Analysis of Molecular Interactions between Yoghurt Bacteria by an Integrated Genomics Approach

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Analysis of Molecular Interactions between Yoghurt Bacteria by an Integrated Genomics Approach

Sander Sieuwerts

Thesis

submitted in partial fulfillment of the requirements for the degree of doctor at Wageningen University by the authority of the Rector Magnificus Prof. dr. M. J. Kropff, in the presence of the Thesis Committee appointed by the Doctorate Board to be defended in public on Tuesday 27 October 2009 at 1:30 PM in the Aula.

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Abstract

The lactic acid bacteria (LAB) are a group of Gram-positive bacteria that ferment sugars such as lactose to produce mainly lactic acid. LAB are a group of industrially important microorganisms that are applied for the production of many fermented foods. These include foods produced with substrates from plant origin (e.g. sauerkraut and wine) and animal origin (e.g. fermented meats and dairy products such as yoghurt). The current market trends regarding sustainability and health-promoting foods demand more efficient and a more diverse range of fermentations. Most fermentations are carried out by multiple strains of different species. The interactions between consortium members are at the base of the performances of the individual microorganisms within a microbial ecosystem and therewith of the whole fermentation. These microbial interactions are often poorly understood. Streptococcus thermophilus and Lactobacillus delbrueckii subsp. bulgaricus are two LAB species that upon fermentation convert (bovine) milk into yoghurt. These two bacteria stimulate each other in growth and acid production. They produce exopolysaccharides (EPS), important for the texture of yoghurt, and characteristic flavor compounds such as acetaldehyde and diacetyl. However, the molecular basis of the mutualistic interactions between these two bacteria was poorly characterized.

In this thesis research, a combination was used of screening, mixed culture transcription profiling, whole-genome metabolic modeling, experimental evolution and next-generation sequencing. This was done to unravel the molecular basis of the interactions between S. thermophilus and L. bulgaricus in milk. The results showed that interactions were primarily based on the exchange of metabolites. Moreover, it was shown which genes or pathways were affected. Evidence was found that S. thermophilus provided L. bulgaricus with formic acid, folic acid (both involved in purine metabolism), long-chain fatty acids (by the action of lipolytic enzymes to break down milk fat) and CO₂. The proteolysis by the exoprotease of L. bulgaricus, in turn, provided both species peptides, which are taken up by the cell and broken down into amino acids (AA) by intracellular peptidases. However, this probably did not yield a sufficient supply of branched-chain and sulfur AA, leading to a higher expression of the genes for biosynthesis of these AA in both species when grown in mixed culture. Moreover, EPS biosynthesis genes were induced in the mixed culture, leading to increased EPS production and a higher viscosity of the yoghurt.

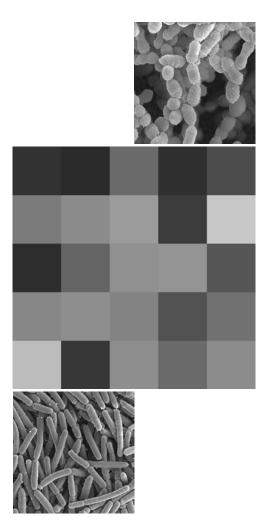
A mixed culture genome-scale metabolic model confirmed that cross-feeding interactions between the yoghurt bacteria were based on purine and AA

metabolism. Moreover, this model was used to show that the interactions provided a significant benefit to both bacteria, i.e. their biomass yield on lactose increased by around 50% in mixed culture.

Experimental evolution revealed that it is possible to co-adapt a novel combination of strains of *S. thermophilus* and *L. bulgaricus*. It was shown that their mutual stimulation increased by optimizing their interactions by fine-tuning expression of pathways involved in the interactions. Furthermore, as little as ~1000 generations of co-culture was sufficient to transform the relatively slow growing mixed culture into one that showed similar performance as commercial starters with respect to key characteristics such as acidification rate and viscosity.

Improved understanding of the described interactions that are at the base of the yoghurt fermentation provides us targets for the rational optimization of existing mixed culture fermentations and the rational development of industrially relevant mixed cultures, such as those containing probiotics. Moreover, the results are in particular interesting for the field of microbial ecology as they show how mutual nutritional dependencies evolve and structure the microbial composition of this ecosystem.

General introduction



Historically, many food products were preserved by fermentation by lactic acid bacteria (LAB). For a large part this can be attributed to the desired functionalities of LAB, such as fast growth and the production of acids, volatile compounds and exopolysaccharides. This makes fermentation by LAB the method of choice for improving the taste and structure of food products. With the industrialization of the fermentation processes during the last century, LAB have even gained importance. For example, the cheese market has a worldwide turnover of more than 75 billion US \$ and the yoghurt market is worth over 35 billion US \$ (59). Most fermentations are carried out by a mixture of species or strains and the last decades it has become clear that the molecular interactions between these different LAB are of key importance for the success of fermentations. In order to control the fermentations and to develop new products, it is important to unravel these interactions. Yoghurt is a relatively well-studied mixed culture fermentation that involves Streptococcus thermophilus and Lactobacillus bulgaricus, but the interactions between the two species are only poorly understood. The low complexity in terms of number of species involved and the high economical value make yoghurt a good model system to study the molecular interactions between the consortium members.

Here, we give an introduction to LAB and their application. In addition, their interactions in industrial fermentations are summarized with an emphasis on the yoghurt consortium. Moreover, new approaches used in modern biotechnology are discussed. Finally, an outline of this thesis is provided.

THE LACTIC ACID BACTERIA

Lactic acid bacteria or *Lactobacillales* are defined as a group of Gram-positive bacteria that ferment sugars such as lactose to produce primarily lactic acid (53). Within the *Lactobacillales* group, three main phylogenetic groups can be identified based on genomic similarity and GC content: *Lactobacillaceae, Leuconostocaceae* and *Streptococcaceae* (53). The LAB can be found ubiquitously on plants, in decomposing plant material, in dairy and in animal mucosa. The great variety in niches reflects that the LAB constitute a group of highly versatile organisms that are able to ferment many different substrates, ranging from simple disaccharides to complex carbohydrates like starch. Because the environments in which LAB occur are often relatively rich in carbon sources, amino acids or peptides and other nutrients, evolution of these organisms is mainly characterized by loss of gene function (see Figure 1) (53, 54), but also by horizontal gene transfer (HGT)

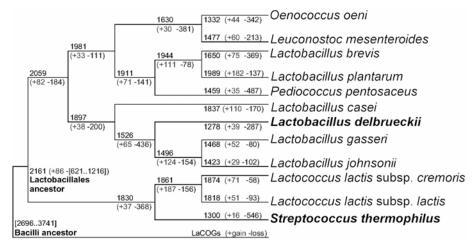


Figure 1. Reconstruction of gene content evolution in *Lactobacillales*. The tree is rooted by using *Bacillus subtilis* as the outgroup. For each species and each internal node of the tree, the inferred number of LaCOGs (*Lactobacillales*-specific clusters of orthologous genes – genes in two species that have a common ancestor gene) present, and the numbers of LaCOGs gained (+) and lost (-) along the branch leading to the given node (species) are indicated. Especially note the low amounts of LaCOGs in *Lactobacillus delbrueckii* (1278) and *Streptococcus thermophilus* (1300) that are caused by reductive evolution in these species (indicated in bold). Figure adapted from Makarova *et al.* (53).

between different LAB species. It was suggested that the last common ancestor of Lactobacillales (estimated genome size 2100 to 2200 genes) has lost 600 to 1200 genes (25 to 30%) and gained less than 100 genes after diverging from the Bacilli ancestor (genome size 2700 to 3700 genes), an event that has taken place billions rather than millions of years ago (54). Only since the rise of mammalian life, i.e. the only natural source of lactose. LAB have become the specialized lactose-utilizing bacteria (19). The adaptation to the relatively nutrient-rich and constant dairy environment was the cause of the reductive evolution (70). An illustrative example of reductive evolution is the case of Lactococcus lactis. This species includes strains that are found on plants while other strains are specifically adapted to the dairy environment and are used for the industrial production of cheese. Genomic and physiological studies have shown that the dairy Lc. lactis strains have lost the ability to ferment many carbohydrates while retaining the capacity to utilize efficiently the milk sugar lactose; conversely, the plant-derived Lc. lactis strains are not capable of fast growth on lactose but have a large capacity to degrade a variety of sugars (58, 81). Similarly, adaptation to milk was shown to often lead to auxotrophy for histidine and branched chain amino acids (BCAA) as a result of the accumulation of mutations mainly in the promoter regions of his genes (21), and nonsense mutations and small deletions in the *ile* and *val* genes (34).

Expression of genes has both costs and benefits, and therefore optimizing the gene repertoire and its expression for a given niche will determine the evolutionary success of a strain (3, 20). In nutritionally-rich environments, it may be advantageous to harvest compounds required for biosynthesis from the medium rather than expressing biochemical pathways needed for *de novo* biosynthesis. As a result these pathways are often not functional in many LAB and one can observe genome decay through the accumulation of mutations that result in loss of function, usually by introducing stop codons by frame shifts. These non-functional genes are annotated as pseudogenes. In addition, gene loss may occur, a process in which genes or major parts of these are completely deleted. Moreover, microorganisms that have a long history of growing together may have optimized their genetic repertoire to support associated growth and develop nutritional interactions. This also occurs frequently among LAB, leading to complex cross-feeding relationships and cooperative behavior as for instance in different types of cheese (73), plantbased food products (29, 82) and beverages (55, 77). Similarly, the close proximities in space and time of different species have facilitated horizontal gene transfer (HGT) leading to genomes containing regions with a deviating GC content originating from other species in the same habitat (4, 5, 53).

LAB ferment sugars in a homofermentative (leading to lactic acid) or heterofermentative (leading to a mixture of lactic acid, carbon dioxide, acetic acid and ethanol) way (40). Most *Lactobacillales* are microaerophilic, meaning that they are oxygen tolerant, but do not perform well in an oxygen-rich (i.e. atmospheric) environment. Recently, it was found that several LAB may respire when cultured in the presence of specific cofactors or their precursors (9, 30). Respiration yields additional ATP per mol of substrate but LAB do not respire in a energy-rich environment such as milk as they have lost the ability to synthesize heme (9, 63). This indicates that the evolutionary strategy followed by most LAB is to optimize their growth and acid production rate rather than their yield (79). The resulting high acidification rate combined with the high acid tolerance makes LAB successful for the preservation of food products by fermentation (12).

INDUSTRIAL FERMENTATIONS WITH LACTIC ACID BACTERIA

LAB have a history of being safely applied in the preservation of food for thousands of years (56). Many LAB species are considered safe for application in fermented food and have acquired the "qualified presumption of safety" (QPS) status in the European Union and the "generally regarded as safe" (GRAS) status in the United states of America dependent on the food they are applied in (43). Since the start of human civilization fermentation has been applied to preserve milk, meat and vegetables and to improve the organoleptic characteristics of foods (12, 28). Initially, these fermentations occurred naturally, but later were started by inoculating the substrate with a small sample of the fermented product. The knowledge on the appropriate techniques was transferred from generation to generation. Only since the rapid scientific progress in the field of microbiology in the 19th century the processes executed by microorganisms that occur during fermentation are being understood (12). It was found that many fermentations relied on the action of mixed cultures of yeasts, filamentous fungi and different species of LAB. The industrialization in the late 19th century together with the isolation and identification of these species in the mid 20th century paved the way for large-scale food production by fermentation to support the increasing growth of the human population (see Table 1). This process continued in the 2nd half of the 20th century with the use of starter cultures to achieve a constant and reproducible quality of the fermented products. These starter cultures, for instance those used for the production of cheese and other fermented dairy products, consisted of either a single strain, multiple strains of one species, or multiple strains of multiple species. The fact that interactions between consortium members play a key role in the performance of a fermentation has only been recognized in the last decades. This notion implies that in the design of starter cultures for mixed fermentations not only single strain traits have to be addressed, but also the interaction potential needs to be included. Mixed strain fermentations have received additional attention with the emergence and rapid growth of the consumer interest in fermented foods containing LAB marketed as probiotics. These probiotics are defined as live microorganisms which, when administered in adequate amounts, confer a health benefit on the host (27). Although some novel probiotic products contain only one – the probiotic - strain, there is much interest in novel strain combinations that typically consist of a traditional starter in combination with one or more probiotic strains. In addition, the probiotic activity may be modulated by the strain's ability to grow in the desired substrate and its interactions with the starter culture. Similar interactions are expected in the multiple strain probiotics that are currently marketed.

Table 1. Examples of fermented foods that are produced at industrial scale with lactic acid bacteria. Adapted from Caplice and Fitzgerald (12). *A., Aspergillus; C., Candida; L., Lactobacillus; Lc., Lactococcus; Ln., Leuconostoc; S., Streptococcus; Sc., Saccharomyces; St., Staphylococcus; LAB, lactic acid bacteria.*

Product	Microorganism(s)	Substrate	Country
Bread	Sc. cerevisiae, other yeasts, LAB	Wheat, rye, other grains	International
Gari	Corynebacterium manihot, other yeasts, LAB (<i>L. plantarum</i> , <i>Streptococcus</i> spp.)	Cassava root	West Africa
Idli	LAB (Ln. mesenteroides, Enterococcus faecalis), Torulopsis, Candida, Trichosporon pullulans	Rice and black gram, dhal	India
Kimchi	LAB	Cabbage, vegetables, occasionally seafood, nuts	Korea
Mahewu	LAB	Maize	South Africa
Ogi	LAB, Cephalosporium, Fusarium, Aspergillus, Penicillium spp., Sc. cerevisiae, and C. mycoderma, C. valida or C. vini	Maize	Nigeria, West Africa
Soy sauce	A. oryzae or A. soyae, Lactobacillus spp, Zygosaccharomyces rouxii	Soybeans and wheat	Japan, China, Filippines
Nan	S. cerevisiae, LAB	White wheat flour	India
Cheese	LAB, (<i>Lc. lactis</i> , <i>S. thermophilus</i> , <i>L. shermanii</i> , <i>L. bulgaricus</i> , <i>Propionibacterium shermanii</i> , <i>Leuconostoc</i> spp), occasionally moulds (<i>Penicillium</i> spp.)	Milk	International
Yoghurt	S. thermophilus, L. bulgaricus	Milk, milk solids	International
Fermented sausages	LAB (lactobacilli, pediococci), catalase positive cocci (<i>St. carnosus, St.</i> <i>xylosus, Micrococcus varians</i>), occasionally yeasts and/or moulds	Mammalian meat, generally pork and / or beef, less often poultry	Southern and central Europe, U.S.A
Sauerkraut	LAB (Ln. mesenteroides, L. brevis, L. plantarum, L. curvatus, L. sake)	Cabbage	International
Pickles	Pediococcus cerevisiae, L. plantarum	Cucumber	International
Olives	Ln. mesenteroides, L. plantarum	Green olives	Mediterranian

INTERACTIONS BETWEEN MICROORGANISMS IN INDUSTRIAL FERMENTATIONS

Because of their ecological importance, there has been considerable interest in defining the nature of the interactions between microbes (25, 33). A total of six classes of interactions have been defined, which are distinguished based on differences in mutual effects on fitness that can occur between microorganisms: neutralism, competition, amensalism, commensalism, parasitism and mutualism (38, 72). Neutralism is the absence of interactions. Therefore, neutralism is not truly considered a class of interaction. In reality, this will not occur often in industrial fermentations because any action of a microorganism (e.g. the consumption of substrate or the production of metabolites) will inevitably have an effect on its neighboring microorganisms. Competition is perhaps the most obvious mode of interaction. Two microorganisms competing for a substrate will negatively affect each other in case the substrate becomes growth limiting. Amensalism is the type of interaction in which one organism adversely affects the other organism without being affected itself. This occurs frequently in mixed culture fermentations (49). Examples include the production of carboxylic acids such as lactic or acetic acid, alcohols (12, 49) and bacteriocins (1, 51). In contrast, when one species benefits from the other, while the second is not affected, it is called commensalism. Examples are fermentations where one microorganism consumes a product that is produced by another (14, 57). Such a trophic interaction can be very valuable in an applied context when a stable combination needs to be obtained or in the cases where a fermentation end metabolite needs to be removed because it is detrimental to the product characteristics. In surface-ripened cheeses, lactic acid is consumed by yeasts. This leads to de-acidification of the cheese surface enabling the outgrowth of aerobic bacteria necessary for the cheese its characteristic flavor (57). In parasitism, one species benefits at the expense of another. Perhaps the most frequently occurring examples are the bacteriophages. Phage attacks have been a longstanding problem. Still today, in an era of increased awareness of the importance of hygiene, it leads to major losses in the food industry. This resulted in the emergence of a complete field of research in mastering phages (76). Finally, mutualistic interactions are positive for both microorganism involved. Many industrial fermentations rely on the mutualistic interactions among LAB species or between LAB, other bacteria and eukaryotes (i.e. yeasts and filamentous fungi). One of the best known mutualistic interactions is that between Streptococcus thermophilus and Lactobacillus bulgaricus, which was reclassified two decades ago into L. delbrueckiii subsp. bulgaricus (31, 83). Amensalism, commensalism, parasitism and mutualism typically result from co-evolution as is exemplified by the co-evolution of *S. thermophilus* and bacteriophages (11). A more extensive overview of these interactions is presented in Chapter 2.

YOGHURT, A MILK PRODUCT FERMENTED BY TWO STRAINS

Yoghurt is a dairy product mostly made from bovine milk that is fermented by the lactic acid bacteria *S. thermophilus* and *L. bulgaricus*. Records of the application of yoghurt as a food product date back to as much as 8000 years ago (28, 77). Only during the last century the two species responsible for this fermentation were identified. In recent years, the genomes of several yoghurt strains have been characterized as is discussed below.

Streptococcus thermophilus

To date, there are three complete genome sequences available of *S. thermophilus*, namely strains CNRZ1066, LMG18311 (4) and LMD-9 (53). The *S. thermophilus* genome is approximately 1.8 Mb large and is predicted to contain 1915 protein-coding genes in strain CNRZ1066, the first strain to be characterized at the genome level (see Table 2 and Figure 2a).

The portion of pseudogenes in *S. thermophilus* CNRZ1066 (10%, see Table 2) is among the highest of all sequenced streptococcal genomes (4). The observation that many genes, mainly involved in transport and the carbohydrate metabolism (both ~30% of all sequences within the category, see Table 3), are nonfunctional (4), indicates that *S. thermophilus* has undergone a process of loss-of-function events. This is probably due to the presence of a single carbon source, lactose, in the dairy environment as was discussed for *Lc. lactis* above (4).

	S. thermophilus	L. bulgaricus
	CNRZ1066	ATCC BAA-365
Genome length (bp)	1796226	1856951
GC content %	39	49
Coding %	83	77
Genes	2000	2040
Protein coding	1915	1721
Pseudogenes	182	192

 Table 2. Comparison of the genomes of Streptococcus thermophilus CNRZ1066 and Lactobacillus bulgaricus ATCC BAA-365.

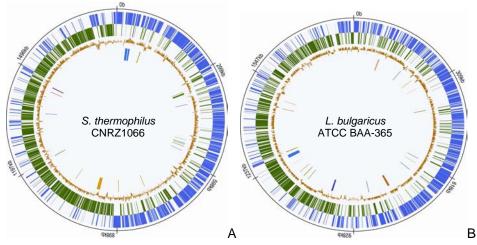


Figure 2. Genome-atlas view of the *S. thermophilus* CNRZ1066 chromosome (left) and the *L. bulgaricus* ATCC BAA-365 chromosome (right), with the predicted origin of replication at the top. In the left panel, the outer to inner circles show (i) positive strand ORFs, (ii) negative strand ORFs, (iii) GC-content and (iv) genes involved in purine biosynthesis and folate cycling (blue), sulfur AA biosynthesis (light green), BCAA biosynthesis and transport (dark green), EPS production (yellow) and the genes *pfl* and *pflA* (red). In the right panel, the outer to inner circles show (i) positive strand ORFs, (ii) negative strand ORFs, (iii) GC-content and (iv) genes involved in purine biosynthesis and folate cycling (blue), sulfur AA biosynthesis (light green), BCAA biosynthesis involved in purine biosynthesis and folate cycling (blue), sulfur AA biosynthesis (light green), BCAA biosynthesis and transport (dark green), long-chain fatty acid biosynthesis (orange) and the gene *prtB* (purple). Figures were made with Microbial Genome Viewer (41) using the ORFs available at NCBI (accession no. NC_006449 for *S. thermophilus* and NC_008529 for *L. bulgaricus*).

Compared to *Lc. lactis* SK11, which has a genome of 2.4 Mb and contains only 6% of pseudogenes (53), the genome of *S. thermophilus* has undergone relatively much decay. Although milk is a protein-rich substrate, the *S. thermophilus* genome contains genes for functional biosynthetic pathways for most amino acids (AA) and this is confirmed by phenotypic analysis. Most *S. thermophilus* strains are auxotroph only for histidine and one of the sulfur AA (62). However, growth may be enhanced when methionine, proline, glutamic acid and valine are added to the growth medium (37, 46). Moreover, as most strains are only weakly proteolytic, *S. thermophilus* generally grows in milk in association with other protease-producing microorganisms and in particular with the PrtB-producing *L. bulgaricus*. It was shown that the exoprotease PrtS, which is present in a minority of *S. thermophilus* strains, does not have any effect on growth when a PrtB-producing *L. bulgaricus* is present (15). The presence of an extensive AA biosynthesis system and the fact that PrtS is not required in mixed cultures with proteolytic *L. bulgaricus* may also explain the absence of a functional exoprotease in most strains (15, 47).

Strikingly, in the S. thermophilus genome there are over 50 insertion sequences of which some display a GC content deviating from the rest of the genome, indicating that they were acquired by HGT. One fragment in the S. thermophilus genome likely originated form L. bulgaricus and contains a metC gene (95% identity to metC in L. bulgaricus) (4). This gene is involved in the biosynthesis of methionine, an amino acid that is present in low concentration in milk and casein. This indicates that the close proximities of S. thermophilus and L. bulgaricus in yoghurt may have led to HGT events (6, 50). Interestingly, a recent in silico study reported that the gene cluster cbs-cblB/cglB-cysE, involved in sulfur AA metabolism, is putatively transferred from L. bulgaricus to S. thermophilus (50). In addition, there are two clusters of genes involved in polysaccharide production in S. thermophilus: the exopolysaccharide (EPS) cluster and the rhamnose polysaccharide cluster. The first may have been acquired from L. bulgaricus (50). The EPS gene cluster codes for the complete pathway for EPS synthesis and secretion and this EPS imparts the viscous texture of yoghurt, one of the key desired properties (8). Although thus far a clear advantage of EPS production in terms of increasing fitness of S. thermophilus has not been identified, obviously, EPS production should confer a benefit that is stronger than the growth burden caused by expressing the genes and producing the EPS.

Lactobacillus bulgaricus

Two fully sequenced genomes of L. bulgaricus strains are publicly available, namely the strains LMG11842 (80) and ATCC BAA-365 (53). The genome of strain ATCC BAA-365 is approximately 1.9 Mb in size and contains 1721 protein coding sequences (see Table 2). Figure 2b gives a representation of the genome of this strain. In L. bulgaricus ATCC BAA-365, about 11% of all genes are pseudogenes and only 77% of the genome consists of (putative) coding sequences. Moreover, the number of rRNA and tRNA genes in L. bulgaricus is 50% higher than the average for a genome of its size (70). This means that the rRNA and tRNA content correspond to a genome of 3-4 Mb instead of its actual size of 1.9 Mb. These three observations indicate that L. bulgaricus is in a process of thorough genome reduction, which can be considered a result of a still ongoing extensive adaptation to the dairy environment (80). This is noteworthy as L. bulgaricus is considered to be a dairy species for already 5000 to 10000 years (31, 45). A relatively high number of transposases and insertion sequence elements (67, 68) may facilitate this process of reductive evolution (32). This reductive evolution likely caused that L. bulgaricus has lost most of its capacity to transport and metabolize sugars other than lactose or glucose. Similarly, the loss of function or even complete absence of pathways involved in AA biosynthesis reflects the steady protein-rich environment *L. bulgaricus* resides in. The availability of the PrtB exoprotease in a protein-rich milk environment can provide a sufficient supply of most AA.

The *L. bulgaricus* genome encodes a complete pathway for the production of EPS and this is the cause of the slimy texture of yoghurt.

Table 3. Comparison of gene content involved in carbohydrate uptake among streptococcal genomes. ^a, TC classification as described at http://tcdb.ucsd.edu/tcdb/background.php; ^b, Genes which are either 3'-truncated, contain one or more frame shift(s), or a point mutation resulting in a stop codon. Adapted from Bolotin *et al.* (4).

Species/strain	Porters ^a	ABC	PTS	Accessory	Total
		transporters	translocators	factors	
S. thermophilus					
CNRZ1066/LMG18311					
Complete genes	1	4	5	3	13
Pseudogenes ^b	0	2	4	0	6
S. pneumoniae TIGR4	0	15	50	3	68
S. pyogenes SF370 (M1)	0	15	28	3	46
S. agalactiae 2603 V/R	0	15	29	3	47
S. mutans UA159	0	13	20	3	36

Protocooperation between the yoghurt bacteria

S. thermophilus and L. bulgaricus were shown to stimulate each others' growth in a mixed culture in milk (64). This was expected to be a result of cross-feeding interactions, involving the exchange of nutrients and growth factors, a process referred to as protocooperation. Indeed, already in mid 20th century some compounds were shown to be produced by one species and to stimulate the other species. These include carbon dioxide (24), formic acid (16, 22) and folic acid (17) provided by S. thermophilus and peptides and amino acids released by the proteolytic action of the PrtB protease of L. bulgaricus (15, 69). The free AA content of milk is very low but the casein content is quite high (~2.5 %). As mentioned, S. thermophilus benefits from the proteolytic activity of L. bulgaricus. In turn, L. bulgaricus grows best in an anaerobic environment and thus the consumption of oxygen and concomitant production of carbon dioxide by the more oxygen tolerant S. thermophilus promotes L. bulgaricus growth. L. bulgaricus lacks pyruvate-formate lyase, which makes it dependent on an exogenous source of formic acid for an optimal purine synthesis. Similarly, a gene involved in the production of para-aminobenzoic acid, a precursor of folic acid, is missing which impedes purine metabolism for an optimal growth in milk (80). This is most likely the result of the long history of co-culture with S. thermophilus. It was shown that folate is secreted by most *S. thermophilus* strains and consumed by *L. bulgaricus* (17). Therefore, exchange of folate is hypothesized as another mode of interaction. In addition, the production of EPS could confer advantages by facilitating exchange of these components by strained close proximities (13). A more detailed overview of the interactions between the yoghurt consortium members can be found in Chapter 2. Yet other modes of interaction exist and these are not all discovered or fully understood. With the classical microbiological methods that were available until the eighties of last century, it was quite difficult to deepen our understanding of interactions in the yoghurt consortium to the molecular level. This has changed with the emergence of genomics technologies that enable more holistic approaches to this well-defined ecosystem.

TRENDS IN MODERN BIOTECHNOLOGY: SCREENING, ~OMICS, MODELING AND EVOLUTION

The last decade the face of biotechnology changed rapidly due to developments that opened new avenues to so far unexplored research lines. One of the most powerful changes is the emergence of whole-genome sequencing and the ~omics technologies, i.e. transcriptomics, proteomics and metabolomics and more recently interactomics (84). The sequencing and annotation of complete genomes have provided insights in cellular regulation, the phylogeny of organisms and the molecular processes that lead to the evolution of species and strain diversity. The field of metagenomics studies the collective genomes of microbial communities, which sheds light on the molecular mechanisms responsible for structuring these communities (66, 84). In that sense, studying the regulation of genes specific for co-culture is essential. Transcription profiling with DNA microarrays is a powerful way of studying genome-wide responses (36). However, the application of microarrays has two major drawbacks in multi-species microbial communities: (i) it is limited to communities of which the genomes of their members is already known and (ii) the lack of variation between genes impedes proper profiling of the expression in closely related species or strains (7). Here, transcriptome profiling using next-generation sequencing (see below) may circumvent these drawbacks (2, 7, 75). Although transcription profiling is very informative for investigating the molecular basis behind responses on changing environmental factors, it does not necessarily reflect the cell's response at protein and metabolite level as these are also dependent on regulation at the posttranslational level, flux kinetics and thermodynamics. The field of proteomics studies the whole protein content of the cell and can be used to determine the differences in protein content upon changing environmental factors and has been applied to *S. thermophilus* for physiological comparison of growth in a complex substrate (milk) with growth in a chemically defined laboratory medium (22). Metabolomics is defined as the study of all metabolites associated with the cell, i.e. substrates, products and intermediates. In order for any ~omics study to make sense, it should be combined with an overview of the reactions occurring in a cell. Taking together the cells' metabolites and protein-coding genes, it is possible to make a genome-scale metabolic model. By integrating ~omics data and, for instance, fermentation data, the link between molecules and physiology is made (10, 48). The field of research performing such analyses, constructing and applying these genome-scale models is systems biology. There are several genome-scale metabolic models available of LAB (60, 61, 78), but never before have these been used to describe co-culture growth or to predict molecular interactions between consortium members.

The sequencing of whole genomes has rapidly increased. With only two fully sequenced genomes in 1995, the amount has risen to an estimated amount of approximately 1500 of completed sequences and approximately 5000 incomplete sequences by the end of 2009 (GOLD database, http://genomesonline.org/). Similarly, the sequencing methods have developed from traditional Sanger sequencing to next-generation technologies such as Roche 454 sequencing and Illumina sequencing (52, 75). The latter is used in this thesis and will be discussed here in more detail (see Figure 3). In short, oligonucleotide adaptors are ligated to fragmented DNA and used for immobilizing the fragments to a substrate by binding. Subsequently, fold-back PCR results in isolated spots of amplified DNA. Fluorescently labeled terminator nucleotides and DNA polymerase are then used to create a complementary-strand DNA leading to fluorescent signals. Images are collected during each cycle. Stacking the images displays the sequence of the fragmented DNA. With Illumina sequencing typically reads of 36 bp are produced, although reads up to 100 bp are possible with optimized procedures (52). Moreover, pair-end sequencing can be applied and offers another option to assemble de novo sequences (44).

Because the method uses an amplification step by PCR, there is a bias in the distribution of sequence reads as amplification is never uniform for all sequences. This results in sequences with high and low coverage (52). Therefore, it is important to acquire a high average coverage, i.e. in the order of 10^2 in order to be able to assemble the short sequences properly. A high coverage (>20) and a high quality score (i.e. a high cut-off for the quality of the reads) are also necessary to reduce read errors (23, 74). Furthermore, the small sequences may prove hard to

assemble if a certain sequence occurs frequently in a genome, e.g. an IS element. However, if a reference genome is already available, the sequences can be aligned with it, facilitating assembly. This makes Illumina sequencing an excellent tool to detect mutations in strains derived from a species for which a genome sequence is available (52, 71).



Figure 3. Schematic representation of the Illumina sequencing procedure. See text for explanation. Figure adapted from MacLean *et al.* (52).

Another field that has undergone major advances the last decade is that of high-throughput screening (HTS). With the availability of new fast screening methods and techniques such as fluorescent activated cell sorting (42), million-well growth chips (39) and rapid head space analysis using CG-MS (61) it becomes possible to screen thousands of strains for a specific trait in a relatively short time.

A field of research that is relatively old is one that deals with adaptation and (experimental) evolution. However, the face of this field changed tremendously the last decade with the application of mentioned ~omics techniques. Evolution studies are often combinations of a theoretical approach and a more experimental approach. The theoretical approach is to identify the underlying mechanisms behind evolution, such as the application of game-theory (65). With the true experimental approach the genetic adaptations in microorganisms in response to certain environmental characteristics are investigated (3, 26). It was shown in *Lc. lactis* that IS elements may cause a higher mutation frequency, especially when the microorganism is stressed (18). This may lead to a faster adaptation to unfavorable conditions. Also the evolution of interspecies interactions in the genomes of the species involved or any transcription profiling studies yet.

In the future, huge advances in mixed culture research can be expected by integrating information derived from HTS, next-generation sequencing, ~omics, modeling and evolution as each method complements what is lacking in the others.

Outline of this thesis

There is a continuous need to develop new fermented food products and to improve the efficiency of existing mixed culture fermentations. Therefore, it is of key importance to understand the microbial interactions that structure a microbial community and that lie at the basis of important product characteristics such as flavor and viscosity. The emergence of new tools and approaches in the genomics era opens up new avenues for research on classic topics in microbiology such as microbial ecology and microbial interactions. The research focus of this thesis is therefore the application of a combined approach of screening, next-generation sequencing, ~omics, modeling and evolution to map and explore the interactions between S. thermophilus and L. bulgaricus. The availability of genome sequences of these two species provided insight in the metabolic potential of these bacteria. Using some of the discussed ~omics technologies we revealed which genes or proteins are affected by co-culture growth. This provided insights in the molecular basis of the mutual stimulation of these two LAB species. Moreover, we applied experimental evolution and whole genome-based metabolic modeling to identify the optimization strategies of the two yoghurt bacteria leading to a mixed culture fermentation that performs better than the sum of the mono-cultures. The used combinations of approaches and technologies (see Figure 4) allow an improved characterization of the yoghurt consortium and the molecular basis behind (industrial) fermentations in general. The new information will facilitate the rational development of new mixed starter cultures or improvement of existing mixed culture fermentations.

Objective				
System description of yoghurt including interactions				
Approaches		Technologies		
A	Biochemical and population profiling of batch fermentations	1	Quantitative extracellular metabolite profiling with HPLC-MS and GC-MS	
		2	Semi-automated CFU enumeration	
в	Interaction analysis: regulatory responses and intervention studies	3	Multi-strain genome scale transcription profiling	
с	Experimental evolution		Technologies 1-3	
		4	Illumina resequencing	
D	System modeling	5	Multi-strain genome scale modeling	

Figure 4. Schematic representation of the approaches and technologies used in this thesis research.

An overview of the current knowledge on microbial interactions in food fermentations is given in **Chapter 2**. Here, in more detail, is described what is the relevance of mixed cultures in industry and which considerations regarding the ecology should be made when designing or applying mixed cultures in food fermentations. Clearly, interactions between the consortium members are of key importance for the performance of the fermentation. Different types of interactions and their effects on mixed cultures are listed as well as what is known about the interactions affecting the yoghurt consortium. Finally the new developments in ~omics and genome-scale metabolic modeling and their possible uses in mixed culture research are further elaborated.

Although ~omics tools and genome scale metabolic modeling have become important and common tools the last decade, classical microbiology remains important and high-throughput screening has also undergone great developments in the past years. One of the methods that determine the amount of screening work that can be done in a fixed amount of time is determining viable counts by plating dilutions of cultures. Therefore, a relatively simple faster method for plating and plate counting was developed that can be incorporated in most laboratories without the need for special equipment. This method is described in **Chapter 3**.

Chapter 4 focuses on the interactions in the yoghurt consortium. Here, transcription profiles of mono and mixed cultures of *S. thermophilus* and *L. bulgaricus* in four different growth phases are compared to each other. These data are underpinned by transcription studies of cultures with additional formic acid and of yoghurt biofilms, and by studies of the effects of components suggested or proven to be involved in or influence the protocooperation.

A new topic in mixed culture research is the application of experimental evolution to unravel interactions between consortium members. **Chapter 5** explains the adaptation of two unfamiliar strains of *S. thermophilus* and *L. bulgaricus* to each other in the course of ~1000 generations under a very strict growth regime. A combination of phenotyping, *in silico* mutation analysis using Illumina sequencing and mixed culture transcription analysis sheds light on the optimization of interactions and shows that as little as 1000 generations can change a relatively inferior mixed culture (i.e. one with a low acidification rate and a low EPS production) into one that is comparable to a commercial starter.

Genome-scale metabolic models of *S. thermophilus* and *L. bulgaricus* are described in **Chapter 6**. Moreover, predictions in terms of growth and metabolite consumption/production (i.e. the carbon and nitrogen fluxes) from these models are compared to fermentation data. Notably the possibility is addressed to combine the

models of both bacteria in order to acquire a mixed culture "system" model that can be used for the prediction of molecular interactions.

Finally, in **Chapter 7** all the information on the interactions from chapters 2 to 6 is gathered and this (i) gives an improved understanding of known interactions between the yoghurt consortium members, (ii) sheds light on the nature of thus far unknown or only expected modes of interaction in this consortium and (iii) provides general concepts for the events that occur in mixed ecosystems, facilitating the rational improvement of existing or design of new industrial fermentations.

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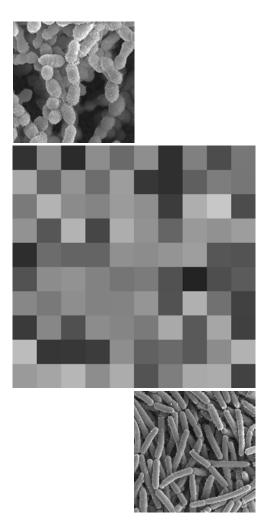
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Unraveling microbial interactions in food fermentations; from classical to genomics approaches



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Fermentation, the microbial degradation of organic compounds without net oxidation, is an important process in the global carbon cycle and is also exploited worldwide for the production and preservation of food. It is one of the oldest food processing technologies known with some records dating back to 6000 BC (50). The link between food and microbiology was laid by Pasteur who found that yeasts were responsible for alcoholic fermentation (106). Since that discovery the scientific and industrial interest in food microbiology started to grow and continues to increase until today. The number of food products that rely on fermentation in one or more steps of their production is tremendous. They form an important constituent of the daily diet and rank among the most innovative product categories in the food industry.

Most of the important microorganisms applied in the production of fermented foods have been studied for decades yielding a wealth of information on their physiology and genetics in relation to product functionalities such as the development of flavor, taste and texture. The recent emergence of genomics has opened new avenues for the systematic analysis of microbial metabolism and the responses of microorganisms to their environment. Additionally, genomics has boosted research on important food microbes (22, 90, 93). Much of this research focuses on the performance of a single strain including its interactions with the food matrix. However, food fermentations are typically carried out by mixed cultures consisting of multiple strains or species. Population dynamics plays a crucial role in the performance of mixed culture fermentations. For many years studies on mixed culture food fermentations have focused on analyzing population dynamics using classical and molecular methods. Many of these studies are mainly descriptive and relatively little is known about the mechanisms governing population dynamics in general and the molecular interactions that occur between the consortium members in particular. The availability of genome sequences for several species that are of industrial importance as well as technological advances in functional genomics enable new approaches to study food microbiology beyond the single species level and allow an integral analysis of interactions and metabolic activity in mixed cultures.

Here we review the current knowledge of important food fermentation processes focusing on the bacterial interactions. In addition, we illustrate how genomics approaches may contribute to the elucidation of the interaction networks between microbes including interactions with the food environment. This information may find application in industry through rational optimization and increased control over mixed culture fermentations.

MIXED CULTURE FOOD FERMENTATIONS – INDUSTRIAL PRACTICE AND CHALLENGES

Traditional fermentation processes relied on transfer of knowledge and methodologies associated with manufacturing from generation to generation. The industrialization of food production together with the blossoming of microbiology in the middle of the 19th century led to optimization and upscaling of many fermentation processes. Similarly, industrially produced starter cultures have emerged, leading to improved and reproducible product quality. Nowadays, the total economic value of fermented food products is huge and the worldwide turnover of fermented fresh products in the dairy segment alone represents a total economic value of 54.2 billion US \$ annually whereas the cheese market is even larger (see Table 1) (111). In recent years there has been massive product diversification and many prebiotic and probiotic products with a high added-value emerged. Simultaneously, artisanal products have gained popularity due to their particular flavor and aroma characteristics (23).

Table 1. Overview of the total turnover in billion US \$ worldwide in 2007 of three categories fermented fresh dairy products and cheese as estimated by Euromonitor International (111).

Category	Turnover (bln US \$)
Yoghurt	34
Fermented dairy drinks	4.3
Fromage frais and quark	7.4
Cheese	74.4

At least two distinct product categories can be distinguished where control of mixed culture performance directly relates to key challenges of innovators in the food industry. The first relates to the dairy market, which includes important products such as cheese and fermented milks. This market is characterized by rapid growth of product varieties with distinct organoleptic properties. Examples include numerous applications in semihard cheeses where adjunct cultures are added to introduce additional flavor notes (49, 114). Additionally, there is an increasing number of product varieties (46). Here, it is important to develop such products while maintaining good organoleptic properties. In low-fat cheese texture may be improved by the application of EPS-producing starter cultures (34). In fermented milks and yoghurts containing probiotic microbes off-flavor problems

may appear due to undesired metabolic activities (99, 152). Furthermore, the success of replacement or addition of the desired probiotic strain in mixed culture fermentation may largely depend on the interaction of this strain with the other strains in the starter culture (64). In general high numbers of viable probiotic bacteria are desired in these products at the moment of consumption. Typically between 5 and 8 logs CFU (Colony Forming Units) per gram of product is considered acceptable (99). Therefore, the growth, survival and activity of the probiotic strain in the product environment is of key importance and these traits are influenced both by specific environmental conditions (35, 152) and by interactions with the starter organisms (72, 99).

A second important product category is formed by food ingredients. Fermentation is widely applied to produce a broad range of ingredients such as amino acids and organic acids. Some of these fermentations are carried out with mixed cultures (54, 155). Challenges in this area include improvement of productivity and stability, and the elimination of unwanted by-products that interfere with down-stream processing. Moreover, such processes may become economically more attractive if cheaper raw substrates can be used with new (combinations of) strains. An example here is improved production of lactic acid from glucose by a mixed culture of *Lactobacillus delbrueckii* NRRL-B445 and *Lactobacillus helveticus* NRRL-B1937, of which the first is a good lactate producer and stimulated by the latter (86). Another example deals with a *S. cerevisiae* strain that was engineered with *L*-arabinose utilization genes from *Lactobacillus plantarum*, allowing it to utilize the *L*-arabinose moiety of lignocellulosic fractions of plant derived biomass (174).

Finally, we are seeing a rapid increase of industrialization of non-western fermented food products in Asia, Latin America and Africa (2, 144). As a result of demographic changes in Europe such products are also of increasing importance in the western market, especially since some are believed to bring specific health benefits (48, 113). Examples include fermented products produced from dairy, cassava, cereals, beans, meat, and fish (7, 167). Challenges here relate to the stability, reproducibility and productivity of fermentations.

MIXED CULTURES VERSUS PURE CULTURES - ECOLOGICAL CONSIDERATIONS

With few exceptions food fermentations rely on mixed cultures of microorganisms. There is a number of important considerations that are at the basis of the ecological success of mixed cultures and these will be discussed in this section. Microorganisms evolve to optimize their fitness and this is often achieved by specialization, e.g. optimization of their metabolism. This is exemplified in a number of elegant experimental evolution studies with *Escherichia coli* in well-defined and homogeneous laboratory systems. In one study in a continuous culture sequentially fed with glucose and acetate this organism differentiated into two ecotypes that displayed a large difference in lag phase when switching to growth on acetate after depletion of glucose (142). Another example with *E. coli* is that a single strain cultured for a prolonged period at glucose limitation diverged into two or three clonal variants in which one variant ferments the glucose and the fermentation products acetate and glycerol serve as growth substrates for the other strains (65, 132).

Most substrates for food fermentations have a highly heterogeneous physicochemical composition which offers the possibility for simultaneous occupation of multiple niches by "specialized" strains, for instance through the utilization of different carbon sources. In these substrates coexisting strains often interact through trophic or nutritional relations via multiple mechanisms as will be discussed below.

Many food fermentations rely on spontaneous fermentation by the indigenous microbiota present in the food substrate. This implies that variations in the indigenous biota may affect the composition and activity of the fermenting community. This has a direct effect on product quality and the reproducibility of fermentations. A recent study showed large variations in the flavor and texture profiles of cheddar blocks produced at different factories (24). This is at least partially due to variations in proteolysis in the cheddar blocks. The application of starter cultures reduces the chance of unexpected population shifts and thereby ensures constant product characteristics and quality. Moreover, in combination with sterilization or pasteurization it allows the food to be fermented by species or strains that would be out competed otherwise.

CLASSIFYING INTERACTIONS ON THE BASIS OF MUTUALLY BENEFICIAL AND DETRIMENTAL EFFECTS ON FITNESS

Microbial interactions in mixed cultures occur via multiple mechanisms. Such interactions may be direct, as for instance through physical contact or via signaling molecules. Alternatively, indirect interactions may occur where changes in the physico-chemical properties of the environment induced by one strain trigger a response in another strain (21, 51). The effects of such interactions on the fitness of the strains involved may either be positive, neutral or negative. Mutual effects on fitness between interacting strains are an effective means of classifying interactions (68). These can be divided into five main classes – amensalism, competition, commensalism, parasitism and mutualism – all of which will be discussed below and illustrated with relevant examples from food fermentations (see Table 2).

Amensalism is an interspecies interaction in which one organism adversely affects the other organism without being affected itself. It frequently occurs in food fermentations since major end products of primary metabolism such as carboxylic acids and alcohols are effective growth inhibitors of the indigenous microbiota and spoilage organisms (23, 89). In fact, the lactic acid bacterial (LAB) metabolism is optimized for fast acid production rather than efficient growth (158). Another example is the production of antimicrobial compounds, such as bacteriocins, that are produced by many food-fermenting LAB and that play an important role in mixed culture population dynamics. Typically, bacteriocin-producing strains produce a dedicated immunity system that protects the host from detrimental effects. Lantibiotics, a special class of bacteriocins produced by LAB and other Gram-positives, have drawn specific attention. Nisin is a well-known lantibiotic produced by Lactococcus lactis and broadly applied as a food preservative. Its activity is based on the permeabilization of the cytoplasmic membrane leading to its depolarization (47, 70). Other potent bacteriocins include plantaricin and pediocin which are widely distributed among L. plantarum and Pediococci, respectively (41, 172). The broad activity spectrum of bacteriocins has been exploited for the inhibition of outgrowth of spoilage microbes and pathogens (4, 91).

The second class of interactions is competition. Microorganisms compete for energy sources and nutrients during fermentation. Carbon sources are often present in high concentrations in food substrates and competition therefore relates to rapid uptake of nutrients and conversion into biomass. In dairy fermentations, nitrogen is limiting and here organisms initially compete for the free amino acids and small peptides available in milk.

Type of interactionProduct(s) or environment(s)Organisms i		Organisms involved	References		
Mutualism	Yoghurt	S. thermophilus L. bulgaricus	(1, 31-33, 43, 53, 66, 119, 140, 151, 154, 163, 179)		
	Dairy	LAB	(108, 153)		
	Cold milk	Lactococcus lactis subsp. cremoris Pseudomonas fuorescens	(80)		
	Dairy, sourdough, laboratory medium	LAB Yeasts Fungi	(26, 108, 137)		
	Milk	LAB Yeasts	(52, 108)		
	Sourdough	Saccharomyces exiguous Candida humilis Lactobacillus sanfranciscensis	(37, 56, 57)		
	Surface-ripened cheese	Different species of moulds, yeasts and bacteria	(30)		
Amensalism	Dairy, vegetable broth	LAB Listeria monocytogenes Pseudomonads Staphylococcus Yersinia Bacillus	(9, 13, 14, 16, 71, 89, 94, 95, 102, 143)		
	Broth culture, laboratory medium, vegetable broth	LAB Escherichia coli Aspergilli Enterobacter Listeria monocytogenes Vibrio Salmonella	(10, 11, 16, 25, 55, 63, 77, 92, 94, 95, 103, 115, 148, 159)		
	Wine	Lactobacillus hilgardii Pediococcus pentosaceus	(94, 131)		
	Yoghurt	S. thermophilus L. bulgaricus	(71, 117, 127, 179)		
	Meat	LAB Listeria monocytogenes	(13)		

 Table 2. Microbial (interspecies) interactions observed during food fermentations and in the fermented products.

Type of interaction	Product(s) or environment(s)	Organisms involved	References
	Wine	Malolactic bacteria Yeasts	(3)
	Surface-ripened cheese	Lactobacillus plantarum Listeria monocytogenes	(91)
	Lettuce	LAB Listeria monocytogenes	(4)
Commensalism	Dairy	LAB	(108, 153, 175)
	Yoghurt	S. thermophilus L. bulgaricus Propionibacteria	(175)
	Yoghurt, dairy	LAB Propionibacteria	(28, 175)
	Milk	LAB Yeasts	(52, 108)
	Wine	Malolactic bacteria Yeasts	(3)
	Surface-ripened cheese	LAB Debaryomyces hansenii Geotrichum candidum Arthrobacter sp. Brevibacterium linens Corynebacterium ammoniagenes Staphyolococci	(107)
	Laboratory medium	Yeasts Bacterium linens	(124)
	Fermented milks, yoghurt, cheeses	Yeasts Bacteria	(165)
Competition	Yoghurt	S. thermophilus L. bulgaricus	(105, 179)
	Dairy	LAB Yeasts	(52, 108)
Parasitism	Laboratory medium	Bacterium Phage	(29, 137)
	Milk	Bacterium Phage	(20, 145)
	Aquatic environments	Bacterium Phage	(169, 170)

In the later stages of fermentation they compete for the peptides released by the action of proteolytic enzymes. For this, they produce proteases, transport systems and peptidases. Growth rate and population dynamics in mixed dairy fermentations are largely determined by the ability to utilize amino acids efficiently (73, 75). Micronutrients such as iron have also been reported to be limiting for strains in the biota of smear cheeses. Strains compete for iron pools through the use of specialized molecular systems for harvesting iron including siderophores (109).

Commensalism is the third class of interactions. This is a situation in which one organism benefits from the interaction while the other strain is not affected. This also occurs in many food fermentations, for instance through trophic interactions. In Swiss-type cheeses propionic acid bacteria utilize the lactic acid produced by LAB starter bacteria (28). Similarly, in surface-ripened cheeses lactic acid is consumed by yeasts, in particular Debaryomyces hansenii, and by the filamentous fungus Geotrichum candidum (107). This leads to de-acidification of the cheese surface enabling the outgrowth of aerobic bacteria such as Arthrobacter species, Brevibacterium linens, Corynebacterium ammoniagenes, and staphylococci. One could argue that in this case the aerobic bacteria benefit while D. hansenii and G. candidum are unaffected. However, it may be difficult to prove that there is no effect if it can not be measured in terms of growth or survival. Another possible form of commensalism takes place in starters for Gouda cheese where PrtP- Lc. lactis strains benefit from the peptides that are released from milk protein through the action of extracellular proteases (PrtP) produced by PrtP+ strains (69, 74) whilst the PrtP+ strains do not directly seem affected. In milk, PrtP+ strains produce more biomass than their isogenic PrtP- variants lacking plasmids containing the protease gene, but growth is slower due to the cost of expressing this protease (173). In pure cultures of PrtP+ strains grown in milk, PrtP- variants rapidly occur. The outcome of long-term propagation of PrtP+ and PrtP- strains in a protein-containing medium like milk is that the strain that makes the least use of the resources in the medium, namely the PrtP- strain, will become dominant. In this case the immediate gain for the PrtP- strain is traded for the long-term community benefit. This particular example is also known as the "prisoner's dilemma" in evolutionary game theory (6, 120). The population dynamics of PrtP+ and PrtPisolates is highly dependent on the growth conditions that influence the costs and benefits of the proteolytic phenotype (69).

The fourth class of interactions is known as parasitism. Parasitism is the interaction in which one species benefits at the expense of another. A well-known example of parasitism in the microbial world is represented by bacteriophages. It is

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well established that food fermentations, especially those repeatedly carried out in the same equipment, are highly vulnerable to phages. Phage attack may suddenly inactivate dominant strains in a fermenting culture leading to failure and product losses in industrial fermentations (145). In recent years our understanding of phage biology and the interactions with their hosts has increased significantly. The biology of bacteriophages has been studied extensively for LAB such as Lc. lactis and Streptococcus thermophilus (20, 145). This work has benefited much from genome sequencing efforts as for instance the genomes of at least seven phages specific for S. thermophilus have been sequenced (146). The diversity and fast evolution of phages typically results in the appearance of strains harboring different phage resistance phenotypes (170). Moreover, the recombination machinery of bacteriophages and their ability to transfer DNA from one bacterial cell to another may accelerate evolutionary processes in bacterial communities and contributes to the diversity in mixed culture fermentation processes, especially when back slopping, the sequential transfer of cultures to fresh medium, is applied (169, 170). Recent studies showed a thus far unknown system present in archaea and bacteria, amongst which S. thermophilus, that is involved in phage resistance (12, In this CRISPR system, bacteria acquire resistance to phages by incorporating phage-specific short transcribed nucleotide sequences into regions of clustered regularly interspaced short palindromic repeats. It was shown that these regions evolve very rapidly, probably driven by the rapid evolution of phages (161).

Finally, during mutualism both participating microorganisms derive a benefit from the interaction. Many food fermentations rely on mutualistic interactions. Probably the best example is the yoghurt consortium, consisting of the LAB S. thermophilus and Lactobacillus delbrueckii subsp. bulgaricus, which will be discussed in detail in the next section. The interactions between the yoghurt bacteria are also often referred to as synergism or protocooperation, interactions in which enhanced growth rate is the main mutual benefit. Cultures consisting of yeasts, LAB and filamentous fungi are of key importance in a broad range of fermented foods in which mutualism is an important mode of interaction. For instance in kefir granules S. cerevisiae raises the pH by utilizing the lactic acid produced by Lactobacillus kefiranofaciens as carbon source enabling more growth of L. kefiranofaciens (26). In the sourdough fermentation there is a synergistic interaction between yeasts such as Saccharomyces exiguous or Candida humilis and LAB, especially Lactobacillus sanfranciscensis (56, 57). Yeast amylase releases maltose from starch which is fermented by L. sanfranciscensis. Part of the glucose derived from maltose is excreted by L. sanfranciscensis and is used as a carbon source by maltose-negative yeasts. In return, the yeasts stimulate growth of *L. sanfranciscensis* by increasing the availability of amino acids and peptides, either through proteolysis or as a consequence of accelerated autolysis (37, 56). In wine interactions between yeasts and LAB also play a major role and these have been reviewed recently by Alexandre *et al.* (3)

YOGHURT CULTURES – THE MIXED CULTURE PARADIGM IN FOOD FERMENTATION

Yoghurt is the product of milk fermented by a defined mixed culture of two thermophilic LAB, *Streptococcus thermophilus* (15) and *Lactobacillus delbrueckii* subsp. *bulgaricus* (93, 163). There are also many fermented milk products that contain only one or neither of these strains, but the name yoghurt is in several countries only allowed for those products that are produced with cultures containing both (82, 151, 179). Nowadays many yoghurts and yoghurt-based drinks are produced that contain probiotic strains, but these do not necessarily contribute to the fermentation. This mixed culture fermentation is of huge economic importance (see Table 1). It represents an attractive model system for research on interactions due to its relatively small complexicity. Some aspects of the yoghurt microbiology have already been reviewed elsewhere (23, 62, 151, 179). Here we present an updated review on comparative analysis with other mixed culture food fermentations.

Although *S. thermophilus* and *L. bulgaricus* are also able to ferment the milk individually, both species were found to be stimulated in growth and acid production in mixed cultures compared to single-strain cultures (119). Proteolysis plays an important role in yoghurt as is illustrated by growth of proteolytic *S. thermophilus* strains in milk (88). After inoculation the cells start growing exponentially using the amino acids, dipeptides, tripeptides and oligopeptides that are freely available. Subsequently, amino acids become limiting and the culture enters a non-exponential growth phase in which the synthesis of extracellular protease is initiated. Finally, in a second exponential phase, the proteolytic system is able to supply sufficient peptides for exponential growth but here the growth rate is lower than in the first exponential phase, probably due to a limited capacity of the peptide uptake system (88).

Most commonly, yoghurt cultures consist of proteolytic *L. bulgaricus* and nonproteolytic *S. thermophilus* (32, 119). During the first exponential phase of *S. thermophilus*, almost no growth of *L. bulgaricus* is observed. In the second phase, *S. thermophilus* growth decreases while *L. bulgaricus* starts to grow exponentially and protease expression is initiated. The cell-wall anchored protease PrtB mainly catalyzes the hydrolysis of the hydrophobic caseins into small peptides, which are subsequently taken up using various peptide transport systems (76, 118). In the cytoplasm the peptides are further hydrolyzed into free amino acids by several endopeptidases and aminopeptidases (133, 135). Growth of *L. bulgaricus* continues in the third growth phase. At this stage the peptides released from milk casein also serve as a source of amino acids for *S. thermophilus* supporting a second exponential growth phase (31, 179).

Most *S. thermophilus* strains exhibit few amino acid auxotrophies and the fact that they have fewer nutritional requirements than *L. bulgaricus* may explain their preferential growth in milk. Only histidine is required by most strains and growth may be enhanced when methionine, proline, glutamic acid and valine are added to growth media (67, 87). With few exceptions, *S. thermophilus* strains do not possess extra-cellular proteases (31, 67). As a result growth of most *S. thermophilus* strains, except some highly proteolytic strains, is strongly stimulated in co-cultures with *L. bulgaricus* strains expressing *prtB* (31, 136).

The mutualistic coexistence of S. thermophilus and L. bulgaricus is also based on other interactions such as the exchange of several growth stimulating factors (see Figure 1). S. thermophilus provides L. bulgaricus with formic acid, pyruvic acid, folic acid (33) and carbon dioxide (43). The positive effects of formic acid and folic acid on growth of *L. bulgaricus* are related to the biosynthesis of purines (53). Formic acid is a precursor for purine synthesis and L. bulgaricus lacks a pyruvateformate lyase, which may explain why it relies on other sources for formate (32). Pyruvate-formate lyase is a highly abundant protein in S. thermophilus grown in milk indicating that S. thermophilus may supply L. bulgaricus with formate during co-cultivation (39). Folic acid is involved as a cofactor in purine and amino acid biosynthesis (149, 168) and was shown to be excreted by S. thermophilus and consumed by L. bulgaricus (33). Genome sequence analysis of L. bulgaricus strain ATCC11842 has shown the absence of a biosynthetic pathway for paraaminobenzoic acid and therefore the biosynthetic pathway for folate in this strain is incomplete (163). S. thermophilus is capable of producing both para-aminobenzoic acid and folate and hence L. bulgaricus may benefit from elevated levels of either compound. A recent report on Lc. lactis shows the involvement of folate in the stimulation of a proteinase positive strain by a proteinase negative strain (121). Carbon dioxide is a precursor for the synthesis of aspartate (128, 166), glutamate (100), arginine and nucleotides (17). In heat-treated milk carbon dioxide levels may be too low for L. bulgaricus (43) and therefore it profits from the carbon dioxide released by S. thermophilus from the urea that is present in milk. In addition, the

urea catabolism plays a role in the synthesis of aspartate and glutamine, both essential amino acids (5, 104).

Yet other compounds may contribute to the mutualistic interaction between the yoghurt LAB. For instance, Partanen *et al.* (116) reported that several long chain fatty acids (LCFA) are stimulatory to *L. bulgaricus*. This is probably due to the fact that *L. bulgaricus* lacks part of the biosynthetic machinery required for *de novo* synthesis of long chain unsaturated fatty acids and one may speculate that *S. thermophilus* is also able to supply *L. bulgaricus* with LCFA. In the recent paper describing the genome sequence of *L. bulgaricus* ATCC11842, Van de Guchte *et al.* hypothesized that ornithine and putrescine may be produced by *S. thermophilus* and *L. bulgaricus*, respectively, and that the exchange of these metabolites mutually increases their resistance to oxidative stress (130, 163). Ornithine is involved in the metabolism of urea and putrescine turns *S*-adenosyl methionine into spermine via the intermediate spermidine. Spermine and spermidine are involved in the stabilization of DNA and DNA replication, respectively.

Growth-detrimental interactions have also been reported. Reddy and Shahani (127) reported that some strains of *L. bulgaricus* produce the bacteriocin bulgarican that inhibits growth of *S. thermophilus* (117). Moreover, some *S. thermophilus* strains were reported to produce peptide bacteriocins (71). Of seven strains of *L. bulgaricus* tested, one was inhibited by this peptide.

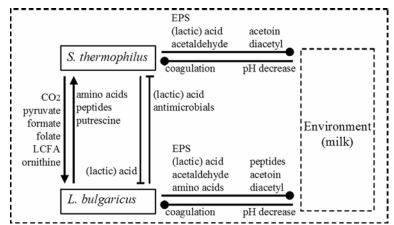


Figure 1. Schematic representation of the validated and hypothesized interactions that occur between *Streptococcus thermophilus*, *Lactobacillus delbrueckii* subsp. *bulgaricus* and their environment, and compounds relevant for yoghurt characteristics. $\mathbf{\nabla}$, positive interactions; \bot , negative interactions; \bullet , interactions that do not specifically promote or decrease growth of the other species. EPS, exopolysaccharides; LCFA, long chain fatty acids. See text for references.

A key sensory attribute that is introduced with fermentation during yoghurt production is its texture. Due to the acidification by the LAB, proteins coagulate and thereby change the viscosity of the milk. Furthermore, the bacteria, and mainly *S. thermophilus*, produce exopolysaccharides (EPS) that form a matrix with the milk proteins resulting in the final yoghurt structure. In kefir, kefiran production by LAB is stimulated by the presence of yeasts induced via direct physical contact (26). Similarly, interactions between yoghurt strains may influence EPS production as for instance by increasing the availability of nitrogen sources or through the interaction with non-EPS-producing *S. thermophilus* strains (38, 177). In general, associations of yeasts and lactic acid bacteria are of key importance for a broad range of fermented foods. However, surprisingly little information is available about molecular interaction mechanisms (165).

QUORUM SENSING AND PHYSICAL INTERACTIONS

Besides the interactions mentioned so far microorganisms may produce diffusible chemicals for the purpose of communication. This includes a process referred to as quorum sensing (QS) that is widely spread among Gram-negatives and Gram-positives and allows regulation at the population level of a wide range of traits, including competence, virulence, and stress responses (58, 78, 150). Two recent reviews link quorum sensing to motility, EPS production, biofilm formation, and toxin production, which are all important phenotypes in food fermentation (44, 59). As described previously, lantibiotics may play an important role in mixed culture population dynamics and their production is often regulated in a density-dependent way via quorum sensing (125, 129). Nisin production in *Lc. lactis* has been studied extensively and it has been shown that it acts as an autoinducer. It regulates its own production at the transcriptional level with the involvement of a two-component regulatory system (for a review see (83)). More recently, the involvement of QS in the regulation in EPS production and monospecies biofilms formation by *L. plantarum* and *Lactobacillus rhamnosus* was reported (85, 147).

Whereas intraspecies communication is quite common, fewer examples exist of interspecies communication and most examples are not related to food microbiology (78). An example of chemical communication has been observed in dental biofilms where *Veillonella atypica* and *Streptococcus gordonii* degrade complex carbohydrates in a way that benefits both species. *V. atypica* produces a yet to be identified signal molecule that induces amylase production in *S. gordonii* and thereby increases the degradation rate (45). A QS system that is present in a major fraction of the bacterial population and allows interspecies signaling is the LuxS system. The LuxS enzyme is responsible for the production of a precursor of autoinducer-2, a signaling molecule involved the regulation of gene expression of for instance virulence factors, competence for genetic transformation, the production of antibiotics and secondary metabolites, and biofilm formation (36, 176). In co-cultures of the hyperthermophiles *Thermotoga maritima* and *Methanococcus jannaschii*, growth and EPS production of the former was stimulated by the presence of the latter. Additionally, a QS signaling peptide in *T. maritima* was upregulated. It was shown that EPS expression was enhanced in presence of this signaling peptide (72). Similar processes may also play an important role in biofilm formation in mixed culture food fermentations.

An example of interspecies communication via QS among lactic acid bacteria is represented by *L. plantarum* NC8, where not only plantaricin itself but also plantaricin-like peptides produced by other Gram-positive bacteria were shown to induce production of plantaricin by *L. plantarum* (96, 97).

Microbes may also interact and influence each others metabolism via physical contact and a few examples of such interactions have been described for mixed culture food fermentations. Cheirsilp *et al.* demonstrated that production of the capsular EPS kefiran was enhanced by physical contact between *Lactobacillus kefiranofaciens* and *S. cerevisiae* (26). The molecular basis of this effect remains to be established. It was postulated that the bacteria and yeasts may benefit from the enhanced kefiran production through interactions that occur in the kefir granules where interspecies contact or the exchange of growth factors is facilitated through physical contact.

GENOMICS APPROACHES FOR MIXED CULTURE RESEARCH

The genomic revolution has opened new avenues for research on mixed cultures. For an increasing number of relevant LAB genome sequences are available (90, 93). In several LAB genomes, amongst which *L. plantarum* (84), *S. thermophilus* (15) and *Lactobacillus salivarius* subsp. *salivarius* (27), there is evidence for horizontal gene transfer (HGT). Interestingly in many cases the acquired sequences appear to originate from species that frequently co-exists and interact. In the genome of *L. bulgaricus* ATCC11842 a region with a GC content of 38 % carrying an operon encoding an ABC transporter that could serve as an uptake transporter for putrescine and/or spermidine was found and proposed to be involved in the interactions between *S. thermophilus* and *L. bulgaricus* (163). This

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GC content is significantly lower than the average value of 49.7% observed for the entire genome. Interestingly, this locus has only been found in a few bacterial genomes whereas it is not even present in the genome of another *L. bulgaricus* strain, ATCC BAA-365 (93) indicating that it may have been acquired recently via HGT (163).

Only a limited number of studies is available where genomics approaches are used to study the interactions in mixed culture food fermentations. Such studies pose at least two technical challenges that need to be addressed. The first relates to the complexity of most food fermentation substrates. The physicochemical composition and especially the high protein or fat content may interfere with experimental procedures for RNA and protein isolation that work well with laboratory media. A number of studies have appeared that describe successful transcriptome or proteome analyses on samples from fermented substrates and even from highly complex material such as fecal samples (81, 178). Most studies on dairy fermentations use skim milk where the precipitation of casein may be prevented by pretreatment with sodium citrate (126, 139). These studies have revealed several previously undescribed metabolic adaptations upon growth in milk such as the induction of pyruvate-formate lyase in S. thermophilus that may serve as a supply of formate required for the biosynthesis of purine bases or other anabolic processes (39) (see also Figure 1). A recent study deals with transcriptome analysis of Lc. lactis grown in milk in co-culture with S. cerevisiae (98). Although no difference in growth was observed compared to a Lc. lactis mono culture, a number of genes was differentially expressed, in particular genes involved in pyrimidine metabolism. Several other regulatory responses could be assigned to the ethanol produced by the yeast.

The potential of using functional genomics approaches for analyzing interactions is well illustrated by recent studies describing the genome-wide analysis of interactions of commensal or pathogenic microbes with their hosts. With the availability of microarray platforms for several plant species and soil bacteria it is possible to elucidate the response of both the host and the microorganism upon interactions as exemplified by the induction of defense proteins in *Arabidopsis thaliana* by *Agrobacterium tumefaciens* (42). Host-microbe interactions in the gastro-intestinal tract are of crucial importance for human health. The overwhelming complexity of this system with respect to composition and activity of the microbiota as well as its heterogeneity and poor accessibility to sampling requires inventive research approaches. The use of germ-free animal models has greatly facilitated the analysis of genome-wide responses of micro-organisms as well as the host upon colonization (18, 134). Other studies report the *in vivo* time

and spatial resolution of the expression of genes specifically expressed in the GI tract in the model probiotic L. plantarum (19). Recently, Sonnenburg et al. have extended these approaches in a study where they co-colonized germ-free mice with Bacteroides thetaiotaomicron, a prominent component of the adult gut microbiota, and Bifidobacterium longum, а frequently used probiotic The results showed that co-colonization prompted B. microorganism. thetaiotaomicron to increase expression of genes involved in the acquisition and metabolism of polysaccharides (141).

Most studies described above relate to the performance to the interactions of microbes in simplified model systems or defined systems composed of a limited microbial complexity. Recent advances in the field of metagenomics provide a radically new approach for very complex ecosystems as well as for ecosystems dominated by a moderate number of species and strains (162, 164). Random sequencing of environmental samples supplies information on the (amount of) species present in an environment, including uncultured microorganisms, as well as information on known and previously unknown genes that occur in that environment. By comparing habitat-specific fingerprints of genes present in various known environments, it is possible to interpret other environments. Tringe et al. (160) clustered similar environmental samples together and found only few genes specific for a certain environment. Based on relative abundance, it was clear that systems for transport of ions and inorganic compounds, energy production and (interspecies) communication were most discriminative between samples from the Sargasso sea, deep sea whale fall and farm soil. Currently, various groups are sequencing metagenomes of and oral microbiota gut (http://www.genomesonline.org/gold.cgi?want=Metagenomes), which will undoubtly boost research on dynamics and interactions within these complex microbial populations and support the development of prebiotics and probiotics.

DESCRIPTIVE AND PREDICTIVE MODELING IN THE GENOMICS ERA

Modeling has played an important role in food microbiology and an extensive review describing different modeling categories has been published recently (156). Historically, most of these studies aim at developing predictive models for the growth of desired or undesired microorganisms in the food matrix. As the demand for minimally processed foods increases, the risk of outgrowth of spoilage or pathogenic microbes rises. Accurate empirical models are of great value as they assist in the definition of processing conditions minimizing the risk of growth of

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these bacteria such as *Bacillus cereus*, lactobacilli, or *E. coli* (95, 101, 122). Similarly, Sodini *et al.* used black box modeling for predicting the acidification of mixed cultures of *S. thermophilus* and *L. bulgaricus* and quantifying the interactions between the two species (140). In another example growth dynamics in a mixed yeast culture of killer and sensitive strains was reported (123). Here, the lethal action of the killer strain showed a lag phase probably due to the necessary accumulation of the toxin before it reached a lethal dose. The existing model was adapted for this effect.

Despite the value of such models in process optimization their predictive value is often limited to specific substrates and conditions and they do not provide additional mechanistic insight as for instance interaction effects. Other modeling strategies aim at predicting the performances of microbes in fermentations on the basis of their metabolic pathways and networks. Such "white box" or mechanistic models have been successfully applied for the optimization of industrial fermentations including food ingredients such as lactic acid and amino acids (8, 138). To our knowledge there are no examples of the integration of interaction effects in such models to the level where they can be used to predict the performance of mixed culture fermentations. However, Gregory *et al.* developed a computing system that allows the modelling of interactions and evolution in bacterial communities (60, 61). This model includes several aspects such as growth stimulatory interactions, antibiotic sensitivity, occurrence of antibiotic resistant mutants and growth on nutrients derived from killed cells in one model.

With the emergence of genomics a radically different modeling approach has drawn increasing attention (see (156) and references therein). Here, genome-scale metabolic models are constructed that allow a systematic exploration of the metabolic capacities and a number of such models have appeared in recent years for important microbes in mixed culture food fermentations like L. plantarum and Lc. lactis (112, 157). These may serve as references for future metabolic models thereby accelerating the process of model construction (110). A genome-scale metabolic model and associated constraint-based modeling techniques were used to analyze the physiology of growth of L. plantarum in a complex medium revealing the importance of amino acid catabolic pathways previously not associated with free-energy metabolism (158). With respect to mixed culture fermentations it will be interesting to see whether it is possible to connect genome-scale metabolic models of the individual components of mixed cultures through a limited number of interactions. Such "multi genome" scale models should be effective tools for the optimization of mixed culture performance with respect to growth and metabolite production.

CONCLUSIONS AND FUTURE PROSPECTS

Mixed culture food fermentations are of primary economic importance. The performance of such cultures, consisting of lactic acid bacteria, yeasts and/or filamentous fungi, is not the simple result of 'adding up' the individual single strain functionalities, but is largely determined by interactions at the level of substrates, exchange of metabolites and growth factors or inhibiting compounds.

Technological breakthroughs in the post-genomic era open up new avenues to study microbial communities and interaction networks beyond simple descriptive models. These are now mainly applied for ecological studies on highly complex systems such as the GI-tract or complex environmental ecosystems. On the other hand studies aiming at understanding more fundamental ecological principals underlying the success of evolutionary strategies typically make use of more artificial laboratory strains and ecosystems (79, 120). Food fermentations may provide a valuable alternative model with a high practical relevance. They typically have moderate microbial complexity and offer excellent possibilities for process control. Moreover, the availability of advanced genomics and genetic tools will allow the integration of mechanistic and evolutionary approaches (171).

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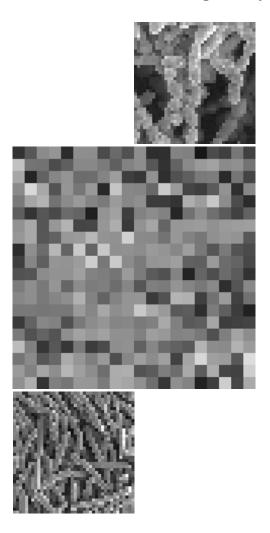
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Chapter 3

A simple and fast method for determining colony forming units



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ABSTRACT

Aims: To develop a flexible and fast colony-forming unit (CFU) quantification method that can be operated in a standard microbiology laboratory.

Methods and results: A miniaturized plating method is reported where droplets of bacterial cultures are spotted on agar plates. Subsequently, minicolony spots are imaged with a digital camera and quantified using a dedicated plug-in developed for the freeware program ImageJ. A comparison between conventional and minicolony plating of industrial microorganisms including lactic acid bacteria, *Escherichia coli* and *Saccharomyces cerevisiae* showed that there was no significant difference in the results obtained with the methods.

Conclusion: The presented method allows downscaling of plating by 100-fold, is flexible, easy-to-use and is more labor-efficient and cost-efficient than conventional plating methods.

Significance and impact of the study: The method can be used for rapid assessment of viable counts of microorganisms similar to conventional plating using standard laboratory equipment. It is faster and cheaper than conventional plating methods.

KEYWORDS

Colony-forming units, plating, faster enumeration, lactic acid bacteria, *Saccharomyces cerevisiae*, *Escherichia coli*

The growth and maintenance of microbes on agar-containing media in Petri dishes has since long been common practice in microbiology. Traditionally, the preferred method for quantitative population analysis of pure and mixed cultures relies on plating of serial dilutions and subsequent counting of colony forming units (CFUs). In recent years a range of alternative, high-throughput (HT), methods relying on quantitative PCR (5, 14), fluorescent labeling (2, 8) or genome probing with micro arrays (1) have gained popularity (9). However, most of these methods measure different entities, i.e. all cells, including non-viable cells. Moreover, these methods may require the use of special equipment or extensive protocol development. In addition, some of these methods are poorly compatible with complex substrates and environmental samples. This largely explains why enumeration of microbes by colony counting is still a widely applied methodology. Presently, microbiology is increasingly moving towards HT analyses, which may require the use of large quantities of plates. This results in serious drawbacks when using conventional plating and colony counting techniques. The preparation of media and plates as well as the counting of colonies is time-consuming and labor-intensive. Moreover, large volumes may lead to significant costs, in particular when expensive indicator or reporter substrates are used. Finally, many methods consume large amounts of materials including disposables, compromising their sustainability.

Several reports describe alternative plating technologies in which the required volumes are down-scaled (6, 7, 13, 16) or the colony counting process is automated (3, 12, 15). However, these examples require equipment that is not present in standard microbiology laboratories (4, 10), may result only in limited downscaling (4, 6, 7), or are poorly suited for automation (6, 13). Building upon this work, we report a simple and flexible method for determining cell counts capitalizing on microtiter plate formats. It integrates rapid miniaturized plating and (semi-) automated counting of minicolonies allowing 100-fold downscaling of the process compared to conventional CFU counting procedures. It can be fully operated with little more than a multichannel pipet, a digital camera and ImageJ, an image processing package that is available as freeware (http://rsb.info.nih.gov/ij/). A number of examples is presented to illustrate the power of the approach for rapid assessment of viable counts of important prokaryotic and eukaryotic industrial microorganisms.

For plating we used 10-fold serial dilutions that were prepared in 96-well micro plates using a Genex Alpha twelve channel pipet. For each dilution, samples of five μ l were pipeted onto a plate containing agar medium using the same pipet. Typically, 60 to 120 droplets were applied per square 12 cm plate. The plates were air dried and then incubated until colonies were visible with an average size of 200 to 500 μ m. Subsequently, these minicolonies were photographed with a Canon EOS 350D high resolution digital camera (Canon 0020X665, Canon Nederland NV) equipped with a Sigma 105 mm macro lens (AF 105MM F2.8 EX MACRO F, Sigma Corporation). Plates were put on a black surface and illuminated from the side in order to achieve a large contrast between colonies and background.

Digital images were further processed in ImageJ using a newly developed plug-in that can be downloaded as supplementary material. The counting process is schematically represented in Figure 1. Briefly, the color images were converted into eight-bit grayscale and inverted. By manual intervention using the 'threshold' function of ImageJ, colonies were selected from the background. Then all pictures were stacked. After inversion, the median was taken from each pixel with its neighboring pixels for noise reduction. The 'watershed' function was used to separate merged colonies and the 'analyze particles' function was used for counting. The output was saved as a text files and subsequently processed in Microsoft Excel.

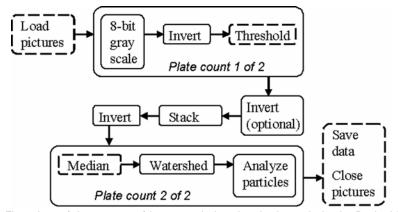


Figure 1. Flow chart of the process of image analysis using the ImageJ plug-in. Dashed boxes are steps that require human intervention. First, a number of pictures is loaded. Thereafter, the pictures are processed with macro 'Plate count 1 of 2' which transfers the pictures into an 8-bit gray scale image (necessary for the 'Threshold' function). Using 'Threshold' manually, the colonies can be selected from the background. This is done for each picture separately, because the images may vary in contrast and brightness. Subsequently, the pictures are stacked so that the following steps can be performed for all pictures simultaneously. For stacking it is necessary to have a black background and white colonies in all pictures, while for the next steps the pictures have to be inverted. In 'Plate count 2 of 2', the median of each pixel with its neighboring pixels is taken to remove noise. 'Watershed' is performed to separate merged colonies, and finally colonies are counted using the 'Analyze particles' function.

In our study we specifically aimed at developing fast CFU counting protocols for industrial microbes including lactic acid bacteria, *Escherichia coli* and *Saccharomyces cerevisiae*. When these strains are enumerated by conventional CFU counting, typically between 30 and 300 colonies per standard agar Petri dish of eight cm in diameter results in optimal counting. Larger numbers may easily result in underestimation as individual colonies can not be discriminated. Low numbers of colonies per plate result in large standard deviations, which is the squared root of the average in Poisson distribution. This implies that in case five colonies are counted the number of cells in the plated samples is between one and nine with 95% confidence whereas for 100 cells these values are 80 and 120. In the latter case the 95% confidence interval is 20% deviation of the average. We therefore aimed at developing a protocol that would allow the counting of at least 100 colonies. This implies that, in any process of downscaling of plate-counting, it is crucial to increase the number of colonies that can be counted per cm² of agar surface. In our experiments, this was achieved by counting minicolonies with a size

of 200 to 500 μ m. Therefore, colonies were counted as soon as minicolonies were visible, which is earlier than normally is done with conventional counting. Moreover, growing many colonies on a relatively small surface area results in smaller colonies for instance due to limited substrate availability (10). This effectively increases the number of colonies that can be counted per cm² of agar surface.

				Incubation of plates		Average CFU/ml (SD)	
Species	Liquid growth medium	Dilution medium	Plating medium	Temp.	Time (h)	Old method	Minicol. method
S. thermophilus	M17 broth + 1% glucose	M17 broth + 1% glucose	M17 agar + 1% glucose	37°C	28 (new method) 40 (Old method)	8.85E+07 (3.25E+07)	2.69E+08 (4.25E+07)
L. lactis	M17 broth + 1% glucose	M17 broth + 1% glucose	M17 agar + 1% glucose	30°C	20	1.88E+08 (3.17E+07)	1.04E+08 (2.30E+07)
L. plantarum	10% skim milk (Nilac) in co-culture with <i>S.</i> <i>thermophilu</i> s	MRS broth	MRS agar + 1% galactose	30°C	24	2.86E+07 (9.21E+06)	1.37E+07 (1.21E+06)
E. coli	TY broth	TY broth	TY agar	30°C	18	2.04E+08 (1.58E+08)	3.12E+08 (8.29E+07)
S. cerevisiae	ME broth	ME broth	ME agar	30°C	18 (new method) 22 (old method)	8.80E+07 (7.29E+07)	4.87E+07 (2.19E+07)

Table 1. Culturing and plating conditions used in the comparison of the conventional plating method and minicolony plating method and resulting average CFU/ml counts with corresponding standard deviations within 12 replicates.

We used the procedures described above to perform viable counting of various industrial microorganisms and bench-marked these data to conventional counting procedures. Therefore, *Streptococcus thermophilus* CNRZ1066, *Lactococcus lactis* MG1363, *Lactobacillus plantarum* WCFS1, *E. coli* DH5 α and *S. cerevisiae* CBS57957 were cultured in appropriate media (see Table 1) for approximately 24 h at 37°C. Culture dilutions were prepared in 96-well plates in 12-fold and these were plated using both methods. For the conventional method 50 µl samples were pipetted onto a round agar plate of eight cm in diameter with a Gilson pipetman P100 and spread using a glass swab. The average CFU counts were comparable and the standard deviations comparable or lower with the minicolony method

confirming the suitability of the method for rapid CFU counting. From the standard deviations in Table 1, it can be concluded that the sensitivity of the fast method is comparable to the conventional method, although the variation between counts may differ with the type of pipets used, as argued previously by Jett *et al.* (7).

For example, *L. plantarum* spots containing minicolonies were around nine mm in diameter and therefore it is possible to count up to 200 colonies per cm^2 efficiently on MRS-galactose agar, which is typically one to two orders of magnitude higher than with conventional plating. We found that the sizes of spots and minicolonies may vary with the type of agar medium, drying time, sample matrice and species of interest (not shown). It may affect the number of colonies that can be enumerated per five µl spot, typically in the range between 10 and 150, but not on the number of colonies that can be counted per cm^2 for this certain species. The detection limit of the minicolony method is similar to that of the conventional method. The dynamic range of the new method was found equal to the conventional method (data not shown).

In recent years high-throughput alternatives and variants have been developed for many conventional microbiological techniques. The best examples are probably liquid batch cultivations for which various multi-well alternatives belong to standard laboratory equipment nowadays. Also several HT alternatives for counting of colony forming units are reported (3, 10, 15). Throughputs are increased by focusing either on automation of the counting process or on the miniaturization of the plating itself. The novelty of the method reported here relies on the integration of these aspects while it requires only standard laboratory equipment, a digital camera, imaging software that is available as freeware, and a dedicated plug-in that is available as supplemental material to this paper at the LAM website. The resulting fast plating and counting protocol is suitable for a quick determination of viable cell counts. The method is highly flexible, because it can easily be implemented for different microbial species and it is easy-to-use. Due to its miniaturization it reduces the amount of necessary materials by approximately 100fold, which makes it a cost and labor efficient alternative for conventional methods. Because the counting is partially automated, the user can monitor critical steps in data acquisition and processing without the variability encountered from manual counting of CFUs (11). We anticipate that this protocol is a valuable tool for routine enumeration of industrial microbes in research and quality control laboratories.

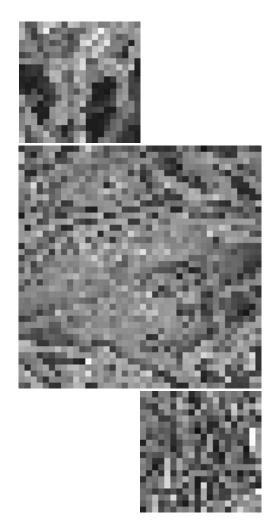
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Mixed culture transcriptome analysis reveals the molecular basis of co-culture growth and its consequences in Streptococcus thermophilus and Lactobacillus bulgaricus



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ABSTRACT

Many industrial food fermentations are carried out by mixed cultures of lactic acid bacteria. Interactions between different strains are of key importance for the performance of these fermentations. The yoghurt fermentation, in which bovine milk is fermented by Streptococcus thermophilus and Lactobacillus delbrueckii subsp. bulgaricus, is one of the best-described mixed culture fermentations. These species are known to stimulate each other's growth by the exchange of metabolites such as folic acid and carbon dioxide. Recently, postgenomic studies have been applied to reveal the global physiological response to mixed culture growth in S. thermophilus (19, 20) but an in-depth molecular analysis of mixed culture growth of both strains remains to be established. Here we report the application of mixed culture transcriptome profiling to unravel the molecular responses associated with co-culture growth of S. thermophilus and L. bulgaricus in milk. The results indicate that the interactions between these bacteria are primarily based on purine, amino acid and long-chain fatty acid metabolism. That is, formic acid and folic acid are provided by S. thermophilus, amino acids by proteolysis executed by L. bulgaricus and long-chain fatty acids possibly by lipolytic action of S. thermophilus. Moreover, we observed that genes involved in iron uptake in S. thermophilus are affected by co-culture growth, and that genes coding for exopolysaccharide production are higher expressed in both organisms in mixed culture.

INTRODUCTION

Many food products are fermented by mixed cultures consisting of bacteria, yeasts or filamentous fungi. Fermented dairy products are typically produced with lactic acid bacteria (LAB), a prominent group of Gram-positive bacteria. Yoghurt is bovine milk fermented by the LAB *Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus* (*L. bulgaricus*). During fermentation, both species contribute to the texture and the flavor of the product by (i) acidifying the medium leading to coagulation of the milk proteins, (ii) producing exopolysaccharides (EPS) and (iii) generating characteristic flavor compounds, such as acetaldehyde and diacetyl (43). *S. thermophilus* and *L. bulgaricus* stimulate each others' growth and acid production in a mixed milk culture, a process also referred to as protocooperation (12). This mutual stimulation is based on the exchange of growth enhancing metabolites (for a recent review, see (35)). *S. thermophilus* provides *L. bulgaricus* with pyruvic acid, formic acid (14) and folic acid (13, 42) and carbon

dioxide (16), compounds that are all associated to purine biosynthesis either as precursors or cofactors. *L. bulgaricus* lacks pyruvate-formate lyase (PFL) and 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase, an essential gene in the biosynthetic pathway of folic acid (13, 45). Other metabolic interactions exist at the level of nitrogen metabolism. Milk contains low levels of free amino acids (AA) and small peptides but milk proteins provide a rich source of AA that can be liberated through the action of extracellular proteolytic enzymes. Typically, the non-proteolytic *S. thermophilus* profits from the proteolytic action of the membrane-resident protease prtB of *L. bulgaricus* (11, 34, 37). Similarly, *L. bulgaricus* was reported to be stimulated by long chain fatty acids (LCFA) such as oleic acid and lauric acid (29), but it remains to be established whether these are provided by *S. thermophilus* in mixed culture.

The metabolic interactions between the yoghurt bacteria have been elucidated mostly with classical microbiological approaches. More recently two postgenomic studies addressed the global response of *S. thermophilus* LMG18311 to growth in milk as a mono or mixed culture with *L. bulgaricus* ATCC11842 (19, 20). These studies revealed several additional metabolic responses to co-culture growth. The down-regulation of genes associated with purine metabolism and the upregulation of *stu0336*, a xanthine/uracil permease, suggested that purine (precursors) were provided by *L. bulgaricus* and consumed by *S. thermophilus*. Additionally the pathways for the biosynthesis of arginine and branched-chain AA (BCAA) were strongly upregulated in *S. thermophilus* in mixed culture. Finally there was a pronounced response in iron metabolism. The authors showed that in response to H_2O_2 produced by *L. bulgaricus*, *S. thermophilus* shows multiple responses that may lead to lower intracellular iron concentrations. (19). In this way *S. thermophilus* appears to minimize damage by reactive oxygen species (ROS) that are generated in the Fenton reaction.

The postgenomic analyses described above are only performed in *S thermophilus*. The global response to mixed culture growth in *L. bulgaricus* remains to be established. In this study we aimed at analyzing the global regulatory responses to co-cultivation in milk in both strains simultaneously. The correlation of the global responses with population dynamics in intervention studies and metabolite production confirmed the importance of purine and AA metabolism, but also showed that *L. bulgaricus* LCFA production genes are down-regulated in mixed culture despite its higher growth rate. This indicates that these LCFA were directly or indirectly provided by *S. thermophilus*. Similarly, the induction of genes responsible for EPS production in both species in co-culture shows a role for EPS in the protocooperation. These results provide further insight in the global

physiology of the yoghurt mixed culture fermentation and may facilitate rational improvement of other fermentations or the development of new (industrial) mixed cultures, for instance by providing targets for engineered nutritional dependencies.

MATERIALS AND METHODS

Strains and culture conditions.

Streptococcus thermophilus CNRZ1066 (3) and Lactobacillus delbrueckii subsp bulgaricus ATCC BAA-365 (25) were maintained as frozen stocks in M17 broth (Difco) and MRS broth (Difco), respectively with 22% glycerol (Scharlau) at -80 °C. Precultures were made as mono-cultures in UHT treated 10% reconstituted skim milk (Nilac, NIZO food research, the Netherlands) for 22 h at 42°C. Final liquid cultures were made by inoculating pre-warmed milk at the same conditions with, precultures of *S. thermophilus* and *L. bulgaricus* to density of approximately 1*10⁵ and 2*10⁴ CFU/mL, respectively.

For biofilm growth, *S. thermophilus* and *L. bulgaricus* mono-cultures in milk were incubated for 1-2 days at 42°C and subsequently pipeted together or separately onto an anopore slide (22) placed on top of a milk agar plate (8% skim milk and 1-1,5% agar). Plates were incubated anaerobically at 42°C for 2-4 days before staining procedures were carried out (see below) or at 45°C for 2 days for transcriptome analysis. Cell density of the inoculum was quantified by plating on MRS agar for *L. bulgaricus* and M17 agar supplemented with 1% (w/v) glucose for *S. thermophilus*.

In order to calculate the amount of lactic acid produced by the different cultures, uninoculated milk was acidified to various pH values with lactic acid. These recorded amounts of added lactic acid were used to calculate the lactic acid content of a culture at a certain pH.

Intervention studies.

Cultures of *S. thermophilus*, *L. bulgaricus* and the mixed culture were prepared in 0.8 volume reconstituted skim milk with 0.2 volume of a solution with compounds for which it has been established or hypothesized that they are involved in interaction (35): Na-pyruvate (1.82 mM), Na-formate (1.47 mM), folic acid (1 mM), nucleobases (10 mg/L each) (all representing purine and pyrimidine metabolism), Tween-20 (105.9 μ M) (as a supply of lauric acid (15, 23)), Tween-80 (110 mg/L) (as a supply of oleic acid (23)), casitone (4 g/L), histidine (650 μ M) (both representing proteolysis), L-ornithine monohydrochloride (590 μ M) and putrescine

(1.13 mM) (both involved in arginine metabolism, urea cycle and tolerance to oxidative stress (7, 35, 45)). Here after these compounds are referred to as 'interaction compounds'. The LCFAs oleic acid and lauric acid are poorly soluble and therefore we used Tween-20 and Tween-80 (29). The effect of each of all interaction compounds on growth and acidification was tested in a single addition and a single omission strategy. Paired comparisons were made of a single compound versus nothing added (neg. control), and of all compounds minus one added versus all (pos. control). Acidification of quadruplicate cultures of 250 µL was measured at 37 °C for 19 h in hydroplates (PreSens - Precision Sensing GmbH, Germany) where after CFU counts were determined using a rapid miniplating method (36). Significant differences in acidification were determined by comparing the maximal acidification rate using a two-tailed Students t-test (p=0.05). Similarly, significant differences were calculated between the final pH values and between the colony-forming units.

Metabolite analyses.

Free amino acid content was determined as follows. Samples (100 µL) were diluted 10x by adding 100 µL 2.5 mM norvaline (Aldrich) as internal standard and 800 µL 0.1 M HCI (Fluka) / 0.2% (w/v) 3,3-thiodipropionic acid (Fluka). In order to remove proteins, this was filtered in a 3000 Da Microcon Ultracel YM-3 microcentrifuge filter (Sigma) by filtration at 3500 G for 30 min. 20 µL of this was mixed with 180 µL of a solution containing 0.15 M NaHCO₃ pH 8.6 to buffer pH. 200 µL 12.4 M dabsyl chloride (Fluka) in acetone (Sigma) was added. The samples were incubated for 15 min at 70°C and mixed with a vortex mixer after 0, 1 and 12 min to derivate the amino acids. This reaction was stopped by placing the samples on ice. The samples were centrifuged at 10000 G for 10 s, where after 400 µL of a solution was added consisting of 50% (v/v) acetonitrile (Sigma), 25% (v/v) ethanol (Sigma) and 25% (v/v) Eluens A (9 M NaH2PO4 pH 7.0 and 0.16% (v/v) triethylamine (Sigma)). The samples were mixed by vortexing and centrifuged at 15000 G for 5 min. Of the supernatants 10 µL was injected in the column for analysis with a Phenomenex ODS (C18), 3 µm SphereClone column and reversedphase HPLC (detection at 436 nm with 738 A (VIS4205) (Applied Biosystems)). The concentrations were calculated by comparing the peak surface with that of a standard series.

For volatile compound analyses Solid Phase Dynamic Extraction (SPDE) head space analysis was performed similar to as described by Bachmann *et al.* (1). In short, triplicate cultures of 5 mL prepared in glass flasks were grown at 37°C for 24 h and subsequently frozen at -80°C. The flasks were incubated at 60°C and 1 mL

headspace was used for the SPDE (PDMS and 1% AC). The volatiles were fixed by cryofixation at -150°C for 0.5 min. Subsequently, the components were separated on a Factor Four V1ms column using a helium flow of 1.5 mL/min. The oven temperature was held at 40°C for 5 min, was increased to 50°C using a ramp rate of 10°C/min, brought to 60°C by 2°C/min, then brought to 150°C by 10°C/min and finally brought to 225°C for 4 min with a ramp rate of 50°C/min. Peak areas were determined and compounds were identified using the mainlib, replib and wiley7 (Nist) libraries in Xcalibur™ (Thermo Fisher Scientific Inc, Waltham, MA, USA). Quantification of components was performed by comparing peak areas with those of calibration series.

Exopolysaccharide isolation.

Different 275 mL yoghurt cultures were grown at 37°C for 24 h. Of this, 80 g was used for EPS isolation. The samples were incubated at 55°C to release all EPS from the cells, where after 5.3 mL of a 60% Na₃Citrate (Merck) solution was added. After stirring at RT for 1 h, the samples were centrifuged for 30 min at 6000 G and 4°C. The supernatant was applied to a flask and adjusted to pH 4.0 with 10 M NaOH (VWR). Dialysis tubes (Medicell International Ltd., England) were boiled in water with a spoon Na₂CO₃ for 5-10 minutes, rinsed with water and boiled in water for 5 min. The samples were applied to the tubes. Dialysis was performed in flowing tap water for 24 h and twice in MQ water for 3 h. Dialyzed samples were freeze dried in an ilShin freeze dryer (IIShin, South Korea) until all water had evaporated.

Microarray design.

Microarrays were spotted on the Agilent 8x15K platform (Agilent Technologies, Santa Clara, CA, USA) with a custom probe design (AMADID 015342) comprising the sequences of both *S. thermophilus* CNRZ1066 (released by NCBI, genbank accession no. NC_006449) and *L. bulgaricus* ATCC BAA-365 (released by JGI, genbank accession no. NC_008529). The probes were designed with the objective to minimize cross-hybridization: the probes were species-specific, i.e. all probes were designed as 60-mers with a target score of 100% to the target gene, allowing no binding of cDNA that is 1 base different (mismatch) if the correct hybridization temperature (65°C) and washing temperature (37°C) are used. In total there are 5438 probes representing 1899 genes of *S. thermophilus* and 4028 spots representing 1709 genes of *L. bulgaricus*. Most genes are represented by 3 probes or more. Only 55 genes in *S. thermophilus* and 77 in *L. bulgaricus* are represented by one probe and only 5 genes of *S. thermophilus* and 31 genes of *L. bulgaricus*.

are lacking. The selectivity of strain specific gene detection was tested by a series of transcriptome profiling experiments of samples from MRS-grown mono-cultures of both strains. Comparative analysis of separate hybridizations and hybridization of a mixture of both samples showed that on average the probes showed 100-fold higher hybridization with RNA samples from the target strain. It was concluded that for a small number of genes strain specific gene expression analysis was not possible. These genes included rRNA genes (14 in *S. thermophilus*, 19 in *L. bulgaricus*), ribosomal proteins (4 and 12, respectively) and hypothetical proteins (8 and 2, respectively). They were excluded from further analysis.

RNA isolation from cultures grown in milk.

The high protein content of milk and the polysaccharide production by the grown microorganisms make cell harvesting problematic. Furthermore, sampling and quenching need to be carried out rapidly in order to prevent the introduction of technical errors in a transcriptomics experiment (10). Several procedures have been developed to "clear" the milk to enable cell harvest by centrifugation without the contamination with milk solids. However, milk cleaning procedures are time consuming and require drastic changes in pH and the addition of large quantities of sodium citrate (9). We considered that this procedure is prone to lead to changes in the transcriptome. Therefore, we developed an alternative method for cell harvesting and RNA extraction from yoghurt cultures suitable for transcriptomic profiling. Yoghurt cultures were quenched in 3 volumes 60% glycerol of -40°C leading to immediate arrest of cellular processes (32) and kept at -20°C for 0.5 h. Then pH was adjusted to 6.5 – 7.0 with 1 M NaOH and the medium was cleared with 4 mL 25% (w/v) Na₃Citrate per 100 mL at -20°C for 0.5 h with gently mixing each 5 min. Cells were spinned down at -20°C and 23000 G for 16 min and dissolved in a solution comprised off 50% (w/v) guanidinethiocyanate (Sigma), 0.5% (w/v) N-laurylsarcosine (Sigma) and 2.5% (v/v) of a 1 M sodium-citrate solution, adjusted to pH 7.0 with 0.1 M NaOH. After another centrifugation, the cells were resuspended in 500 µL 1xTE and applied to an RNA extraction tube containing 250 µL acidic phenol (Sigma), 250 µL chloroform (sigma), 30 µL NaAc (Merck) pH 5.2, 30 µL 10% SDS (Sigma) and 500 mg zirconium beads with 0.1 mm diameter (Biospec products Inc., OK, USA) which was immediately frozen in liquid nitrogen and kept at -80°C until RNA extraction.

For RNA isolation, a method was used that was already established for isolation from lactobacilli (39). Briefly, cells were disrupted 3 times 45 s in a Fastprep (Qbiogene Inc., France) at 5.5 m/s separated by 1 min on ice. After centrifugation for 1 min at 20800 G, 500 μ L of the aqueous phase was purified with

400 µL chloroform and a second centrifugation step. The aqueous phase was used for RNA isolation with a High Pure kit (Roche Diagnostics, Mannheim, Germany), which included 1 h of treatment with DNase I. RNA was stored at -80°C. Quantity and quality were checked using a ND-1000 photospectrometer (Nanodrop Technologies, Wilmington, DE, USA) and capillary electrophoresis on a RNA 6000 Nano LabChip® kit (Agilent Technologies, Santa Clara, CA, USA) in a 2100 Bioanalyzer (Agilent).

cDNA synthesis, labeling and hybridization.

Five to seven μ g of RNA was used for cDNA synthesis and labelling as described before (40). For each array, 0.3 μ g of cDNA labeled with Cyanine 3 and Cyanine 5 was hybridized. Hybridizations were performed with solutions and following the protocol delivered by Agilent (version 5.5) for 8x15K slides. Arrays were hybridized at 65°C for 17 h. Hybridization schemes were designed that allowed duplicate comparisons between different stages within a fermentation experiment as well as and between mono and mixed cultures (see Figure 1). Here after, the microarray slides were washed according to the manufacturer's instructions (buffer 1: room temperature, buffer 2: 30-37°C) with the buffers supplied by Agilent. We found that washing at lower temperatures resulted in major cross-hybridization when hybridising *S. thermophilus* cDNA labelled with Cy5 and *L. bulgaricus* cDNA labelled with Cy3 simultaneously, but not when applying only one cDNA sample.

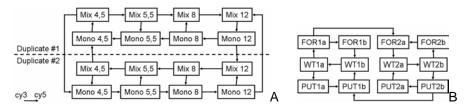


Figure 1. Hybridization schemes of the micro arrays performed in this study. Panel A, Mixed cultures were compared with mono-cultures in duplicate at four time-points in the fermentation: 4.5, 5.5, 8 and 12 h corresponding to the first exponential phase, transition phase, second exponential phase and stationary phase, respectively. Mono indicates a mixture of RNA from the mono-cultures of *S. thermophilus* and *L. bulgaricus*. Panel B, Mixed cultures without supplement (WT) were compared to mixed cultures supplemented with formic acid (FOR) and putrescine (PUT) at the transition phase (a) and the second exponential phase (b). The numbers 1 and 2 indicate biological duplicates.

Array analysis.

Slides were scanned using an Agilent microarray scanner (G2565BA), Laser lights of wavelengths at 532 and 635 nm were used to excite Cyanine3 and Cyanine5 dye, respectively. Fluorescent images were captured as multi-image-tagged image

file format and analyzed with Imagene software (Axon) (BioDiscovery, Marina del Rey, USA). The extent of hybridization was derived from a median value of pixelby-pixel ratios. *S. thermophilus* and *L. bulgaricus* spots were normalised separately using Lowess (47). Differential regulation was determined by false-discovery rate (FDR) from the Cyber-T *p*-values by means of multiple testing connection (2, 48). Differential regulation was defined as a two-fold or higher differential expression with a FDR cut-off value of 0.05 or lower. Regulated genes were divided into functional classes as described by NCBI (*S. thermophilus*) and JGI (*L. bulgaricus*). Using Hierarchical clustering, principle component analysis and MicroPreP (46), the quality of the different hybridizations was verified. Finally, results were visualized by plotting onto KEGG maps, Simpheny (Genomatica Inc., San Diego, CA) metabolic maps (30, 44) and Minomics (6).

Staining, imaging and processing of biofilms.

For SybrGold staining, anopore strips containing minicolonies were transferred right-side up to a microscope slide covered with a 1-mm-thick film of 1% (w/v) solidified low-melting-point agarose (Sigma, The Netherlands) containing 1µl/10ml 10000x concentrated SybrGold (Invitrogen, The Netherlands). Staining was for 20 min at room temperature. These procedures allowed staining of the organisms on the anopore surface through the pores without disruption of the microcolonies. Strips were then imaged directly (without coverslip, immersion oil, or fixative) using an Olympus BX-41 fluorescence microscope equipped with U-MWIBA filters (excitation spectrum of 460 to 490 nm, diachronic mirror splitting at 505 nm, and an emission spectrum of 515 to 550 nm, used for SybrGold) (Olympus, Japan). Scanning and examination of microcolonies were performed with 4x and 10x UMPIanF1 objective lenses, and observation of individual cells used a 50x UMPIanF1 objective (Olympus). Image capture was done with a charge-coupled device (CCD) camera controlled by Kappa Image Base software (Kappa, Germany).

Scanning electron microscopy (SEM) of biofilms.

Samples were cultured on anopore strips on milk agar plates for 2-4 days and fixed in situ by placing the anopore strips on MRS agar plates with 2.5% glutaraldehyde (w/v) for at least 2-3 hours. The strips were then washed three times with MQ water. Here after, samples were stained with 1% osmium in water for 15 min, and dehydrated through a series of ethanol/water mixtures with increasing ethanol content (10, 30, 50, 70, 90, 100%) for 10 min per treatment (twice with 100%) and then critical point dried.

Anopore strips cultured with bacteria were glued on a sample holder with conductive carbon cement (Leit-C, Neubauer Chemicalien) and frozen in liquid nitrogen. Samples were transferred under vacuum to the dedicated cryo-preparation chamber (Oxford Cryo-system, CT 1500 HF) onto a sample stage at -90°C. The samples were freeze-dried for 4 min at -90°C in a 3x10⁻⁷ Pa vacuum to remove water vapor contamination. Subsequently, the sample surface was sputter-coated with 10 nm platinum, and it was transferred to the cold sample stage (-190°C) inside the Cryo-FESEM (JEOL 6300F Field Emission SEM) and subsequently analyzed with an accelerating voltage of 5 kV. Images were digitally recorded (Orion, E.L.I.).

RESULTS

Population dynamics of S. thermophilus and L. bulgaricus.

To study the interaction of *S. thermophilus* and *L. bulgaricus* in milk growth and acid production in mono-cultures and in a mixed culture were compared (see Figure 2). While the *L. bulgaricus* mono-culture showed only one exponential phase, a typical 4 growth-phase behavior, following the lag phase, was observed in the *S. thermophilus* and the mixed cultures: (i) a first exponential phase, (ii) a transition phase at which the growth rate decreased, (iii) a second exponential phase, and (iv) a stationary phase (12, 24).

Intervention studies.

Several compounds are known or hypothesized to play a role in the interaction between the two yoghurt bacteria. We systematically analyzed the effect of these compounds on acidification and outgrowth in mono and mixed cultures. Therefore, mono and mixed cultures were prepared with single additions, a mixture of all components added, and all components with single omissions. The effects of these medium interventions on the evolution of pH were analyzed by scoring effect of key parameters of the acidification profile. That is, the maximal or minimal acidification rate in each growth phase (see Figure 2B) and the final pH. The final viable counts were also taken as measures for the paired comparisons (see Table 1). A higher cell count, lower final pH, higher acidification rate and a shorter time to reach this rate are considered stimulatory effect of the intervention compared to the control.

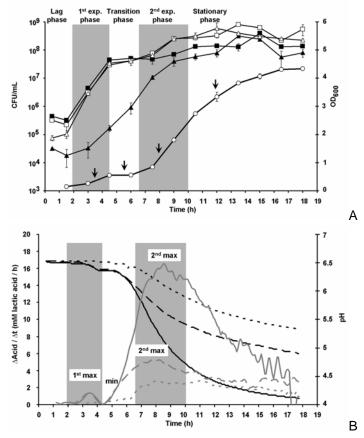
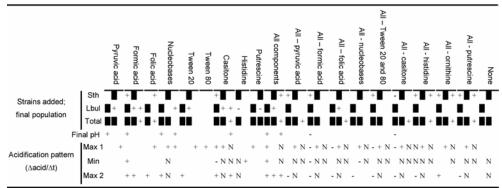


Figure 2. Growth and acidification of mono and mixed cultures grown in 10% reconstituted skim milk at 42 °C. Panel A, Colony-forming units per mL of *S. thermophilus* in mono-culture (\blacksquare) and mixed culture (\Box), and *L. bulgaricus* in mono-culture (\blacktriangle) and mixed culture (Δ), and the OD₆₀₀ of the mixed culture (\circ). Error bars indicate standard deviations of triplicate measurements. Gray and white boxes indicate the five distinct growth phases of the mixed culture. Arrows indicate sampling points for transcriptomics. Panel B, pH (black lines) and acidification (Δ mM lactic acid / h) (grey lines) of typical milk fermentations of *S. thermophilus* (striped), *L. bulgaricus* (dotted) and the mixed culture (solid). The three distinct phases (1st exponential phase, decreased growth phase, 2nd exponential phase) with a maximal, minimal and another maximal acidification rate are present in the *S. thermophilus* and mixed cultures, but not in the *L. bulgaricus* culture.

Acidification by *S. thermophilus* was stimulated by the following compounds in decreasing order: formic acid, casitone, pyruvic acid, folic acid and Tween-20. *L. bulgaricus* acidification was stimulated the most by formic acid and nucleobases, whereas pyruvic acid, folic acid, Tween-20 and Tween-80 showed a small stimulatory effect. Acidification of the mixed cultures was still stimulated by pyruvic

acid, formic acid and casitone, but in all cases stimulatory effects were less than with the mono-cultures. Only formic acid and casitone led to a higher final cell count of *S. thermophilus. L. bulgaricus* cell counts were higher when pyruvic acid or Tween-20 was supplied. These effects were less evident in mixed cultures, indicating the importance of purine and AA acquisition and a possible role of LCFA in the interactions between the two bacteria.

Table 1. Stimulation of growth and acidification by components potentially involved in the interactions between *S. thermophilus* and *L. bulgaricus* in milk. The final populations presented were determined from duplicate plating of quadruplate cultures. The acidification rates and final pH values were calculated from the same quadruplicate cultures in which one, all, or all minus one compound(s) were added. The pH was monitored for 19 h where after dilutions were plated for cell enumeration. Significant effects were determined by a two-tailed t-test (p=0.05). Cultures containing one component were compared to cultures without additions (single additions). Cultures containing all components minus one were compared to the cultures containing all (single omissions). Components that showed no difference with the reference in any of the measurements are left out from the table (i.e. Tween-80 on both monocultures and ornithine on all three cultures). Sth, *S. thermophilus*; Lbul, *L. bulgaricus*; +, positive effect (higher cell count, lower end pH, higher acidification rate, earlier maximal rate); -, negative effect (lower cell count, higher end pH, lower acidification rate, later maximal rate); N, not present; **L**, this species is not added in the culture.



Transcriptome analysis of mono and mixed cultures

In order to identify genes that are differentially expressed in both species upon coculture, we performed transcriptome profiling on mixed cultures and compared those to mono-cultures at four different growth phases, i.e. the first exponential phase (3.5 h after starting the fermentation), transition phase (5.5 h), second exponential phase (8 h) and stationary phase (12 h). Similarly, we compared these four distinct growth phases within a culture. Finally, transcriptome profiling was performed on cultures in early and mid second exponential phase mixed cultures supplemented with the interaction compounds formic acid and putrescine. These studies allowed analysis of global regulatory responses and the development of the interactions throughout the fermentation. DNA micro arrays were used that contained probes targeting strain-specific sequences ensuring minimal cross-hybridization for the genomes of both *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365. An RNA extraction method based on quenching by rapid freezing the culture and clarification by citrate was specifically designed for these experiments and proved to be crucial for the acquisition of high quality RNA samples from yoghurt cultures. Although we defined genes that were two-fold or more up or down-regulated with a FDR value of lower than 0.05 as significantly differentially expressed, also the more general effects were considered (e.g. all genes in a pathway are significantly upregulated by 1.5-fold).

Differential expression between mixed and mono-cultures was high in all four growth stages (see Table 2, Supplementary Tables 1 and 2 provide an overview of all significantly differentially expressed genes). The interactions affected S. thermophilus mainly in the second exponential phase (23% of all genes was more than 2-fold differentially expressed), which is in agreement with the observation that only at this growth phase S. thermophilus is profoundly stimulated by L. bulgaricus (see Figure 2A) (19). The major functional groups affected included 'Amino acid transport and metabolism' (15-42% of the genes in the category), 'Inorganic ion transport and metabolism' (14-32%) and 'Nucleotide transport and metabolism' (10-47%). The presence of S. thermophilus stimulates L. bulgaricus growth already in the early stages of the fermentation, which is exemplified by the higher portion of differentially expressed genes in L. bulgaricus in the two early growth phases compared to S. thermophilus (24% versus 7% in the transition phase). A major part of the differential expression in both species could be attributed to the increased growth rate as is exemplified by the induction of primary metabolism including the genes involved in the production of important end products such as diacetyl, contributing to the typical yoghurt flavor. Indeed, this compound was present in larger quantities in mixed culture than in mono-culture (see Table 3). The major affected functional groups related to interactions included 'Amino acid transport and metabolism' (21-36% of the genes in the category), 'Inorganic ion transport and metabolism' (20-28%) and 'Nucleotide transport and metabolism' (18-44%).

Below we will first describe the global physiological responses of both strains. Subsequently, regulatory responses for the major pathways affected will be described in more detail.

Global regulatory responses analysis of L. bulgaricus. In the L. bulgaricus mono-culture there was little difference in gene expression between the different growth phases except that from 8 h on (growth slows down and the culture enters stationary phase, see Figure 2A) many pathways were down-regulated, especially those associated with the biosynthesis of folic acid, purines, LCFA and AA and genes related directly related to growth such as those encoding ribosomal proteins and enzymes involved in cell wall biosynthesis. In the mixed culture there was a clear lower expression of genes associated with folic acid and purine biosynthesis, LCFA biosynthesis and sulfur AA metabolism in the transition phase compared to the first exponential phase. This may be due to the lower growth rate in the transition phase. In the second exponential phase, however, expression of purine and LCFA biosynthesis genes remained at a low level despite the higher growth rate compared to the transition phase. Moreover, LBUL 0106, encoding 1-acyl-snglycerol-3-phosphate acyltransferase was expressed 13-fold higher, suggesting that this acyltransferase was loaded with LCFA harvested from the medium. In addition, genes involved in EPS and sulfur AA metabolism were higher expressed in the second exponential phase than in the transition phase.

Global regulatory responses in S. thermophilus. In the S. thermophilus mono-culture, the gene pfIA (4.6-fold) for the production of formic acid and the pathway for purine biosynthesis were higher expressed in the transition phase compared to the first exponential phase despite the lower growth rate. Similarly, BCAA import and production genes were 2.9-3.0-fold higher expressed in the transition phase suggesting a shortage of these AA relatively early in the fermentation. Expression of genes for the production of other AA was in general lower in the transition phase compared to the first exponential phase. There was little difference in the second exponential phase compared to the transition phase except the up regulation of sulfur AA metabolism, as was also described by Hervé-Jimenez et al. (20). The trends in differential expression between the first exponential phase and the transition phase were comparable in S. thermophilus in mixed culture and the mono-culture, except for the fact that the higher expression of BCAA acquisition genes did not occur in the mixed culture. In the second exponential phase in mixed culture, purine biosynthesis genes were lower expressed than in the transition phase, but many pathways involved in AA acquisition were higher expressed, especially those for BCAA (2-3.1-fold) and sulfur AA (2.2-61.5-fold) suggesting an increased requirement for these AA. In the stationary phase, growth-related pathways were lower expressed. It is noteworthy that EPS biosynthesis genes of S. thermophilus were significantly higher

Table 2. Global patterns in differential gene expression. Numbers of genes two-fold or more up and down-regulated (FDR=0.05) in mixed culture compared to the mono-culture, cultures supplemented with formic acid compared to a culture without supplements. "All" refers to the number of genes that were differentially expressed at all four time-points. 'Early exponential' and 'mid exponential' correspond to 6.5 and 8 h in the fermentation without formic acid, respectively.

	S. ther	mophilus	L. bulgaricus			
	Up	Down	Up	Down		
Mixed versu	us mono	o-culture				
3.5 h	96	103	77	431		
5.5 h	58	93	96	702		
8 h	270	223	342	344		
12 h	246	514	489	411		
All	4	4	6	0		
Supplemen	tation of	formic aci	d			
Early exp.	105	122	53	80		
Mid exp.	89	63	61	93		
Both	5	7	8	20		

Table 3. Production of volatile compounds important for yoghurt flavor by the different cultures (µM).

	acetaldehyde	methanethiol	2-propanone	dimethylsulfide	2-methylpropanal	diacetyl	2-butanone	bthylacetate	3-methylbutanal	2-methylbutanal	2-pentanone	2,3-pentanedione	dimethyldisulfide	2-heptanone	dimethyltrisulfide
S. thermophilus	410	9.87	1020	2.27	4.50	74.00	41.67	13.67	1.63	0.87	14.00	3.63	0.90	18.00	0.73
L. bulgaricus	108	2.07	317	6.17	2.00	730	38.00	11.67	0.30	0.20	1.33	41.67	0.13	1.77	0.23
Mixed culture	252	21.67	1290	9.37	7.63	2333	68.00	25.67	1.40	0.60	8.57	423	1.03	9.40	1.60

expressed in the second exponential phase and stationary phase compared to the earlier growth phases in mixed culture, but not in mono-culture.

Purine metabolism. In a proteome study of *S. thermophilus*, Dezelle *et al.* (14) found that pyruvate-formate lyase (PFL) was highly abundant during growth in milk. We also found that the two genes, *pfl* and *pflA* were higher expressed in mixed culture, especially in the first exponential phase (3.0 and 4.1-fold, respectively) compared to mono-cultures. Expression was down-regulated 3.8 and 5.7-fold when formic acid was supplied indicating that the physiological role of the enzyme was (in part) ensuring sufficient supply of formic acid. Expression of genes of the biosynthetic pathway for folic acid production was not affected, but expression of folic acid cycling genes (C1 pool) corresponded to the expression of genes for the production of purines. However, the incomplete folate biosynthetic

pathway in *L. bulgaricus* was lower expressed, especially at the first two growth stages. Genes in the purine biosynthesis pathway in *S. thermophilus* were higher expressed in the mixed culture in the two earlier growth stages, but, in accordance to the study by Hervé-Jimenez *et al.* (19), less expressed in the second exponential phase despite the higher growth rate. Similarly, purine metabolism in *L. bulgaricus* was lower expressed in mixed culture, especially after 5.5 h, potentially due to the lower growth rate in mixed culture at this phase (see Figure 2A). When formic acid was supplied, expression of genes involved in biosynthesis of purines and folic acid cycling was lower in the early (second) exponential phase but higher in the mid exponential phase in both species.

Amino acid and carbon dioxide metabolism. Interactions occur at the level of nitrogen metabolism (proteolysis (19) and carbon dioxide utilization(16)). Nitrogen metabolism was poorly affected in L. bulgaricus with few exceptions. In co-culture we observed considerable higher expression levels of the prtB gene, LBUL 1105, which was 8.9-fold higher expressed in the second exponential phase in co-culture. This can be explained by the fact that peptides generated upon casein hydrolysis by the protease are more rapidly consumed when S. thermophilus is also present. This demands higher protease activity to sustain growth of both bacteria. In addition, genes involved in the biosynthesis of the sulfur AA cysteine and methionine were highly upregulated in mixed culture, e.g. the gene that converts O-acetyl-L-serine into cysteine, LBUL_1235, was expressed 23.1-fold higher in the mixed culture during the second exponential phase (see Figure 3A). This indicates that the proteolysis of casein does not allow the supply of sufficient cysteine for both organisms. Indeed, the cysteine content of casein is only 0.35% (41). Moreover, the free methionine content of a milk culture is negligible and the free cysteine is rapidly consumed, i.e. cysteine does not accumulate in L. bulgaricus mono-culture and mixed culture, while several other AA do (for an overview, see Supplementary Table 1). In S. thermophilus, the higher peptide abundance due to the proteolysis executed by the protease that is produced by L. bulgaricus led to the upregulation of peptide import systems, such as the ABC transport system encoded by amiC, amiD, amiE and amiF1 (2.5-2.8fold), and peptidolysis, as exemplified by the upregulation of the gene encoding peptidase PepN (2.4-fold) in the second exponential phase. In addition, genes encoding the biosynthesis of the three BCAA (2.0-fold) and uptake (1.0-1.3-fold) were slightly higher expressed in mixed culture. Similarly, in L. bulgaricus in mixed culture LBUL_0431, encoding a branched-chain amino acid permease, was 2.3fold higher expressed during the second exponential phase. That was anticipated since especially the S. thermophilus mono-culture and the mixed culture displayed a very low BCAA content, in particular of isoleucine. Similarly, in S. thermophilus there was a higher expression of pathways that convert serine into cysteine and methionine (1.5-1.9-fold). The pathways for de novo production of arginine out of glutamine and glutamate were upregulated in mixed culture. Glutamate is converted into ornithine mediated by four genes, argJ, argB, argC and argD, which were all 1.8-3.3-fold higher expressed in mixed culture at the second exponential phase. In addition, carA, one of the genes responsible for the conversion of glutamine into carbamoyl phosphase, was 1.8 fold higher expressed. This all indicates that the urea cycle is running faster in S. thermophilus in the second exponential phase when grown in co-culture with L. bulgaricus. Moreover, cah, encoding carbonate dehydratase in S. thermophilus, was 3.8 to 15.8-fold higher expressed in mixed culture, in particular in the earlier growth phases. By liberating CO_2 from carbonate this enzyme may play a role in providing the CO_2 required for biosynthesis of aspartate, glutamate, arginine and nucleotides (4, 27, 49) in both species. These results are in accordance with the results described by Hervé-Jimenez et al. (19), who argued that BCAA and arginine metabolism in S. thermophilus were upregulated in presence of L. bulgaricus.

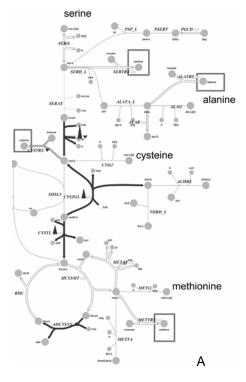
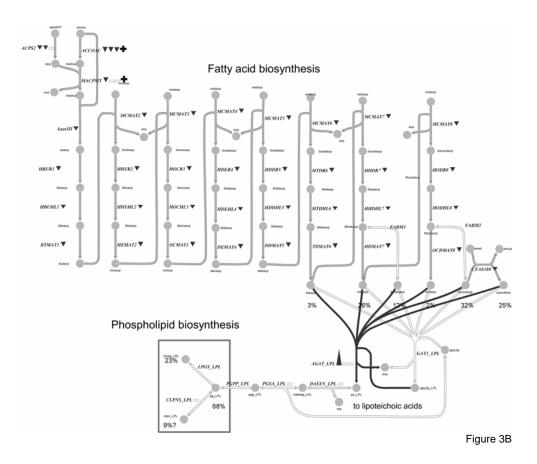


Figure 3. Differential gene expression in L. bulgaricus between mixed cultures and mono-cultures in the second exponential phase plotted on SimPheny metabolic maps. These maps are based on the gene content of the presented organism. Circles represent metabolites. Thick arrows indicate reactions catalyzed by proteins present in this species; thin arrows indicate that the genes encoding the protein catalyzing have not been identified in the genome. Dark arrows indicate a higher expression in the mixed culture; lighter arrows a higher expression in monoculture and white arrows indicate no differential expression. Pyramids indicate the extent of differential expression. Multiple pyramids indicate that there are multiple genes associated with this reaction. Panel A, Sulfur AA metabolism of L. bulgaricus. acser, O-acetyl-L-serine; CYSS, cysteine synthase; CYSTRS, cystenyl-tRNA synthetase; CYSTGL, cystathionine g-lyase; CYSTL, cystathionine b-lyase; HCYSMT, homocysteine s-methyltransferase; AHCYSNS, adenosylhomocysteine nucleosidase. Panel B, Fatty acid biosynthesis of L. bulgaricus in mixed culture compared to mono-culture at the second exponential phase. apoACP, apoprotein [acyl carrier protein]; accoa, acetyl-coA; acp, acyl carrier protein; tdeacp, tetradecanoyl-acp; hdeacp. hexadecanoyl-acp; 2chdeacp, cis-hexadec-2-eonylacp; ocdacp, octadecanoyl-acp; 2cocdacp, cisoctadec-2-eonyl-acp; cpocdacp, cvclopropanol AGAT-LPL, octadecanoyl-acp; 1-acyl-glycerol-3phosphate acyltransferase; pa_LPL, phosphatydic acid.



Iron metabolism and H_2O_2 resistance. We found that 6 of 7 genes involved in iron transport in *S. thermophilus* were differentially expressed in mixed culture compared to mono-culture. In contrast to the findings of Hervé-Jimenez *et al.* (19), the iron complex ABC transporter consisting of *fatA*, *fatB*, *fatC* and *fatD* was expressed 2.7-4.5-fold higher in mixed culture during the second exponential phase. However, the putative iron transport regulator *fur* and the iron chelator *dpr* were 2.4 and 2.9-fold lower expressed in the mixed culture in this growth phase. In stationary phase, these genes were 1.5 and 1.2-fold higher expressed, which is in accordance with a previous study (19), in which it was concluded that *S. thermophilus* lowers its iron uptake in presence of *L. bulgaricus* (26). Indeed, the expression of *fur* and *dpr* is correlated to the expression of *LBUL_2034*, the homologue of *pox1* in *L. bulgaricus* LMG11842, but not with *LBUL_1421* and *LBUL_1955*, the homologues of *pyrD2* and *pyrD1* (19).

EPS biosynthesis. Sugar nucleotide precursors that are used for EPS biosynthesis are also used as intermediates in sugar catabolism, the assembly of peptidoglycan and other glycan-containing cellular polymer, both important for growth. EPS is mainly produced in the later stages of fermentation (5). We observed that S. thermophilus EPS genes (epsA - epsM) were higher expressed in the second exponential phase and especially in the stationary phase compared to the earlier growth phases. In addition, all these genes were higher expressed at these two later phases in the mixed culture compared to the mono-culture, i.e. 2.1 -5.1-fold in the second exponential phase and 2.2-4.0-fold in stationary phase (the transcriptional activator epsA 2.0 and 1.9-fold). Similarly, in the L. bulgaricus (poly)saccharide metabolism many genes were higher expressed in mixed culture compared to mono-culture at the two later growth phases, including several genes in EPS synthesis, indicating that more EPS is produced in mixed cultures. Indeed, the amount of EPS increased from 0.80±0.02 g/L in a S. thermophilus monoculture and 1.18±0.12 g/L in a L. bulgaricus mono-culture to 1.46±0.04 g/L in the mixed culture. However, this increase in EPS production in the mixed culture compared to the mono-cultures (1.3-1.8-fold) is less than would be expected based on the increase in total biomass (4.5-8.5-fold).

Fatty acid metabolism in *L. bulgaricus.* In the three later phases of fermentation, the genes encoding LCFA synthesis by *L. bulgaricus* were 3.3-9.6-fold lower expressed in mixed culture, while in the second exponential and the stationary phase *LBUL_0106* and *LBUL_1256* (both 1-acyl-sn-glycerol-3-phosphate acyltransferase) were 3.1 and 15-fold higher expressed in mixed culture, respectively (see Figure 3B). Therefore, it is likely that this acyltransferase is loaded with fatty acids from the medium in presence of *S. thermophilus*, e.g. liberated from milk fat by its lipolytic activity (33).

Biofilm studies

In order to explore whether the responses to mixed culture growth in milk identified above are generic, we studied interactions with cells residing in a different environment while growing on the same substrate. It has been well documented that cells growing in biofilms are in a physiological state very different from that during planctonic growth (17, 38). In addition, in mixed culture biofilms the high proximity and/or physical contact is likely to amplify interaction response and the phenotypic responses can be easily explored by staining and microscopy or SEM. A series of experiments was performed on mono and mixed cultures growing in biofilms on anopore placed on top of milk agar which aimed to explore the effect on growth as well as regulatory responses at the transcriptome level. Figures 4A-C

show SEM photographs of *S. thermophilus*, *L. bulgaricus* and mixed biofilms. In the mixed biofilm, *L. bulgaricus* cells in particular showed a remarkable increase in cell length compared to mono-culture biofilms. We also observed elongated cells of both species in mixed liquid cultures. This elongation is due to incomplete septation (21) as is exemplified by a transmission electron microscopy photograph of a *S. thermophilus* cell (see Figure 4D).

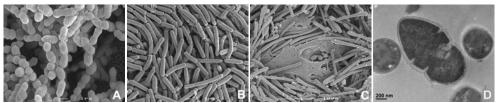


Figure 4. Minicolonies in biofilms grown on anopore slides placed on top of milk agar plates. A-C, SEM images of mono-cultures of *S. thermophilus* (A), *L. bulgaricus* (B) and the mixed culture (C). D, Cross section of a *S. thermophilus* cell displaying the characteristic ring pattern associated with incomplete septation.

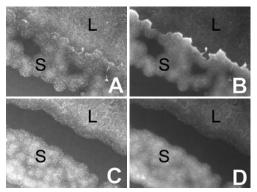


Figure 5. Minicolonies grown in biofilms on anopore slides on milk plates stained with SybrGold (A, C) and Wheat Germ Agglutin (WGA) (B, D). In A and B, colonies of *S. thermophilus* and *L. bulgaricus* are in physical contact leading to a higher staining of WGA at the interphase compared to C and D. S, *S. thermophilus*; L, *L. bulgaricus*.

In addition, there was a large quantity of extracellular matrix present in the mixed biofilm, which was only present at low levels in the mono-culture biofilms. It was hypothesized that this matrix mostly consist of EPS for the following 3 reasons: (i) it is specifically stained with Wheat Germ Agglutin (WGA), a lectin that is suitable for specific staining of EPS in yoghurt (18); (ii) if not protected by osmium tetroxide, the structure collapses as is typically observed with a highly hydrated biopolymer. (iii) Moreover, colonies of *S. thermophilus* and *L. bulgaricus*

in physical contact led to an increase of WGA stain at the interface relative to the interface of two colonies of the same species or to the colonies that are not in contact (see Figure 5). Additional support is provided by a transcription profiling study of mono-culture and mixed culture biofilms (data not shown). There was little differential expression between mono and mixed culture biofilms. However, most of the EPS biosynthesis genes were higher expressed in the mixed culture biofilm (1.2-3.4-fold for *S. thermophilus* and 2.0-5.1-fold for *L. bulgaricus*).

DISCUSSION

The growth pattern with the four distinct growth phases following the lag phase in our study was similar to what was described before (12, 19). Differences may be due to strain-to-strain variation and to our relative low inoculation level $(10^4-10^5 \text{ CFU/mL} \text{ in stead of } 10^6 \text{ CFU/mL} \text{ in the two cited references})$ that was chosen in order to follow the complete fermentation and to be able to identify when in the fermentation interactions between the bacteria become of importance, i.e. around 10^5-10^6 . Growth and acidification was mainly stimulated by formic acid, folic acid, casitone (*S. thermophilus* only) and Tween-20. That is in accordance with literature (11, 13, 14, 16, 29).

The physiology of mixed culture fermentation and strain interaction was further explored with transcriptome analysis in mono and mixed cultures. Transcriptome analysis of *S. thermophilus* in mono (20) and in mixed culture (19) has been reported previously, but only at the second exponential phase. We analyzed gene expression related to the interactions between the yoghurt bacteria through the fermentation. Also the analysis of *L. bulgaricus* is a novel aspect of our study. Gene expression data are supported by the intervention studies and by physiological data (see below). We confirmed that interactions are based on the exchange of folic acid and purine (precursors) and on proteolysis. Moreover, we found that availability of LCFA to *L. bulgaricus* by lipolytic action of *S. thermophilus* is likely a novel mode of interaction and that the genes for EPS synthesis are induced in both strains in co-culture leading to a higher EPS content.

Formic acid and folic acid support growth of *L. bulgaricus*. The high abundance of PFL in *S. thermophilus* in milk and the stimulatory effect of formic acid and folic acid on acidification growth of both species show that purine availability in milk is too low to sustain optimal growth. The folic acid and purine biosynthesis pathways were very highly expressed in *L. bulgaricus* mono-culture, indicating that it was difficult to acquire sufficient purines. The down regulation of

these pathways in combination with the up regulation of PFL and folic acid production in *S. thermophilus* show that formic acid and folic acid were indeed provided by *S. thermophilus* for *L. bulgaricus*. These two components support *L. bulgaricus* growth already during the first exponential phase. The stimulatory effect of nucleobases is evident as they are the end products of purine (and pyrimidine) metabolism.

Amino acid and carbon dioxide metabolism. The proteolytic activity of L. bulgaricus plays a key role in the co-fermentation of S. thermophilus and L. bulgaricus as is exemplified by the large stimulatory effect of addition of hydrolyzed casein to a S. thermophilus culture and the smaller effect to a mixed culture. L. bulgaricus has a very degraded AA synthesis system, which makes the bacterium highly dependent on its proteolytic activity when growing in milk (45) both in monoculture and in mixed culture. That may explain the relatively small number of changes in the expression of AA biosynthetic genes between mono-culture and mixed culture. The cleavage of casein into peptides by PrtB and the higher expression of peptidases in S. thermophilus support higher growth rates of both species in mixed culture. However, the upregulation of BCAA (present 6-7% w/w in casein), arginine (4%) and cysteine (0.35%) biosynthesis pathways shows that the proteolysis by PrtB did not supply a sufficient amount of these AA, as they are relatively highly abundant in the predicted proteins of S. thermophilus (19) and L. bulgaricus (http://www.cbs.dtu.dk/services/GenomeAtlas) compared to their content in casein (41). It was reported before that sulfur AA become limiting for growth of S. thermophilus in the second exponential phase in mono-culture (20) and BCAA in mixed culture as well (19). Our study confirms this observation for S. thermophilus. In addition, cysteine and methionine biosynthesis were overexpressed by both organisms in mixed culture indicating a shortage of these AA in mixed culture. This may also explain why BCAA and sulfur AA pathways remained functional in *L. bulgaricus* unlike many other AA biosynthetic pathways. The up regulation of the urea cycle and carbonate dehydratase shows that CO_2 production is stimulated in mixed culture which favors growth of *L. bulgaricus* (16).

Iron metabolism and H_2O_2 resistance. In stationary phase of the mixed culture, *dpr* and *fur* were higher expressed than in the *S. thermophilus* monoculture. It was shown before that this relates to the expression of *pyrD1* and *pyrD2* and the concomitant production of H_2O_2 by *L. bulgaricus* LMG11842 (19). In our study differential expression of *fur* and *dpr* was comparable to the differential expression of pyruvate oxidase, *LBUL_2034*, in strain ATCC BAA-365. Thus, the intake of iron by *S. thermophilus* is negatively correlated to H_2O_2 production by *L. bulgaricus*, minimizing the damage caused by ROS.

EPS biosynthesis increases upon co-culture. Previously, it was found that EPS production increases in the late exponential and stationary phase in fermentation in mono-culture as well as in mixed culture, but no induction of expression of EPS related genes was observed (20), contradicting our results. We clearly observed the upregulation of genes coding for EPS biosynthesis and secretion in both *S. thermophilus* and in *L. bulgaricus* in liquid mixed culture compared to mono-culture. This was confirmed in biofilm growth using polysaccharide staining, SEM and transcriptome profiling. The higher EPS synthesis may be a direct response to the lower pH in the mixed species systems, since low pH was shown to trigger EPS production by *L. bulgaricus* (31). To date, there has not been assigned a biological function for EPS production by these microbes in yoghurt, but it is not unlikely that EPS causes increased acid resistance (28) or facilitates exchange of metabolites by forcing close proximities or even physical contact between the two species, as is the case in kefir (8, 35).

In conclusion, we have performed a gene expression study of the whole yoghurt system and provided evidence for the involvement of purine metabolism (formic acid and folic acid), proteolysis and LCFA in the interactions between the two consortium members. In addition, we showed that in mixed culture genes for EPS formation are induced leading to a higher EPS content of yoghurt. Finally, iron uptake by S. thermophilus is correlated to its growth rate, but decreased in the later stages of co-fermentation due to the increased production of H₂O₂ by L. bulgaricus. The stimulatory effect of pyruvic acid can be easily explained as this compound plays a central role in the primary metabolism and many other pathways but we found no evidence that the exchange of pyruvic acid is a mode of interaction. Putrescine and ornithine did not show any positive effect on acidification and outgrowth. Neither did we find any obvious differential regulation in transport or processing related to these two compounds between both mono-cultures and the mixed culture, nor any differential expression when putrescine was or was not added to the culture. However, it can not be excluded that there is exchange of these compounds despite the absence of regulatory responses at the RNA level.

Our study provides important information on the molecular basis of this mixed culture fermentation in an industrial or natural environment rather than a laboratory medium. These findings may help to understand other mixed culture systems and provide prospects for engineering interacting mixed cultures, for instance by introducing nutritional dependencies in dairy systems containing probiotics.

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SUPPLEMENTARY MATERIAL

ed culture ove

Supplementary Table 1. Free amino acid content (μ M) of milk and three different cultures after 12 and 24 h of fermentation. ND, not determined, below detection limit.

	Time (h)	Asp	Glu	Asn	Gln	Ser	Thr	Gly	Arg	Ala	Pro	Val	Met	lle	Leu	Trp	Phe	Cys	Lys	His	Tyr
Milk		61	361	1114	541	174	601	145	ND	132	31	ND	ND	19	14	5	10	354	35	24	12
S thermophilus	12	219	389	1083	868	84	554	74	ND	47	61	30	ND	ND	36	ND	42	285	9	21	16
S. thermophilus	24	161	301	1118	1006	339	438	118	49	53	75	44	ND	ND	49	ND	36	234	14	27	20
L. bulgaricus	12	291	633	ND	931	1555	286	960	55	319	486	426	ND	129	371	17	110	394	318	330	303
E. bulganous	12 24	136	632	ND	1122	ND	1447	ND	63	ND	532	378	ND	87	473	16	115	190	331	262	226
	12	108	456	2000	187	1096	1061	262	161	302	372	108	26	19	154	10	80	250	141	71	122
WINEG CUILUIE	24	603	1059	2196	115	584	626	98	170	146	741	342	55	152	266	ND	111	248	245	129	175

Supplementary Table 2. Significant (\geq 2-fold FDR \leq 0.05) differential expression of *S. thermophilus* genes between mixed and mono-cultures and between cultures supplemented with formic acid and cultures without any supplement, per functional category. Values represent ratios between the first and the second condition. Columns 3-6 contain ratios of mixed cultures over mono-cultures in the first exponential phase (3.5 h), reduced growth phase (5.5 h), second exponential phase (8 h) and stationary phase (12 h), respectively. Columns 7 and 8 contain ratios of a culture supplemented with formic acid over one without supplement in the early exponential phase and mid exponential phase, respectively.

			mone	o-culture		Formic ac	id over none	_
Locus ID	Locus	1st exp phase	Transition phase	2nd exp. phase	Stationary phase	1st exp. phase	2nd exp. phase	Product
And an and		ind metabolis						
str0023	prsA1	ind metabolis	m	0.424	0.202	0.283		ribose-phosphate pyrophosphokinase
str0025	araT			0.424	0.317	0.203	2.099	hypothetical protein
str0063	pepS				0.392	0.483	2.033	aminopeptidase PepS
str0125	amiA2				0.253	0.405		oligopeptide ABC transporter substrate-binding protein
str0158	ami/12				2.038			amino acid (glutamine) ABC transporter ATP-binding protein
str0159				3.273	2.047	0.405		amino acid (glutamine) ABC transporter substrate binding protein/permease protein
str0172				0.446			0.420	dipeptide/oligopeptide ABC trasporter permease protein, truncated
str0229	pepC				0.248			cysteine aminopeptidase C
str0283	ureC				0.416			urea amidohydrolase (urease) alpha subunit
str0296	-	0.361	0.056		0.082	6.942		amino acid ABC transporter substrate binding protein, putative
str0298	-		0.149		0.011			succinyl-diaminopimelic descuccinlyasadipeptidase, truncated
str0300	-		0.117		0.013	2.665		succinyl-diaminopimelic descuccinlyasadipeptidase, truncated
str0303	dctA	0.470	0.269		0.174	3.492		dicarboxylate/amino acid:cation (Na+ or H+) symporter
str0352	metB1	0.092	0.025		0.052	7.589		cystathionine gamma-synthase
str0353	-	0.111	0.045		0.117	7.405		aminotransferase (class II)
str0360	livH					0.477		branched-chain amino acid ABC transporter permease protein
str0366	cysM1	0.445	0.100		0.314	6.449		cysteine synthase
str0377	asnA				0.269			asparagine synthetase AsnA
str0430	gdhA				0.500			glutamate dehydrogenase
str0454 str0463	pepB aspC3		0.113		0.165	7.519		oligopeptidase hypothetical protein
str0463 str0464	aspC3		0.219			7.519	0.384	N-acetyl-gamma-glutamyl-phosphate reductase
str0466	argB		0.219				0.355	acetylglutamate kinase
str0466	argD		0.201		2.578		0.335	acetylogiutainate kinase acetylognithine aminotransferase
str0469	hom			2.148	2.570			homoserine dehydrogenase
str0470	thrB			2.140		2.034		homoserine kinase
str0526	carA				2,121	0.445		carbamoyl-phosphate synthase small subunit
str0527	carB				2,145	0.428		carbamoyl-phosphate synthase large subunit
str0555		0.169	0.365	3.100		2.874		alanine dehydrogenase, truncated
str0556		0.319		2.301		8.274		alanine dehydrogenase, truncated
str0583	-	0.468			0.240	6.095		amino acid permease
str0584	mmuM	0.401	0.449		0.317	7.337		homocysteine methyltransferase
str0590	bcaT	2.012			0.304			branched-chain amino acid aminotransferase
str0629	pepQ				2.015			dipeptidase
str0645	aroA				2.798			3-phosphoshikimate 1-carboxyvinyltransferase
str0646	aroK				4.274			shikimate kinase
str0647	pheA				3.613			prephenate dehydratase
str0771	pabB				3.038	0.407		para-aminobenzoate synthetase component I
str0785 str0786	metE	0.036	0.016 0.027		0.019 0.045	8.497 7.964		5-methyltetrahydropteroyltriglutamatehomocysteine methyltransferase
str0786 str0846	metF cvsM2	0.043	0.027		0.415	7.964		5,10-methylenetetrahydrofolate reductase
str0846 str0877	cysiviz				0.415	0.367	0.321	cysteine synthase amino acid (glutamine) ABC transporter, substrate binding protein
str0904						4.197	0.321	hypothetical protein
str0905		0.309	0.227			7.913		hypothetical protein
str0908		0.435	0.273			3.666		ABC transporter substrate binding protein
str0923	als	0.455	0.275	2.128	3.987	5.000		alpha-acetolactate synthase
str0970	dtpT		0.331	2.120	0.144		2,192	di-/tripeptide transporter
str0974	-			2.771	2.366	0.297		ABC transporter substrate binding protein, truncated
str0975				3.287	4.384			ABC transporter substrate binding protein, truncated
str0976	-			3.198	2.549			ABC transporter permease protein, truncated
str0977	-				3.949			ABC transporter permease protein, truncated
str0984	dagA			3.153		0.389	2.263	sodium/alanine glycine symporter
str0987	cysD	0.278	0.201	3.232	0.089	7.222	2.300	O-acetylhomoserine sulfhydrylase
str1007	pepN			2.374	0.451		2.050	lysyl-aminopeptidase, aminopeptidase N
str1061	-			0.353	2.485			hypothetical protein

str1127	pepV				0.489		0.481	dipeptidase amino acid (glutamine) ABC transporter ATP-binding protein
str1161 str1163	-				2.379		0.481	amino acid (glutamine) ABC transporter ATP-binding protein amino acid (glutamine) ABC transporter permease protein
str1164	-				2.715			amino acid (glutamine) ABC transporter permease protein
str1181	aroH				0.306			hypothetical protein
str1203 str1211	leuA				0.333 2.060			2-isopropylmalate synthase
str1222	- metA	0.284	0.263		0.130	2.066		hypothetical protein homoserine O-succinyltransferase
str1287				2.523			3.974	transcriptional regulator, putative
str1297	dapA			2.506	0.400			dihydrodipicolinate synthase
str1298 str1309	asd proWX	0.372			0.429	18.333		aspartate-semialdehyde dehydrogenase proline/glycine betaine ABC transporter
str1310	proV	0.424		2.816		16.210		proline/glycine betaine ABC transporter ATP-binding protein
str1312	proWZ	0.468		2.173	0.291	29.876		proline/glycine betaine ABC transporter substrate-binding protein
str1317	sdaA		0.263		2.109			L-serine dehydratase alpha subunit
str1346 str1347			0.263	0.353				amino acid (glutamine) ABC transporter ATP-binding protein ABC transporter amino acid permease protein
str1357	brnQ			0.555	0.217		2.850	branched chain amino acid transport system II carrier protein
str1389	-						4.027	amino-acid efflux protein, putative
str1438	amiF1	0.488	0.389	2.748		3.921		oligopeptide ABC transporter ATP-binding protein
str1439 str1440	amiE amiD	0.447	0.229	2.451		2.141		oligopeptide ABC transporter ATP-binding protein oligopeptide ABC transporter membrane-binding protein
str1441	amiC	0.111	0.301	2.784	0.393	3.075		oligopeptide ABC transporter membrane-binding protein
str1442	-				0.239			oligopeptide ABC transporter substrate-binding protein, truncated
str1443 str1445	- amiA3		0.438	2.350	0.423 0.323	2.564	2.127	oligopeptide ABC transporter substrate-binding protein, truncated
str1445 str1447	-		0.432	3.331	0.323	4.711	2.127	oligopeptide ABC transporter substrate-binding protein oligopeptide ABC transporter ATP-binding protein, truncated
str1448	-			0.440	0.249			oligopeptide ABC transporter ATP-binding protein, truncated
str1461	nifS3	2.109						aminotransferase (class V), putative
str1519 str1527	serB serA			2.089	4.050 0.169		2.536	phosphoserine phosphatase D-3-phosphoglycerate dehydrogenase
str1529	serC		0.373	2.445	0.196		2.000	phosphosphograde denydrogenase
str1579	-	0.305	0.158	2.084	0.236	12.993		amino acid (glutamine) ABC transporter substrate binding protein
str1580	-	0.249	0.138		0.140	18.328		amino acid (glutamine) ABC transporter ATP-binding protein
str1581 str1582	-	0.263	0.158		0.208	13.125 16.197		amino acid (glutamine) ABC transporter permease protein amino acid (glutamine) ABC transporter permease protein
str1589	- trpF	0.200	0.176		0.140	23.120		N-(5'-phosphoribosyl)anthranilate isomerase
str1590	trpC					2.615		indole-3-glycerol-phosphate synthase
str1591	trpD					23.842		anthranilate phosphoribosyltransferase
str1592 str1593	trpG trpE					9.455 2.894		anthranilate synthase component II
str1636	aspC2				0.463	2.034		anthranilate synthase component I aspartate aminotransferase
str1652	-	0.461	0.425	2.091	0.405	2.352		ABC transporter ATP-binding protein, amino acid
str1653	-	0.467	0.423	2.354	0.489			ABC transporter amino acid permease protein
str1654 str1710	- proA		0.380	2.320	0.331 0.180			ABC transporter substrate-binding protein, amino acid gamma-glutamyl phosphate reductase
str1710	proA				0.192			gamma-glutamyl kinase
str1812	argH			0.218				argininosuccinate lyase
str1813	argG			0.445				argininosuccinate synthase
str1839 str1871	dapD ilvC				0.342		2.069	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase, putative
str18/1 str1872	ilvC ilvN				0.351		2.069	ketol-acid reductoisomerase acetolactate synthase small subunit
str1873	ilvB				0.231			acetolactate synthase large subunit
str1972	-				0.393			hypothetical protein
str1973	-				0.394	3.484		hypothetical protein
	roto tropoport	and motobol	l'ana					
Carbohyd								
Carbohyd str0114	gpmB	2.969	lism	0.487	0.487			phosphoglycerate mutase
str0114 str0189	gpmB -	2.969	lism	0.487		0.376		PTS glucose-specific enzyme IIABC components, truncated
str0114 str0189 str0190	gpmB -	2.969	lism	0.487	0.433	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated
str0114 str0189	gpmB - -	2.969	lism	0.487		0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated
str0114 str0189 str0190 str0191 str0194 str0219	gpmB - - - pgi -	2.969	iism	0.487	0.433 0.422 0.420	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DecR family
str0114 str0189 str0190 str0191 str0194 str0219 str0312	gpmB - - - pgi - tkt	2.969	iism	2.855	0.433 0.422	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0399	gpmB - - pgi - tkt fruR	2.969	lism	2.855 0.475	0.433 0.422 0.420	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional regressor
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0399 str0400	gpmB - - - pgi - tkt	2.969	lism	2.855	0.433 0.422 0.420	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional repressor fructose-1-phosphate kinase
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0399 str0400 str0401 str0405	gpmB - - pgi - tkt fruR	2.969		2.855 0.475 0.335 0.324 0.307	0.433 0.422 0.420	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional repressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0309 str0400 str0405 str0407	gpmB - - pgi - tkt fruR fruB - -	2.969	1.SM 2.297	2.855 0.475 0.335 0.324	0.433 0.422 0.420 0.369	0.376		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transcriptional regulator, DeoR family transcriptional repressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0309 str0400 str0401 str0407 str0488	gpmB - - pgi - tkt fruR fruB - - tpiA	2.969		2.855 0.475 0.335 0.324 0.307	0.433 0.422 0.420 0.369 0.372	0.376		PTS glucose-specific anzyme IIABC components, truncated PTS glucose-specific anzyme IIABC components, truncated PTS glucose-specific anzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional regulator, DeoR family fructose-1-phosphate kinase PTS fructose-specific anzyme IIABC components, truncated PTS fructose-specific anzyme IIABC components, truncated PTS fructose-specific anzyme IIABC components, truncated PTS fructose-specific anzyme IIABC components, truncated
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0399 str0400 str0401 str0405 str0407 str0488 str0501	gpmB - - pgi - tkt fruR fruB - -	2.969		2.855 0.475 0.335 0.324 0.307	0.433 0.422 0.420 0.369		0.314	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-photophate isomerase transcriptional regulator, DeoR family transcriptional genesion transcriptional genesion Transcription T
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0302 str0400 str0401 str0405 str0407 str0488 str0501 str0512	gpmB - - - tkt fruR fruB - - tpiA nagA - -	2.969		2.855 0.475 0.335 0.324 0.307	0.433 0.422 0.420 0.369 0.372 0.498	0.376	0.314 0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional repressor https://www.internet.org/ https://wwww.internet.org/ https://www.internet.org/ https://www.internet.org/ https://www.internet.org/ https://wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww
str0114 str0189 str0190 str0191 str0194 str0219 str0219 str0219 str0400 str0400 str0405 str0405 str0405 str0408 str0501 str0488 str05501 str0513 str0541	gpmB - - - tkt fruR fruB - - tpiA nagA - nagB	2.969	2.297	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372			PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional repressor fructose-1-phosphate isomerase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated truncated enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated trutosethosphate isomerase trutosethosphate isomerase beta-glucosite-specific PTS system IIABC component, truncated beta-glucosite-specific PTS system IIABC component, truncated plucosamine-chopsphate isomerase
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0399 str0400 str0405 str0407 str0405 str0407 str0488 str0501 str0512 str0513 str0541 str0535	gpmB - - - tkt fruR fruB - - tpiA nagA - - nagB eno	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307	0.433 0.422 0.420 0.369 0.372 0.498 0.448			PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional regulator, DeoR family tructose-1-phosphate isomerase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated trustose-toposphate isomerase N-activglucosamine-6-phosphate deacetvipsen beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase
str0114 str0189 str0190 str0191 str0194 str0219 str0219 str0219 str0400 str0400 str0405 str0405 str0405 str0408 str0501 str0488 str05501 str0513 str0541	gpmB - - - tkt fruR fruB - - tpiA nagA - nagB	2.969	2.297	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372 0.498			PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerane transcriptional regulator, DeoR family transcriptional regressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated troscephosphate isomerase N-acatylglucosamine-6-phosphate leadontylesa N-acatylglucosamine-6-phosphate IIABC component, truncated beta-glucosatio-specific PTS system IIABC component, truncated beta-glucosatio-specific PTS system IIABC component, truncated beta-glucosatio-specific PTS system IIABC component, truncated phosphopyrovate hydratase phosphopyrovate hydratase
str0114 str0180 str0190 str0191 str0194 str0219 str0219 str0219 str0312 str0312 str0400 str0400 str0405 str0407 str0405 str0407 str0501 str0551 str0551 str0551 str0551 str0551 str0687 str0895 str09895	gpmB - - - tkt fruR fruB - - tpiA nagA - - nagB eno	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016	0.377		PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transcriptional regulator, DeoR family Transcriptional regulator, DeoR family PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated trosephosphate isomerase N-acetylglucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated phosphopynovale hydratase phosphopynovale hydratase transcriptional regulator inositiol monphosphatase family protein
str0114 str0189 str0191 str0194 str0219 str0219 str0212 str0399 str0400 str0405 str065 str0605	gpmB - - - - - - - - - - - - -	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232		0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transketolase transcriptional regulator, DeoR family transketolase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated tritosephophate isomerase N-acetylglucosamine/Enzyme IIABC component, truncated bits/glucosamine/Enzyme IIABC component, truncated glucosamine/6-phosphate isomerase phosphopyuvaria hydratase phosphopyuvaria hydratase phosphopyuvaria mutase transcriptional regulator inostiol monophosphatase family protein dycogen phosphorykase
str0114 str0189 str0190 str0191 str0194 str0219 str0302 str0309 str0401 str0407 str0407 str0408 str0407 str0408 str0512 str05512 str05512 str0551 str05512 str0697 str08999 str1012 str018999	gpmB - - - - - - - - - - - - - - - - - - -	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016	0.377	0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transcriptional regulator, DeoR family TS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated TTS fructose-specific enzyme IIABC component, truncated trosephosphate isomerase N-acetylglucosamine-6-phosphate leacetylase beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase phosphophysele phosphate isomerase transcriptional regulator transcriptional regulator transcriptional regulator inostoil monpohosphatase family protein apdicogen phosphorykase matose-imatodextrin ABC transporter permease protein, truncated
str0114 str0189 str0191 str0194 str0219 str0219 str0212 str0399 str0400 str0405 str065 str0605	gpmB - - - - - - - - - - - - - - - - - - -	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016	0.377	0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transktolase transcriptional regulator, DeoR family truncase-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated trusseptophate isomerase beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase phosphopyruvale hydratase phosphopyruvale hydratase phosphopyruvale hydratase phosphopyruvale hydratase matose/matodextrin ABC transporter permease protein, truncated hydrogen phosphorylase matose/matodextrin ABC transporter permease protein, truncated hydrogen phosphorylase
str0114 str0189 str0190 str0191 str0194 str0219 str0219 str0401 str0401 str0400 str0400 str0400 str0400 str0400 str0407 str0407 str0513 str0551 str0551 str0599 str0513 str05999 str1017 str1077 str1120	gpmB - - - - - - - - - - - - - - - - - - -	0.450	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332 0.458 2.082	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016	0.377	0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerse transcriptional repressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated truse-tephosphate isomerse IIABC components, truncated PTS fructose-specific enzyme IIABC component, truncated truse-tephosphate isomerse hoter-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated phosphopyrovate hydratase phosphopyreate nutase transcriptional regulator inosiolin omophosphates fransporter mutase dycogen phosphopyreate many set transporter protein dycogen phosphopyreater protein typophetical protein exoptysaccharide polymerization protein phosphopyrounder bydrates
str0114 str0189 str0190 str0191 str0194 str0219 str0219 str0400 str0400 str0400 str0405 str0405 str0405 str0405 str0405 str0405 str0408 str0512 str0513 str0521 str0553 str059 str059 str059 str01012 str0685 str0999 str1012	gpmB - - - - - - - - - - - - - - - - - - -	2.969	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332 0.458 2.082	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016 2.175	0.377	0.357 0.500 3.862	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transluctogenetic enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase phosphopyrunate hydratese phosphopyrunate hydratese phosphopyrunate hydratese phosphoptic regulator inositol monophosphates and the protein matlose-matinedextrin ABC transporter permease protein, truncated hypothetical protein exponytasecharde polymerization protein phosphoptic protein phosphate isomerase A
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0312 str0400 str0401 str0405 str0407 str04488 str0511 str06512 str0405 str0657 str0657 str0657 str06999 str1012 str1017 str1028 str1017 str1121	gpmB - - - - - - - - - - - - - - - - - - -	0.450	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332 0.458 2.082	0.433 0.422 0.369 0.372 0.498 0.448 7.232 10.016 2.175	0.377	0.357	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulation, DeoR family transcriptional regulation, DeoR family transcriptional regulation, DeoR family PTS fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC component, truncated PTS fructose-specific enzyme IIABC component, truncated trosephosphate isomerase N-aactylglucosamine-6-phosphate laced beia-glucosatio-expecific PTS system IIABC component, truncated beia-glucosatio-expecific PTS system IIABC component, truncated glucosamine-6-phosphate Isomerase phosphopyrovate hydratase phosphopyrovate hydratase transcriptional regulator inositiol monphosphatase family protein glycogen phosphoryneate family protein phosphopyroterate phosphopyroterate mutase transcriptional regulator inosition monphosphatase family protein glycogen phosphopyreates phosphopyroterate mutase transcriptional regulator inosition monphosphatase family protein phosphopyroterate mutase transcriptional segulator inosition monphosphatase family protein phosphopyroterate mutase transcriptional segulator inosition monphosphate isomerase A phosphopyroteratemutase
str0114 str0189 str0190 str0191 str0194 str0219 str0219 str0400 str0400 str0400 str0400 str0401 str0405 str0405 str0405 str0408 str0512 str0513 str0521 str0523 str0533 str0513 str0523 str0533 str052	gpmB - - - - - - - - - - - - - - - - - - -	0.450	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332 0.458 2.082	0.433 0.422 0.420 0.369 0.372 0.498 0.448 7.232 10.016 2.175 0.250 2.514	0.377	0.357 0.500 3.862	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transluctures transcriptional regulator, DeoR family Transluctures Transluctures Truncated enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC component, truncated PTS fructose-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase phosphopyruvate hydratase phosphopyruvate hydratase matiose/matiodextrin ABC transporter permease protein, truncated hydrogen riposphoralise matiose/matiodextrin ABC transporter permease protein, truncated hydrogen phosphopyruse matiose/matiodextrin ABC transporter permease protein, truncated hydrogen phosphopyrusae matiose/matiodextrin ABC transporter permease protein, truncated hydrogen phosphopyrusae matiose/matiodextrin ABC transporter permease protein, truncated hydrogen phosphopyrusae hydrogen phosphate isomerase A phosphopyruser protein phosphopyruser protein phosphate isomerase A phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphate isomerase A phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyruser protein phosphopyr
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0400 str0400 str0405 str0405 str0405 str0405 str0405 str0405 str0405 str0512 str051	gpmB - - - - - - - - - - - - - - - - - - -	0.450	2.297 2.230	2.855 0.475 0.335 0.324 0.307 0.332 0.458 2.082	0.433 0.422 0.369 0.372 0.498 0.448 7.232 10.016 2.175 0.250 2.514 2.914	0.377	0.357 0.500 3.862	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomerase transcriptional regulator, DeoR family transletubase transcriptional regulator, DeoR family transletubase transcriptional regulator, DeoR family PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated trossephosphate isomerase N-acetylglucosamine-6-phosphate deacetytese beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase phosphopyruate hydratese phosphopyruate hydratese phosphopyruate hydratese matloseimatiodextirn ABC transporter permease protein, truncated hydrogen phospholatese matloseimatiodextirn ABC transporter permease protein, truncated hydrogehate isomerase A phosphopyrumutase transcriptional protein phosphopyrumutase, putative phosphopyrumutase, protein phosphopyrumutase, putative phosphopyrumutase, putative phosphopering protein Pr(histidine-containing protein)
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0312 str0401 str0401 str0405 str0407 str0405 str0405 str0407 str0405 str0405 str0405 str0405 str0407 str0505 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str0407 str0405 str040	gpmB 	0.450	2.297 2.230 2.020	2.855 0.475 0.324 0.325 0.307 0.307 0.332 0.458 2.082 2.629	0.433 0.422 0.369 0.372 0.496 0.448 7.232 10.016 2.175 0.250 2.514 2.514 2.514 2.53	0.377	0.357 0.500 3.862	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-t-phosphate isomerase transcriptional regulator, DeoR family transcriptional regulator, DeoR family TS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC component, truncated trosephosphate isomerase N-acetylglucosamine-6-phosphate leacetylase beta-glucoside-specific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase hosehophosphates pecific PTS system IIABC component, truncated glucosamine-6-phosphate isomerase transcriptional regulator inositol monpohosphatase family protein aptosematicated polymerization protein phosphophophates family phosphophophates family phosphophophates family phosphophophates family phosphophophates family phosphophophophates fami
str0114 str0189 str0190 str0191 str0194 str0219 str0312 str0400 str0400 str0405 str0405 str0405 str0405 str0512 str0408 str0512 str051	gpmB 	0.450	2.297 2.230 2.020	2.855 0.475 0.335 0.324 0.327 0.352 0.458 2.082 2.629 0.482	0.433 0.422 0.369 0.372 0.498 0.448 7.232 10.016 2.175 0.250 2.514 2.914	0.377	0.357 0.500 3.862 2.348	PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated PTS glucose-specific enzyme IIABC components, truncated glucose-t-phosphate isomerase transcriptional repressor fructose-t-phosphate isomerase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated truse-tephosphate isomerase Holds enzyme IIABC component, truncated beta-glucoside-specific PTS system IIABC component, truncated beta-glucoside specific PTS system IIABC component, truncated hypothetical protein matose-5-phosphate isomerase A phosphoglucoremutase truse-5-phosphate isomerase, truncated phosphognetic protein Protein phosphognetic protein Protein
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Mixed culture transcriptome analysis

str0131 str0163	- rgpG				0.363 0.193			mechanosensitive ion channel, putative polysaccharide biosynthesis protein
str0349	murE	2.269	2.484		4.340			UDP-N-acetylmuramoylalanyl-D-glutamate2,6-diaminopimelate ligase
str0563	gcaD			2.064				UDP-N-acetylglucosamine pyrophosphorylase
str0569	-				0.451			glycosyl transferase, family 1
str0636 str0699	-			3.109	6.616 4.189			hypothetical protein endolysin, putative
str0721	-				4.189			hypothetical protein
str0733	divIB				2.539			cell division protein
str0762	dltB			2.551	2.312			integral membrane protein
str0764 str0873	dltD glmS			2.119 2.988	2.627		4.304	extramembranal protein D-fructose-6-phosphate amidotransferase
str0873 str1046	gims			2.966			4.304	endolysin, putative, truncated
str1073	epsX			0.001	0.075		0.200	lipopolysaccharide 1,6-galactosyltransferase
str1077	epsL			2.629				exopolysaccharide polymerization protein
str1080	epsl			4.044	3.657			exopolysaccharide biosynthesis protein, sugar transferase
str1082 str1083	epsG	0.456		5.117 2.507	3.457 2.470			exopolysaccharide biosynthesis protein, glycosyltransferase exopolysaccharide biosynthesis protein, UDP-galactopyranose mutase, truncated
str1085	- epsE			2.178	2.470			exopolysaccharide biosynthesis protein
str1167	murA				0.401			UDP-N-acetylglucosamine 1-carboxyvinyltransferase
str1242	rmIB				3.221			dTDP-glucose-4,6-dehydratase
str1297	dapA			2.506			2.110	dihydrodipicolinate synthase phosphinothricin acetyltransferase, putative
str1301 str1311	- proWY	0.401	0.392	2.415		15.697	2.110	prosprinotrincin acetytransferase, putative proline/glycine betaine ABC transporter membrane-spanning protein
str1400	galE1	0.401	0.002	2.410	0.477	10.001		UDP-glucose 4-epimerase
str1413	-	5.956					2.766	putative glutamatecysteine ligase
str1467 str1468	rgpF	0.470		2.689				polysaccharide biosynthesis protein
str1468 str1469	rgpE rgpD	0.478		4.034 3.622				polysaccharide biosynthesis protein/putative glycosyltransferase polysaccharide ABC transporter ATP-binding protein
str1470	rgpC	0.364		4.327				polysaccharide ABC transporter membrane-spanning protein
str1471	rgpB			2.627				polysaccharide biosynthesis protein/putative rhamnosyl transferase
str1472	rgpA			3.881				polysaccharide biosynthesis protein/putative rhamnosyl transferase
str1476 str1478		0.486		2.267 2.508				glycosyl transferase glycosyl transferase, truncated
str1479		0.488		6.948				glycosyl transferase
str1485	-			2.031				glycosyl transferase, family 2
str1560	murZ			3.757	0.347	0.485		UDP-N-acetylglucosamine 1-carboxyvinyltransferase
str1576 str1607	murF			3.151	0.486			UDP-N-acetylmuramoylalanine-D-glutamyl-lysineD-alanyl-D-alanine ligase hypothetical protein
str1629		0.272			0.400	8.226		hypothetical protein
str1869	pbp1B				0.350			penicillin-binding protein 1B
str2006	-				0.028			conserved hypothetical protein, LysM domain protein
Cell motili	y and secretic	m						
str0356	clpP					0.386		ATP-dependent Clp protease proteolytic subunit
str0722	pilD			0.335				prepilin peptidase type IV
str0889 str0896	ffh dprA			0.339	3.075		3.346	signal recognition particle DNA processing protein, Smf family
str1730	secA			2.020	3.075			translocase
str1860	-			0.222				competence protein, putative
str1862	comGD	2.599		0.174				competence protein
str1863 str1864	comGC comGB			0.180 0.168				late competence protein, exogenous DNA-binding protein late competence protein, ABC transporter subunit
str1865	comGA	0.348		0.054	0.237			late competence protein, ABC transporter subunit
str1914	secY			2.036				preprotein translocase SecY
Coenzym	e metabolism							
str0092	panE		0.337		0.116			2-dehydropantoate 2-reductase (ketopantoate reductase)
str0123	thiD				2.113			phosphomethylpyrimidine kinase
	pncB				0.398			nicotinate phosphoribosyltransferase
str0226								
str0227	nadE folC1	2.105			0.434		0.420	NAD(+) synthetase
str0227 str0409	nadE folC1 -	2.105 3.888			0.434 3.675		0.439	NAD(+) synthetase folylpolyglutamate synthase / dihydrofolate synthase
str0227 str0409 str0545 str0590					0.434		0.439 7.274	NAD(+) synthetase folyboydjutamate synthase / dihydrofolate synthase molybdopterin biosynthesis protein (HesAMoeB/ThiF family protein), putative, truncated branched-chain amino acid aminotransferase
str0227 str0409 str0545 str0590 str0771	folC1 - bcaT pabB	3.888 2.012			0.434 3.675 0.273		0.439 7.274	NAD(+) synthetase folyloplyglutamate synthase / dihydrofolate synthase molydopterin biosynthesis protein (HesA/MeeB/ThF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzotate synthetase component I
str0227 str0409 str0545 str0590 str0771 str0789	folC1 - bcaT pabB dfp1	3.888 2.012 2.110			0.434 3.675 0.273 0.304		0.439 7.274	NAD(1+) synthetase foly/polyditamate synthase / dihydrololate synthase motybdopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopantothonyclysteine synthase/decarboxylase
str0227 str0409 str0545 str0590 str0771 str0789 str0790	folC1 - bcaT pabB dfp1 dfp2	3.888 2.012		2 044	0.434 3.675 0.273 0.304 3.038		7.274	NAD(+) synthetase (bi/polyglutamate synthase / dihydrofolate synthase molybdopterin biosynthesis protein (HesA/MoeB/ThF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzotale synthase component I phosphopantothenoy(cysteine synthase/decarboxylase hypothetical protein
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826	folC1 - bcaT pabB dfp1	3.888 2.012 2.110		2.044	0.434 3.675 0.273 0.304		0.439 7.274 2.600	NAD(P) synthetase foly/polyditamate synthase / dihydrololate synthase motybdopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopantothonyclysteine synthase/decarboxylase hypothetical protein 6-pyruxyl tetralydroblopterin synthase, putative
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA	3.888 2.012 2.110 2.124			0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122		7.274	NAD(1+) synthetase foly/colydiamate synthase / dihydrotolate synthase motybdopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branchet-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopantohenov(tysteine synthase/decarboxylase hypothetical protein 6-pyruvoyl tetralydroblopterin synthase, putative alpha-acetolactate synthase [poate-protein liase
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK	3.888 2.012 2.110		2.128	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056		7.274	NAD(P) synthetase foly/polyditurante synthase / dihydrotolate synthase motyAcopterin biosynthesis protein (HesA/MoeB/ThF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphogantothenov(pysteine synthase/decarbox/tase fis-privacyl terahydrotolopterin synthase, putative alpha-aceditactate synthase lipoate-protein ligase 5-adenosylmethoniene synthetase
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172 str1284	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA	3.888 2.012 2.110 2.124 0.404		2.128	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122		2.600	NAD(1+) synthetase foly/colyditurante synthase / dihydrotolate synthase motybdopterin biosynthetas protein (HesA/MoeB/ThiF family protein), putative, truncated branchet-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopartohenov(tysteine synthase/decarboxylase hypothetical protein 6-pyruxoyl tetralydroblopterin synthase, putative alpha-acetolactate synthase [poate-protein ligase 5-adenosylmethionine synthetase pyridoxine kinase
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK	3.888 2.012 2.110 2.124		2.128	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056		7.274	NAD(P) synthetase foly/polyditurate synthase dolydpolyditurate synthase (dihydrotolate synthase motydoopterin biosynthetass protein (HesA/MoeB/ThF family protein), putative, truncated branched-hain amino acid aminotransferase para-aminobenzoate synthetase component I phosphoganothenov(pysteine synthase/decarbox/Jase hypothetical protein gatha-acedicated synthase lipoate-protein ligase S-adenosyntemionine synthetase pyrtidoxine kinase putative glidamate-cysteine ligase
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172 str1284 str1413 str1527 str1529	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK pdxK - serA serC	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195		7.274 2.600 2.766	NAD(P) synthetase foly/oplyditurate synthase (dilydotopterin biosynthetas protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopantofinon/cysteine synthase/decarboxytase hypothetical protein 6-privroyl teta/ydotopterin synthase, putative apha-aeotolactate synthetase S-adenosynthetionine synthetase pytidoxine kinase putative dutamate-cysteine ligase D-3-phosphosphocyterate dehydrogenase
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172 str1284 str1413 str1527 str1529	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK pdxK - serA serC trpG	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.169	9.455	7.274 2.600 2.766	NAD(P(+) synthesize foly(c))quitants synthase dihydrotolatants synthase dihydrotolatants synthase dihydrotolatants synthase para-aminobenzoate synthetase component I phosphopantohenoy(systeine synthase/decarboxylase hydrothenoy(systeine synthase/decarboxylase hydrothenoy(systeine synthase) e/pruvoy Iteralydroblopterin synthase, putative alpha-acetolactate synthase Boate-protein ligase S-adenosylmethionine synthase putative glutamate-cysteine ligase D-3-phosphoyloverate ddirytogenase phosphoserine aminotransferase anthranitate synthase component II
str0227 str0249 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172 str1284 str1413 str1527 str1592 str1593	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK pdxK - serA serC trpE	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196	9.455 2.894	7.274 2.600 2.766 2.536	NAD(P) synthetase ' foly/colyditurate synthase dihydrotolate synthase motyAdopterin biosynthetas protein (HesA/MoeB/ThiF family protein), putative, truncated branchet-chain amino acid aminotransferase para-aminobenzoate synthetase component I phosphopantolinenoy(bysteine synthase/decarbox/lase hypothetical protein 6-privroyl tetrahydrobiopterin synthase, putative alpha-acetolactate synthese lipotate-protein ligase pyridovine kinase pyridovine kinase pyridovine kinase putative glamate-cysteine ligase D-3-phosphospine aminotransferase anthraniate synthase component I
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0826 str0923 str1009 str1172 str1284 str1413 str1527 str1592 str1592 str1593 str1871	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpE ilvB	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.169	2.894	7.274 2.600 2.766 2.536 2.069	NAD(P) synthesize foly/polyditurate synthase motyAdopterin biosynthesis protein (HesA/MeeB/ThiF family protein), putative, truncated branchet-chain amino acid aminotransferase para-aminobenzoate synthesize component I phosphopantoheno/tysteine synthase/acarbox/lase trypothetical protein 6-privucyl tetrahydrobiopterin synthase, putative alpha-acetolacitate synthase S adenosylmethicnine synthesize S adenosylmethicnine synthesize polarity protein aminotransferase polarity protein aminotransferase polarity protein aminotransferase anthraniate synthase component II hortsphosen aminotransferase anthraniate synthase component II ketol-acid reductoisomerase acetolacitate synthase subunit
str0227 str0249 str0545 str0590 str0771 str0789 str0790 str0826 str0826 str0823 str10023 str10023 str10284 str1413 str1527 str1529 str1529 str1593 str1871	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA metK petK - serA serC trpG trpE ilvC	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.196		7.274 2.600 2.766 2.536	NAD(P) synthelase ' folylopbyttamate synthase dihydrotolate synthase motydopterin biosynthelas protein (HesA/MoeB/ThF family protein), putative, truncated branched-hain amino adid aminotransferase para-aminoberizoate synthelase component I phosphoganothenov/psiane synthase/decarboxylase dipase-totelase synthases, putative alpha-acetotacted synthase ipoate-protein ligase S-adenosynthetionine synthetase pyridoxine kinase putative glutamate-cysteline ligase D-3-phosphoglycerate dehydrogenase anthraniate synthase component II anthraniate synthase component II anthraniate synthase component II
str0227 str0409 str0545 str05590 str07789 str07789 str0789 str0789 str0789 str0789 str0789 str0789 str0789 str0789 str0789 str0789 str1284 str1527 str1592 str1592 str1592 str1592 str1873 str1873	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpE ilvB	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089 2.445	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.196	2.894	7.274 2.600 2.766 2.536 2.069	NAD(P) synthelase i dylopolydiumate synthase divlycholydiumate synthase divlycholydiumate synthase para-aminobenzoate synthelase component I phosphogantohnovi(systeine synthase/decarbox/lase typothelad protein typothelad protein synthase/decarbox/lase typothelad protein synthase/decarbox/lase typothelad protein synthase by typothelase typothelad protein synthase by typothelase typothelad by typothelase phosphospine aminotransferase anthranilate synthase component I anthranilate synthase by typothelad by thase by typothelad by thase by typothelad by thase by typothelad by thase by typothelad by typothe
str0227 str0409 str0545 str05590 str07789 str07780 str0780 str0780 str0780 str0780 str0783 str0780 str0783 str0783 str0783 str1274 str1529 str1529 str1553 str1553 str1553 str1573 str1544 Defense n str0874	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.196	2.894 3.726	 7.274 2.600 2.766 2.536 2.069 3.868 	NAD(P) synthetase (bly/pc)gutanate synthase / dihydrololate synthase motydoopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthesiae component I phosphopantothenoy(bysteine synthase), putative alpha-acetolactate synthesiae portactive transformation (poate-protein ligae S-adenosylmethionine synthese putative glutamate-cysteline ligae D-3-phosphojoverate derlyndogenase phosphoserine aminotransferase anthranilate synthase component I anthranilate synthase component I anthranilate synthase component I acrotocates pythase lange suburit bacteriocin biosynthesis protein, putative
str0227 str0409 str0545 str05590 str07789 str07789 str0789 str0789 str0789 str0789 str0789 str1029 str1284 str1029 str1284 str1592 str1593 str	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.196 0.351 0.231	2.894	7.274 2.600 2.766 2.536 2.069 3.868 5.179	NAD(P) synthesiae iolylopbylutanate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-hain amino acid aminotransferase para-aminobenzoate synthesiae component I phosphopantofinonyloysteine synthase/decarboxylase hypothetical protein 6-privroyl tetralydrobloprerin synthase, putative alpha-aetolactate synthase S-adenosynthethonine syntheses pytidixvine kinase putative glutamate-cysteine ligase D-3-phosphogthogycerate dehydrogenase anthraniate synthase component II ketol-acid reductoiscomerase actolactate synthase toutine bactelicine biosynthesis protein, putative hypothetical protein bactelicine biosynthesis protein, putative
str0227 str0409 str0545 str05590 str07789 str07789 str0789 str0789 str0789 str0789 str0789 str1274 str1529 str1529 str1529 str1553 str1553 str1544 Defense n str0874	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404	0.373	2.128 0.230 2.089 2.445	0.434 3.675 0.273 0.304 0.304 0.215 3.987 2.122 0.056 0.195 0.195 0.195 0.195 0.195	2.894 3.726	 7.274 2.600 2.766 2.536 2.069 3.868 	NAD(P) synthesiae iolylopbylutanate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-hain amino acid aminotransferase para-aminobenzoate synthesiae component I phosphopantofinonyloysteine synthase/decarboxylase hypothetical protein 6-privroyl tetralydrobloprerin synthase, putative alpha-aetolactate synthase S-adenosynthethonine syntheses pytidixvine kinase putative glutamate-cysteine ligase D-3-phosphogthogycerate dehydrogenase anthraniate synthase component II ketol-acid reductoiscomerase actolactate synthase toutine bactelicine biosynthesis protein, putative hypothetical protein bactelicine biosynthesis protein, putative
str0227 str0409 str0545 str0590 str0771 str0780 str0780 str0780 str0780 str0828 str1093 str1093 str1227 str1243 str1433 str1592 str1593 str1595 str159	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.196 0.351 0.231	2.894 3.726	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024	NAD(P) syntheliae ' folylopbytimate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF family protein), putative, truncated branched-hain amino adid aminotransferase para-aminoberizoate synthesis ecomponent I phosphoganuthenyolystaine synthase/decarbox/tase brosphoganuthenyolystaine synthase/decarbox/tase epyruxoyl tertahydrotolopterin synthase, putative ajpha-acetotactate synthase syntaes/decarbox/tase pyridoxine kinase putative glutamate-cysteline ligase D-3-phosphogiverate derlydrogenase partificatione synthase component I anthranitate synthase component II anthranitate synthase component II anthranitate synthase component II anthranitate synthase component II bacteriocin biosynthesis protein, putative, truncated bacteriocin bielinmmuthy protein, putative, truncated bacteriocin bielinmmuthy protein, putative, truncated peptide ABC transporter ATP binding/permesse protein, truncated peptide ABC transporter ATP binding/permesse protein, truncated
str0227 str0409 str0545 str0550 str0771 str0789 str0789 str0789 str0789 str0782 str0782 str0782 str1022 str1284 str1284 str1413 str1527 str1284 str1413 str1527 str1592 str159	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453 0.387	0.434 3.675 0.273 0.3038 0.215 3.987 2.122 0.056 0.195 0.196 0.351 0.231	2.894 3.726	7.274 2.600 2.766 2.536 2.069 3.868 5.179	NAC(P) synthesize ' folycolygiturate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminofransferase para-aminobenzoate synthesiae component I phosphopantolinony(systeine synthase), epitative alpha-acetolactate synthesiae optimum synthesiae pyridovine kinase pyridovine kinase pyritekine pyritekine pyritekine pyritek ABC transporter ATP binding/permesse protein, funcated peptide ABC transporter ATP binding/permesse protein, funcated pyridovine kinase pyritekine pyritekinekine pyritekine pyritekine pyritekine pyritekine pyritekine py
str04227 str0409 str0545 str0590 str0771 str0780 str0780 str0780 str0828 str10923 str10923 str10923 str10923 str1172 str1243 str1413 str1527 str1582 s	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.351 0.231 0.251 0.231	2.894 3.726	7.274 2.600 2.766 2.536 3.868 5.179 8.024 8.181	NAC(P) synthesize ' folycolygiturate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-hain amino acid aminofransferase para-aminobenzoate synthesiae component I phosphopantolinony(systeine synthase), epitative alpha-acetolactate synthesiae optimum synthesiae pyridovine kinase pyridovine kinas
str0227 str0409 str0545 str0590 str0771 str0789 str0790 str0790 str1029 str1029 str1284 str1413 str1529 str1553 str1553 str1553 str157	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK pdxK - serA serC trpG trpG trpE ilvB mccB	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453 0.387	0.434 3.675 0.273 0.3038 0.215 3.987 2.122 0.056 0.195 0.196 0.351 0.231	2.894 3.726	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256	NAC(+) synthesize ' folycolyditurante synthase dihydrotolate synthase motydoopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branched-chain amino acid aminofransferase para-aminobenzoate synthesiae component I phosphopantolinenoy(systeine synthase), epitative alpha-aetolacitate synthesiae optimum lise Soate protein lise Soate protein lise Soate protein lise Dava-phosphoghocyntae lise Soate protein aminotransferase Dava-phosphoghocyntae lise Soate protein aminotransferase Soate protein aminotransferase anthraniate synthase component I anthraniate synthase component II bacteriocin biosynthesis protein, putative hypothetical protein putative, truncated bacteriocin sid-immunity protein, putative, truncated peptide ABC transporter ATP bindingpermease protein, funcated peptide ABC transporter ATP bindingpermease protein, funcated peptide ABC transporter ATP bindingpermease protein, funcated peptide ABC transporter ATP bindingpermease protein, funcated ABC transporter ATP bindingpermease protein, funcated ABC transporter ATP bindingpermease protein, funcated ABC transporter ATP binding protein
str0227 str0409 str0545 str0590 str0771 str0780 str0790 str0790 str1029 str1029 str1284 str1413 str1529 str1553 str1553 str1553 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str1573 str1574 str157	folC1 - bcaT pabB dfp1 dfp2 ptpS als lplA metK updK serA serA serC trpE liWC mcB mecehanisms - - - -	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453 0.387 4.012	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.196 0.196 0.196 0.351 0.231 0.260 0.391 0.2411	2.894 3.726 2.533	7.274 2.600 2.766 2.536 3.868 5.179 8.024 8.181	NAC(+) synthesize ' folycologitumate synthase dihydrotolate synthase motydoopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated branchet-chain amino acid aminotransferase para-aminobenzoate synthesiae component I phosphopantohenolycysteine synthase/decarboxylase hypothetical protein 6-privroyl tetrahydrobiopterin synthase, putative alpha-acetolactate synthesiae opticate protein ligae bydrotome kinase bydrotome kinas
str0227 str0409 str0545 str0590 str0771 str0789 str0789 str0789 str0780 str1028 str1029 str1284 str1413 str1529 str1525 str1523 str15553 str15554 str1555454 str1555454 str1555454 str155545454545454545454545454545454545454	folC1 - bcaT pabB dfp1 dfp2 ptpS als lpIA als lpIA reatK pdKK - serA serC trpG wccB wccB mccB - - - - - - - - - - - - - - - - - -	3.888 2.012 2.110 2.124 0.404		2.128 0.230 2.089 2.445 0.453 0.387	0.434 3.675 0.273 0.304 3.038 0.215 2.927 0.398 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.231 0.231	2.894 3.726 2.533	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256	NAC(P) synthesiae ' folyopolytimate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF family protein), putative, truncated branched-hain amino acid aminotransferase para-aminobenzoate synthesise component I phosphoganothenov(pysteine synthase/decarbox/sae hypothecial protein gatha-acedicated synthesise protection of the synthase of the synthase of the synthase lipoate-protein ligase para-aminobenzoate synthese soladno-synthesise organized and synthase lipoate-protein ligase putative glutamate-crystein ligase D-3-phosphospine aminotransferase anthranilate synthase component I exclusion in the synthase of the synthase anthranilate synthase component I keti-lacid reductive/merase anthranilate synthase component I bacteriocin biosynthesis protein, putative bacteriocin biosynthesis protein, putative, truncated bacteriocin self-immunity protein, putative, truncated bacteriocin self-immunity protein, putative, truncated bacteriocin self-immunity protein, putative, truncated peptide ABC transporter ATP binding permease protein, runcated peptide ABC transporter ATP binding permease protein, runcated patiet aBC transporter ATP binding permease protein, putative ABC transporter ATP binding permease protein, putative ABC transporter ATP binding permease subunit ABC transporter ATP binding permease subunit ABC transporter ATP binding permease protein
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str0227 str0409 str0545 str05545 str05545 str05545 str05545 str0526 str0526 str0771 str07271 str12841 str0228 str1029 str12841 str12841 str12841 str12841 str12841 str12841 str12842 str15533 str12841 str15533 str15533 str15533 str15533 str15741 str1873 str15741 str1873 str15741 str1873 str15741 str1873 str15741 str15741 str15741 str15741 str15741 str15741 str0559 str0529 s	folC1 - bcaT bcaT pabB dfp1 dfp2 dfp2 dfp2 pla pla pla pla serC serC serC tipE tipE tipE tipE tipE tipE tipE - - - hsdS1 hsdS1 hsdM1 - - hsdS2 hsdS2 - hsdS2 - hsdS1 hsdS1 hsdS1 hsdS1 hsdM1 - - - - - - - - - - - - -	3.888 2.012 2.110 2.124 0.404 5.956	0.310	2.128 0.230 2.089 2.445 0.453 0.453 3.575 0.270 2.338 2.277	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.196 0.351 0.231 0.240 0.391 0.411 3.145 4.865 2.492 2.991 2.112 2.412 2.492 2.492 2.449 0.381 0.201	2.894 3.726 2.533 4.408 2.749 0.122 5.864 0.460 0.120	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256 0.378 0.356	NAC(+) synthelase ' folyloplytimate synthase dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF Family protein), putative, truncated branchet-chain amino add aminotransferase para-aminoberizoate synthesis ecomponent I protein ' hypothelical protein ' c-pruvoyl tetrahydrotolopterin synthase, putative alpha-acetolacate synthase component i potate-protein ligase putative glutanate-cysteline ligase putative glutanate-cysteline ligase Do-phosphogienamate-cysteline ligase Do-phosphogienamate-cysteline ligase putative glutanate-cysteline ligase anthraniate synthase component I anthraniate synthase component I anthraniate synthase component I bacteriocin biosynthesis protein, putative, truncated bacteriocin biosynthesis protein, putative, truncated peptide ABC transporter ATP binding/permease protein, truncated peptide ABC transporter ATP binding/permease protein ABC transporter ATP binding porteinse ABC transporter ATP binding portein ABC transporter ATP binding porteinse ABC transporter ATP binding porteins
str0227 str0409 str0545 str0545 str0781 str0781 str0783 str0783 str0783 str0783 str0783 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0944 str09555 str09555 str09555555555555555555555555555555555555	folC1 - bcaT pabB dfp1 dfp1 dfp2 ptpS uptpS tp2 ptpS uptpS uptp tp2 uptpS uptp	3.888 2.012 2.110 2.124 0.404 5.956	0.310	2.128 0.230 2.089 2.445 0.453 0.453 3.575 0.270 2.338 2.277	0.434 3.675 0.273 0.304 3.038 0.215 3.987 0.195 0.196 0.196 0.196 0.195 0.196 0.196 0.351 0.231 0.231 0.240 0.304 0.391 0.411 3.145 2.991 2.112 0.435 2.025 2.449 0.201 0.201	2.894 3.726 2.533 4.408 2.749 0.122 5.864 0.460 0.120 0.460	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256 0.378 0.356	NAC(+) synthesize ' folyopolytimate synthase d dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF Family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthesise component I phosphogantomoviny tankin for protein protein synthase, putative alpha-acidatate synthase upoate-protein ligase porta-brotein ligase porta-brotein ligase porta-brotein ligase porta-brotein ligase phosphogantame-crystein ligase D-3-phosphogantome- phosphogantame-crystein ligase anthranilate synthase component I anthranilate synthase component I bacteriocin biosynthesis protein, putative activationate constraint activationate component I bacteriocin biosynthesis protein, putative bacteriocin biosynthesis protein, putative, truncated bacteriocin self-immunity protein ABC transporter ATP binding premases protein ABC transporter ATP binding premases protein ABC transporter permease protein ABC transporter permease protein ABC transporter ATP binding protein putative, truncated ABC transporter ATP binding protein putative, truncated ABC transporter ATP binding protein p
str0227 str0409 str0545 str0545 str0580 str07713 str06826 str07713 str0828 str0928 str0928 str0928 str0928 str0928 str1224 str1224 str1224 str1222 str1222 str1222 str1533 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1944 str0778 str0788 str1873 str1873 str0788 str0788 str0788 str0788 str0788 str0788 str0788 str1888 str1888 str1888 str1888 str1888 str0788 str	folC1 - bcaT pabB dfp1 dfp1 dfp2 ptpS uptpS tp2 ptpS uptpS uptp tp2 uptpS uptp	3.888 2.012 2.110 2.124 0.404 5.956	0.310	2.128 0.230 2.089 2.445 0.453 0.453 3.575 0.270 2.338 2.277	0.434 3.675 0.273 0.304 3.038 0.215 3.987 2.122 0.056 0.195 0.195 0.195 0.195 0.195 0.351 0.231 0.231 0.231 0.240 0.391 0.391 0.391 0.391 0.391 0.411 3.145 2.492 2.991 2.112 2.492 2.492 2.491 2.112 0.381 0.201	2.894 3.726 2.533 4.408 2.749 0.122 5.864 0.460 0.120 0.460	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256 0.378 0.356	NAC(+) synthelize ' folyloplytimate synthase d dhydrololate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF Family protein), putative, truncated branched-hain amino add aminotransferase para-aminoberuzoate synthesis e component I phosphoganotheron/tystalme synthase/decarbox/sise Prosphoganotheron/tystalme synthase/decarbox/sise Prosphoganotheron/tystalme synthase/decarbox/sise Prosphoganotheron/tystalme synthase/ e-prynovyl tetrahydrobopterin synthase, putative alpha-acotolacate synthase pyridoxine knase pyridoxine knase pyridoxine pyridoxine pyridoxine pyridoxine knalle knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyridoxine knase pyrid
str0227 str0409 str0545 str0545 str0781 str0781 str0783 str0783 str0783 str0783 str0783 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0923 str0924 str0944 str09555 str09555 str09555555555555555555555555555555555555	folC1 - bcaT pabB dfp1 dfp1 dfp2 ptpS uptpS tp2 ptpS uptpS uptp tp2 uptpS uptp	3.888 2.012 2.110 2.124 0.404 5.956	0.310	2.128 0.230 2.089 2.445 0.453 0.453 3.575 0.270 2.338 2.277	0.434 3.675 0.273 0.304 3.038 0.215 3.987 0.195 0.196 0.196 0.196 0.195 0.196 0.196 0.351 0.231 0.231 0.240 0.304 0.391 0.411 3.145 2.991 2.112 0.435 2.025 2.449 0.201 0.201	2.894 3.726 2.533 4.408 2.749 0.122 5.864 0.460 0.120 0.460	7.274 2.600 2.766 2.536 2.069 3.868 5.179 8.024 8.181 5.256 0.378 0.356	NAC(+) synthesize ' folyopolytimate synthase d dihydrotolate synthase motydopterin biosynthesis protein (HesA/MoeB/ThF Family protein), putative, truncated branched-chain amino acid aminotransferase para-aminobenzoate synthesise component I phosphogantomoviny tankin for protein protein synthase, putative alpha-acidatate synthase upoate-protein ligase porta-brotein ligase porta-brotein ligase porta-brotein ligase porta-brotein ligase phosphogantame-crystein ligase D-3-phosphogantome- phosphogantame-crystein ligase anthranilate synthase component I anthranilate synthase component I bacteriocin biosynthesis protein, putative activationate constraint activationate component I bacteriocin biosynthesis protein, putative bacteriocin biosynthesis protein, putative, truncated bacteriocin self-immunity protein ABC transporter ATP binding premases protein ABC transporter ATP binding premases protein ABC transporter permease protein ABC transporter permease protein ABC transporter ATP binding protein putative, truncated ABC transporter ATP binding protein putative, truncated ABC transporter ATP binding protein p

str0036	· .			0.454				IS861, transposase (orf1), IS3 family, truncated
str0056	ruvA				0.442			Holliday junction DNA helicase motor protein
str0060 str0062	recA polC			3.019	0.382	0.296		recombinase A DNA polymerase III subunit alpha
	poic				0.432	0.290		
str0067 str0069	-			0.474	0.432			ISSpn1, transposase, IS3 family, truncated
str0069 str0105	- tnp1239				0.394		2.206	ISSpn1, transposase, IS3 family, truncated
str0105	uip1239		2.028		0.384		2.200	IS1239 transposase
str0126			2.020		0.434			truncated IS1216 transposase truncated IS1193 transposase
str0206				0.464	0.353			IS861, transposase (orf2), IS3 family, truncated
str0200				0.404	0.353			IS861, transposase (orf2), IS3 family, truncated
str0223	tnp1239				0.492			IS1239 transposase
str0234	1101200			2.033	0.402			hypothetical protein
str0244				2.000	0.398			ISSpn1, transposase, IS3 family, truncated
str0259	xer2				4.244			tyrosine recombinase
str0320	dnaB				0.330			chromosome replication initiation / membrane attachment protein DnaB
str0321	dnal				0.445			primosomal protein Dnal
str0368	comFA				2.482		0.376	late competence protein required for DNA uptake
str0490	dnaH			0.491	0.477			DNA polymerase III subunit delta
str0588	parE			2,701				DNA topoisomerase IV subunit B
str0589	parC			3.330	4,738	0.428		DNA topoisomerase IV subunit A
str0601	-	2.531						conserved hypothetical protein, MutT/nudix family protein
str0614	recR			2.501		0.314		recombination protein RecR
str0658	-				0.356			hypothetical protein
str0679					2.898			MutT/nudix family protein
str0742						127.988		truncated IS1193 transposase
str0743	-				0.444			truncated IS1193 transposase
str0765	-				0.444			IS861, transposase (orf2), IS3 family, truncated
str0783	int2				0.330			integrase/recombinase, phage associated
str0813	dinG	0.459		2.941				ATP-dependent DNA helicase
str0822	-				0.417			truncated IS1193 transposase
str0841	-			0.365				truncated IS1191 transposase
str0849	tnp1191			0.412				IS1191 transposase
str0879	-						0.344	SOS responce UmuC protein, truncated
str0885	sthIM			5.974	5.172			type III restriction-modification system methylation subunit
str0894	rnhB				5.545			ribonuclease HII
str0896	dprA			0.339	3.075			DNA processing protein, Smf family
str0897	topA			2.948	3.771			DNA topoisomerase I
str0956	-				0.355			hypothetical protein
str0986	pcrA			2.036				ATP-dependent DNA helicase
str1035	-			0.458				truncated IS1191 transposase
str1045	tnp1193				0.493			IS1193 transposase
str1074	-				0.339			truncated IS1216 transposase
str1126	-	0.406						hypothetical protein
str1198	dnaE			2.156	3.573			DNA polymerase III subunit alpha
str1213	recN				2.044			DNA repair and genetic recombination protein
str1220	nth	0.259	0.303		0.260	3.137		endonuclease III, DNA repair
str1221	dnaD	0.223	0.329		0.199	3.214		DNA replication protein dnaD
str1224	recJ			2.222				single strand DNA-specific exonuclease
str1300	alkD		2.234					DNA alkylation repair protein
str1304	-				0.355			truncated IS1193 transposase
str1385	umuC1			2.900			0.104	SOS responce UmuC protein
str1394	sbcC		2.851		4.240			ATP-dependent dsDNA exonuclease
str1395	sbcD			0.439				ATP-dependent dsDNA exonuclease
str1425	pknB			2.757				protein kinase
str1449				0.448	0.195			hypothetical protein
str1489	dnaG			2.384				DNA primase
str1496	· _				0.451			MutT/nudix family protein
str1521	gyrB				3.237			DNA gyrase subunit B
str1550	exoA	2.539			0 700			3'-exo-deoxyribonuclease
str1567	·				2.796	0.434		hypothetical protein
str1568	rheA			2.454				ATP-dependent RNA helicase
str1601	dnaQ	0 700		0.314		0.313		DNA polymerase III subunit epsilon
str1638	-	3.762		0.166	2.414			ISSth3, transposase, IS30 family, truncated
str1656	dinP					4.585		DNA polymerase IV
str1699	rheB		2.174					ATP-dependent RNA helicase
str1725	recG						0.483	ATP-dependent DNA helicase
str1753	ssbB			2.584	0.328		2.392	single-strand DNA-binding protein
str1757	mutY	2.824	0 500					A/G-specific adenine glycosylase
str1762	mutS2	2.529	2.568	2.312	2.220			DNA mismatch repair protein
str1765	rnhB		2.933	2.047 2.955				ribonuclease HIII
str1767	recD		2.933	2.955				exodeoxyribonuclease V
str1783	-				0.426			IS657, transposase, IS200 family, truncated
str1784	-				0.466	0.215		IS861, transposase (orf1), IS3 family, truncated
str1807	tnp657		0.458		0.419	0.215		IS657, transposase, IS200 family single-strand DNA-binding protein
str1845	ssbA		0.408	0.474	0.273	10.252		angio-auanu Dhiw-binung protein ISSth4 transposoo IS20 family trungst-1
str1897	-			0.474				ISSth4, transposase, IS30 family, truncated
str1904 str1945	-			0.353	0.493			ISSth4, transposase, IS30 family, truncated truncated IS1191 transposase
str1945 str1948					0.329			hypothetical protein
str1948 str1957	- cshA			0.486	0.328			chromosome segregation helicase
str1957 str1988	uaries .			0.400	0.396	0.429		conserved hypothetical protein, MutT/nudix family
str1999	- holB				0.390	0.423		replicative DNA helicase
str2015	recF			2.036	0.110			recombination protein F
302013								
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Energy or		conversion						
Energy pr str0246	roduction and	conversion 3.406						
str0246	roduction and acyP	conversion 3.406			0.112			acylphosphatase
str0246 str0478	roduction and acyP atpE	conversion 3.406			0.112			acylphosphatase proton-translocating ATPase, c subunit
str0246 str0478 str0480	roduction and acyP atpE atpF	conversion 3.406			0.198			acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B
str0246 str0478 str0480 str0481	roduction and acyP atpE atpF atpH	conversion 3.406			0.198 0.249			acylphosphatae proton-translocating ATPase, c subunit ATP synthaes subunit B ATP synthaes subunit D
str0246 str0478 str0480 str0481 str0482	roduction and acyP atpE atpF	3.406			0.198 0.249 0.399			acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A
str0246 str0478 str0480 str0481	roduction and acyP atpE atpF atpH atpA	2.525		0.309	0.198 0.249		0,338	acylphosphatae proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleoide-disulifide oxidoreductase
str0246 str0478 str0480 str0481 str0482 str0557	roduction and acyP atpE atpF atpH	3.406			0.198 0.249 0.399 2.436		0.338	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit A ATP synthase subunit A ATP synthase subunit A pyrdine nucleotide-disulfide oxidoreductase isopententy pyrophosphate isomerase
str0246 str0478 str0480 str0481 str0482 str0557 str0562	roduction and acyP atpE atpF atpH atpH - idi	3.406			0.198 0.249 0.399 2.436 2.882		0.338	acylphosphatae proton-translocating ATPase, c subunit ATP synthaes subunit B ATP synthaes subunit D ATP synthaes subunit A pyridine nucleoide-disulfide oxidoreductase isopentenyl pyrophosphate isomerase L-2-hydroxycocproted dehydrogenase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0644 str1049	roduction and acyP atpE atpF atpH atpA - idi hdhL acoC	3.406			0.198 0.249 0.399 2.436 2.882 3.233		0.338	acylphosphatae proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit A ATP synthase subunit A pryntine nucleotide-disulfide oxidoreductase isopententy prophosphate isomerase L-2-hydroxyisocaproate dehydrogenase dihydroilgoandie acetyltransferase
str0246 str0478 str0480 str0481 str0482 str0557 str0552 str0562 str0644	roduction and acyP atpE atpF atpH atpH - idi hdhL	3.406			0.198 0.249 0.399 2.436 2.882 3.233 0.491		0.338	acylphosphatae proton-translocating ATPase, c subunit ATP synthaes subunit B ATP synthaes subunit D ATP synthaes subunit A pyridine nucleoide-disulfide oxidoreductase isopentenyl pyrophosphate isomerase L-2-hydroxycocproted dehydrogenase
str0246 str0478 str0480 str0481 str0482 str0482 str0557 str0562 str0644 str1049 str1050 str1051	roduction and acyP atpE atpF atpH atpA - idi hdhL acoC acoB acoA	3.406 2.525		0.309	0.198 0.249 0.399 2.436 2.882 3.233 0.491	0.224		acytphosphatae proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit C ATP synthase subunit C Supportery prophosphate isolaride and and subunit compared and and and and supporter of the subunit acetion dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex, E1 component, alpha subunit
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0644 str1049 str1050 str1051 str1149	roduction and acyP atpE atpF atpH atpA - idi hdhL acoC acoB acoA nfrA	3.406		0.309 0.456	0.198 0.249 0.399 2.436 2.882 3.233 0.491	0.224	0.338	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleolid-disulfide oxidoreductase isopentenyl pyrophosphate isomerase L-2-hydroxyscoprate dehydrogenase dihydrolipoamide acetyltransferase acetoin dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0644 str1059 str1051 str1149 str1266	roduction and acyP atpE atpF atpH atpA - idi hdhL acoB acoB acoA nfrA icd	3.406 2.525		0.309	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261	0.224		acytphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit D ATP synthase subunit C ATP synthase subunit C ATP synthase subunit C ATP synthase subunit L 2-Phytropense complex, E1 component, beta subunit netroin dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase isocitrate dehydrogenase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0644 str1050 str1051 str1149 str11266 str1280	roduction and acyP atpE atpF atpH atpA - idi hdhL acoC acoB acoA nfrA	3.406 2.525		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261	0.224		acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleidd-disulfide oxidoreductase isopentenyl pyrophosphate isomerase L2-hydroxycocoprate dehydrogenase dihydrolipoamide acetyltransferase acetion dehydrogenase complex, E1 component, teta subunit acetion dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase isocitrate dehydrogenase
str0246 str0478 str0480 str0481 str0482 str0557 str0557 str0562 str0644 str1050 str1051 str1149 str1280 str1280 str1253	roduction and acyP atpE atpF atpH atpA - idi hdhL acoB acoB acoA nfrA icd	3.406 2.525 3.210		0.309 0.456	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261	0.224		acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleotide-disulfide oxidoreductase isopentenyi pyrophosphate isomerase L-2-hydroxyscaprcate dehydrogenase acetoria dehydrogenase complex, E1 component, beta subunit acetoria dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase L-lacata dehydrogenase L-lacata dehydrogenase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0564 str1050 str1050 str1050 str1050 str1050 str1266 str1280 str1353 str1369	roduction and acyP atpE atpH atpH atpA - idi hdhL acoC acoB acoA nfrA icd idh -	3.406 2.525		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240	0.224		acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit B ATP synthase subunit A pyrdine nucleotide-disulfide oxidoreductase isopententy pyrophosphate isomerase L-2-hydroxyisocaproate dehydrogenase dihydroilgoanide acetyltranslerase acetoin dehydrogenase complex, EI component, beta subunit acetoin dehydrogenase complex, EI component, alpha subunit nition/lawn reductase isopensenty pyrdrogenase complex, EI component, alpha subunit nition/lawn reductase L-Lacitate dehydrogenase, funcated NAD(P)H ritioreductase, putative
str0246 str0478 str0480 str0481 str0481 str0557 str0562 str0564 str1051 str1149 str1266 str1280 str1280 str1363 str1369 str1455	roduction and acyP atpE atpF atpH atpA - idi hdhL acoC acoB acoA nfrA icd Idh - pta	3.406 2.525 3.210		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180		0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleid-di-subified oxidoreductase isopentenny pyrophosphate isomerase L-2-hydroxyscoprcate dehydrogenase dhydrollpoanside acetyltransferase acetoin dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex truncated L-lacata dehydrogenase ghycerol dehydrogenase, putative hybosphate acetyltransferase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0562 str1050 str1050 str1050 str1050 str1149 str1266 str1280 str1353 str13657	roduction and acyP atpE atpH atpH atpA - idi hdhL acoC acoB acoA nfrA icd idh -	3.406 2.525 3.210 2.270		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180	0.224		acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleid-disulfide oxidoreductase isopenteny pyrophosphate isomerase L2-hydroxyscoparate dehydrogenase dhydroilpoamide acetylransferase acetion dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex, E1 component, alpha subunit mitration dehydrogenase subcitatia dehydrogenase subcitatia dehydrogenase gylovoril dehydrogenase, putative phosphate acyltransferase pyruvate formate-lyase thoredoxin
str0246 str0478 str0480 str0481 str0481 str0482 str0567 str0562 str0664 str1050 str1051 str1149 str1280 str1280 str1353 str1369 str1455 str1657 str1803	roduction and acyP atpE atpH atpH atpA - idi acoC acoA nfrA icd ldh - pta pfl	3.406 2.525 3.210 2.270		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129		0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit A pyridine nucleid-di-subified oxidoreductase isopentenny pyrophosphate isomerase L-2-hydroxyscoprcate dehydrogenase dhydrollpoanside acetyltransferase acetoin dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex truncated L-lacata dehydrogenase ghycerol dehydrogenase, putative hybosphate acetyltransferase
str0246 str0478 str0480 str0481 str0482 str0557 str0562 str0644 str1049 str1050 str1051 str1149 str1260 str1280 str1353 str13657 str1803 str1805 str1805	roduction and acyP atpE atpH atpH atpA - idi hdhL acoB acoB acoA nfrA idd ldh - - pta pfl trxA1	3.406 2.525 3.210 2.270		0.309 0.456 0.412	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180		0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit D ATP synthase subunit A pyridine nucleid-disulfide oxidoreductase isopenteny pyrophosphate isomerase L2-hydroxyscoparate dehydrogenase dihydroipoamaide acetyltransferase acetoin dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex, E1 component, alpha subunit mitroffwin reductase isocitata dehydrogenase, chuckted ghydroid dehydrogenase, truncated NADP(PH nitroreductase, putative phosphate acetyltransferase pyruvate formate-lyase thoredoxin bacteriocin transport accessory protein, putative thoredoxin
str0246 str0478 str0480 str0481 str0482 str0482 str0557 str0562 str1050 str1050 str1050 str1050 str1280 str1353 str1363 str1365 str1455 str1657 str1803	roduction and acyP atpE atpF atpH atpA atpA idi hdhL acoC acoA nfrA icd idh idh idh idh idh idh trXA1 bta	3.406 2.525 3.210 2.270		0.309 0.456 0.412 0.343 0.151	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129 0.277 0.340		0.204	acytiphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit C ATP synthase subunit Ade oxidoreductase bisopenneny prophosphate iconerasas L-2-hydroxyisocaproate dehydrogenase dihydroilgoanide acetyltransferase acetoin dehydrogenase complex, E1 component, beta subunit acetoin dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase isocitrate dehydrogenase L-atatte dehydrogenase ghycerol dehydrogenase pipurota formate-lyase provate formate-lyase provate formate-lyase provate formate-lyase bacterioin transport accessory protein, putative thioredoxin acetate kinase
str0246 str0478 str0480 str0481 str0482 str0557 str0557 str0562 str0557 str0562 str1050 str1050 str1050 str1050 str1280 str1280 str1280 str1455 str18803 str18805 str18857 str18857 str18857	roduction and: acyP atpE atpF atpH atpH idi hdhL acoB acoA acoB acoB acoB idd ldh - pfi trxA1 bta trxA1 bta trxA2	3.406 2.525 3.210 2.270		0.309 0.456 0.412 0.343 0.151 0.264	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129 0.277		0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit A ATP synthase subunit A pyridine nucleotide-disulfide oxidoreductase isopententy pyrophosphate isomerase L-2-hydroxyisocaproate dehydrogenase dihydroilgoanide acetyltransferase acetoin dehydrogenase complex, EI component, taba subunit acetoin dehydrogenase complex, EI component, alpha subunit nitroffixen reductase isopententy pyrotechase isopentential pyrotechases isopentential charater dehydrogenase, truncated NAD(P)H ritrofeuductase, putative phosphate acetyltransferase thioredoxin bacterioxin transport accessory protein, putative hosphation
str0246 str0478 str0480 str0481 str0482 str0552 str0552 str0552 str1049 str1050 str1050 str1050 str1050 str1280 str1280 str1280 str1353 str1369 str1455 str18803 str1855 str1849 str18879 str18879 str18879	roduction and: acyP atpE atpF atpH atpH idi hdhL acoB acoA acoB acoB acoB idd ldh - pfi trxA1 bta trxA1 bta trxA2	3.406 2.525 3.210 2.270		0.309 0.456 0.412 0.343 0.151 0.264 0.184	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129 0.277 0.340		0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit A ATP synthase subunit A pyridine nucleotide-disulfide oxidoreductase isopententy pyrophosphate isomerase L-2-hydroxyisocaproate dehydrogenase dihydroilgoanide acetyltransferase acetoin dehydrogenase complex, EI component, taba subunit acetoin dehydrogenase complex, EI component, alpha subunit nitroffixen reductase isopententy pyrotechase isopentential pyrotechases isopentential charater dehydrogenase, truncated NAD(P)H ritrofeuductase, putative phosphate acetyltransferase thioredoxin bacterioxin transport accessory protein, putative hosphation
str0246 str0478 str0480 str0481 str0482 str0557 str0557 str0562 str0557 str0562 str1050 str1050 str1050 str1050 str1280 str1280 str1280 str1455 str18803 str18805 str18857 str18857 str18857	roduction and: acyP atpE atpF atpH atpH idi hdhL acoB acoA acoB acoB acoB idd ldh - pfi trxA1 bta trxA1 bta trxA2	3.406 2.525 3.210 2.270		0.309 0.456 0.412 0.343 0.151 0.264	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129 0.277 0.340 0.479		0.204	acytiphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit Ad oxidoretuctase pyridhen nudeotide-toghate isomerases toghate and the subunit and the subunit activity transferase L-2-hydroxytisocaproate dehydrogenase dihydrotipoantide activitytransferase acetoria dehydrogenase complex, E1 component, beta subunit acetoria dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase L-actate dehydrogenase L-actate dehydrogenase pycerol dehydrogenase pycerol dehydrogenase pycerol dehydrogenase pycerol afbydrogenase pycerol afbydrogenase pyc
str0246 str0478 str0480 str0481 str0482 str0552 str0552 str0552 str1049 str1050 str1050 str1050 str1050 str1280 str1280 str1280 str1355 str1369 str1455 str18803 str1855 str18803 str1885 str1887 str1887 str1887	roduction and: acyP atpE atpH atpH atpH dthL acoC acoB acoA acoA acoA acoA acoA acoA acoA acoA bidh icd ldh - - - - - - - - - - - - -	3.406 2.525 3.210 2.270 3.035		0.309 0.456 0.412 0.343 0.151 0.264 0.184	0.198 0.249 0.399 2.436 2.882 3.233 0.491 0.268 0.261 0.423 0.415 0.240 2.180 0.129 0.277 0.340 0.479 0.323	0.265	0.204	acylphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit A ATP synthase subunit A prydine nucleotide-disulfide oxidoreductase isopententy purphosphate isomerase L-2-hydroxyisocaproate dehydrogenase dihydroilgoanide acetyltransferase acetoin dehydrogenase complex, EI component, taba subunit acetoin dehydrogenase complex, EI component, alpha subunit nitiorfilavin reductase sectori dehydrogenase, truncated NAD(P)H ritroductase, truncated NAD(P)H ritroductase, truncated NAD(P)H ritroductase, truncated interaction transport accessory protein, putative bacterioin transport accessory protein, putative hacterioin transport accessory protein, putative alcohol-acetaldehyde dehydrogenase, truncated alcohol-acetaldehyde dehydrogenase, truncated
str0246 str0478 str0480 str0481 str0482 str0552 str0552 str0564 str1050 str1051 str1149 str1266 str1286 str1285 str1657 str14855 str16857 str1880 str18857 str18857 str18857 str18857 str18857	roduction and acyP atpE atpF atpH atpH atpA - idi acoA acoA acoA acoA acoA acoA idd - - pta pta bta bta trxA1 bta - - - - - - - - - - - - -	3.406 2.525 3.210 2.270		0.309 0.456 0.412 0.343 0.151 0.264 0.184 0.184	0.198 0.249 0.249 0.399 2.436 2.862 3.233 0.491 0.268 0.261 0.423 0.421 0.240 0.261 0.240 2.180 0.240 0.240 0.240 0.240 0.240 0.240 0.240 0.240 0.241 0.240 0.241 0.243 0.425		0.204	acytiphosphatase proton-translocating ATPase, c subunit ATP synthase subunit B ATP synthase subunit D ATP synthase subunit Ad oxidoretuctase pyridhen nudeotide-toghate isomerases toghate and the subunit and the subunit activity transferase L-2-hydroxytisocaproate dehydrogenase dihydrotipoantide activitytransferase acetoria dehydrogenase complex, E1 component, beta subunit acetoria dehydrogenase complex, E1 component, alpha subunit nitroffavin reductase L-actate dehydrogenase L-actate dehydrogenase pycerol dehydrogenase pycerol dehydrogenase pycerol dehydrogenase pycerol afbydrogenase pycerol afbydrogenase pyc

Function str0022								
	pcsB				0.095	0.398		glucan binding protein
str0064	-				0.301	0.000		hypothetical protein
str0113	-				0.241		2.223	hypothetical protein
str0124	-				2.424			hypothetical protein
str0260	scpA				6.205			segregation and condensation protein A
str0268 str0276	-			4.060	0.118	0.282		hypothetical protein membrane protein
str02/0		0.382	0.208	2.008	0.165	4.699		hypothetical protein
str0340		0.002	0.200	2.176	0.100	4.000		hypothetical protein
str0491	sip			0.485	0.430			signal-petidase-like protein
str0492	-				0.407			hypothetical protein
str0504					0.459	0.000		hypothetical protein, truncated
str0552 str0595	-				0.136	3.069 0.500		hypothetical protein hypothetical protein
str0632				0.484		0.500		hypothetical protein
str0634	-	2.374	2.351		2.283			hypothetical protein
str0643	-				3.300			hypothetical protein
str0652	mip			3.699		24.134		macrophage infectivity potentiator-related protein, putative
str0657		3.089			0.231			hypothetical protein
str0661 str0673		3.089	2.817		2.615			hypothetical protein hypothetical protein
str0676			2.017	0.496	2.015			hypothetical protein
str0698	-		2.158		6.101	0.470		transcriptional regulator
str0884	sthIR			2.535	9.595			DNA endonuclease, type III restriction and modification system
str1063	-			0.221				hypothetical protein
str1157 str1248	•			0.434	4.334			hypothetical protein
str1252				0.434	2.431			hypothetical protein hypothetical protein
str1256	-				3.261			hypothetical protein
str1377	-	2.025						hypothetical protein
str1422	-			2.457		0.426		conserved hypothetical protein, putative transporter
str1425	pknB			2.757				protein kinase
str1466	•			2.535	0.294			hypothetical protein
str1506 str1551				0.438	0.384			hypothetical protein hypothetical protein, citrulline cluster-linked gene
str1723				0.100	0.381			conserved hypothetical protein, Cof family
str1961					0.361			hypothetical protein
str1967						0.499		hypothetical protein
str1980 str1982					0.343		0.494	hypothetical protein
str1982 str1993					0.206	0.358	0.494	hypothetical protein hypothetical protein
str1996					0.358	0.313		hypothetical protein
str2014	-			2.063	0.415	0.394		hypothetical protein
str2019	-				0.416			hypothetical protein
str2023	-				0.349	2.633		hypothetical protein
0		lation and .						
str0022	unction pred pcsB	action only			0.095	0.398		glucan binding protein
str0059	cinA				0.365	0.384		competence damage-inducible protein A
str0066	-					0.476		hypothetical protein
str0188	-				0.270	0.357		ABC transporter permease protein, putative malate permease
str0193	-				0.435			hypothetical protein
str0217 str0218					2.829 2.985			hypothetical protein hypothetical protein
str0218	- recU			2.026	0.433			hypothetical protein
str0248	-			0.405	0.100			conserved hypothetical protein, putative hydrolase
str0249				0.378				conserved hypothetical protein, membrane protein
str0257	-				3.826			hypothetical protein
str0258					4.330			hypothetical protein
str0316 str0334		0.082	0.147		0.191 0.202	34.356		hypothetical protein hypothetical protein
str0335		2.179	0.147		0.202	34.330		conserved hypothetical protein, Cof family
str0336		2.110					2.711	conserved hypothetical protein, soft family conserved hypothetical protein, xanthine/uracil permease family
str0337						0.483		hypothetical protein
str0346	-							hypothetical protein, truncated
str0347 str0364				2.118				hypothetical protoin, admouted
	-	0.040		2.118	2.268			hypothetical protein, truncated
	- -	2.210		2.118 2.296	2.268 2.464	0.259		hypothetical protein, truncated acetoin utilization protein, truncated
str0369	- comFC recX	2.210		2.118 2.296	2.464	0.258		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein
str0369 str0375 str0379	- comFC recX -	2.210 2.499		2.118 2.296	2.464 2.466			hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative
str0369 str0375 str0379 str0443	recX -			2.118 2.296	2.464 2.466 0.137	0.258		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein
str0369 str0375 str0379 str0443 str0451	recX - - metG			2.118 2.296	2.464 2.466 0.137 0.365			hypothetical protein, truncated action utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein metrionine-HRAN ligase
str0369 str0375 str0379 str0443 str0451 str0453	recX -			2.296	2.464 2.466 0.137 0.365 0.221			hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methicnineRNA ligase competence protein, transcription factor
str0369 str0375 str0379 str0443 str0451 str0453 str0455	recX - - metG	2.499	0.188	2.118 2.296 2.029	2.464 2.466 0.137 0.365	0.341		hypothetical protein, truncated acetoni utilization protein, truncated late competence protein RecA regulator RecX beiges protein RecX beiges protein and the set of the set of the beiges protein protein methodina-effect and the set of the set of the methodina-effect and the set of the se
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462	recX - - metG		0.188	2.296	2.464 2.466 0.137 0.365 0.221 0.431			hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methionineIRNA ligase competence protein, transcription factor methythransferase, putative hypothetical protein
str0369 str0375 str0379 str0443 str0453 str0453 str0455 str0462 str0474 str0493	recX - metG coiA - -	2.499 0.290 3.480		2.296 2.029 2.222 0.298	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266	0.341 4.264		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methionineRNA ligase competence protein, transcription factor methyfuransferase, putative hypothetical protein tetrapyrotei emethyase family protein
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462 str0462 str0474 str0493 str0554	recX - - metG	2.499 0.290 3.480 0.227	0.188	2.296 2.029 2.222	2.464 2.466 0.137 0.365 0.221 0.431 2.739	0.341		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methorinina–RNA ligas glucan binding protein methyritical protein tambyritical protein hypothetical protein tetrapyrole methylase tamily protein aminoacylaseM-acyL-amino acid amidohydrolase/hippurate hydrolase
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462 str0474 str0493 str0554 str0601	recX - metG coiA - -	2.499 0.290 3.480		2.296 2.029 2.222 0.298	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203	0.341 4.264		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methioninaRNA ligase competence protein, transcription factor methyfuransferase, putative hypothetical protein tertapyrotei enthylase family protein aminoacylase/N-acy/L-amino acid amidohydrolase/hippurate hydrolase conserved hypothetical protein
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462 str0474 str0493 str0554 str05601 str0679	recX - metG coiA - -	2.499 0.290 3.480 0.227		2.296 2.029 2.222 0.298	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203 2.898	0.341 4.264 4.536		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-Phosphoglucomutase, putative glucan binding protein methicninaRNA ligase glucan binding protein methicninaRNA ligase organization protein methicninaRNA ligase protein transportein transport methypothetical protein hypothetical protein tetrapyrole methylase family protein tetrapyrole methylase family protein minoacylaseN-acyL-amino acid amidohydrolase/hippurate hydrolase conserved hypothetical protein, MutT/mudx family protein MutT/mudx family protein
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462 str0474 str0493 str0554 str0601 str0696 str0704	recX - metG coiA - -	2.499 0.290 3.480 0.227		2.296 2.029 2.222 0.298	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203	0.341 4.264		hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methioninaRNA ligase competence protein, transcription factor methyfuransferase, putative hypothetical protein tertapyrotei enthylase family protein aminoacylase/N-acy/L-amino acid amidohydrolase/hippurate hydrolase conserved hypothetical protein
str0369 str0375 str0379 str0443 str0451 str0453 str0455 str0462 str0474 str0493 str0554 str0696 str0679 str0696 str0704	recX - metG coiA - -	2.499 0.290 3.480 0.227 2.531 2.975 5.745	0.291	2.296 2.029 2.222 0.298 3.927	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203 2.898 3.211 2.658	0.341 4.264 4.536		hypothetical protein, truncated acetoni utilization protein, truncated late competence protein RecA regulator RecX RecA regulator RecX biological protein antionion-approximation entrylowina-frames, putative proteince protein, transcription factor methytiransfrease, putative hypothetical protein tetrapyrrole methylase family protein aminoschysies/work-usimic acid amidohydrolase/hippurate hydrolase minoschysies/work-usimic acid amidohydrolase/hippurate hydrolase aminoschysies/protein tetrapyrole in adhylase family protein MutTinudxi family protein oxidoreductase, short chain dehydrogense/reductase family conserved hypothetical protein, DHH subtamily
str0369 str0375 str0379 str0443 str0451 str0455 str0462 str0474 str0493 str0554 str0601 str0679 str0696 str0704 str0748 str0748	recX - metG coiA - -	2.499 0.290 3.480 0.227 2.531 2.975	0.291	2.296 2.029 2.222 0.298 3.927 2.222	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203 2.898 3.211 2.658 0.285	0.341 4.264 4.536	3.038	hypothetical protein, truncated acetoin utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucomutase, putative glucan binding protein methicnineRNA ligase competence protein, transcription factor methythransferase, putative hypothetical protein tampyrotemical protein tampyrotemical analy protein tampyrotemical protein development of the statistic statistic statistic protein and statistic statistic statistic trutter and the statistic statistic statistic hypothetical protein development of the statistic statistic conserved hypothetical protein, MutT/mudix family protein hypothetical protein conserved hypothetical protein, devidyogenase/reductase family conserved hypothetical protein, DHH subfamily hypothetical protein
str0369 str0375 str0379 str0443 str0453 str0453 str0455 str0462 str0474 str0493 str0554 str0696 str0704 str0696 str0704 str0825	recX - metG coiA - - - - hipO1 - - - - - -	2.499 0.290 3.480 0.227 2.531 2.975 5.745	0.291	2.296 2.029 2.222 0.298 3.927	2.464 2.466 0.137 0.365 0.221 0.431 2.739 0.266 0.203 2.898 3.211 2.658 0.225 0.326	0.341 4.264 4.536	2.874	hypothetical protein, truncated acetoni utilization protein, truncated late competence protein RecA regulator RecX beta-Phosphoglucomutase, putative methonina-eTNA ligase competence protein, transcription factor methytiransfrease, putative hypothetical protein tetrapyrrole methylase family protein aminoacylaseN-acyL-amino acid amidohydrolase/hippurate hydrolase conserved hypothetical protein, MulT/nudX family protein MulT/nudX family protein MulT/nudX family protein bookdmeticale, short chain dehydrogenase/reductase family conserved hypothetical protein, DHH subfamily hypothetical protein conserved hypothetical protein, DHH subfamily hypothetical protein
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str0365 str0375 str0379 str0379 str0443 str0443 str0445 str044	recX metG colA - - - hipO1 - - - adcA - - - - - - - - - - - - - - - - - - -	2.499 0.290 3.480 0.227 2.531 2.975 5.745 0.381 0.380 4.074 3.407 0.202 0.212	0.291 0.479 0.385 0.432 2.834 0.281	2.296 2.029 2.222 0.288 3.927 2.292 2.197 0.319 2.767 2.922 4.644 4.784 0.119 0.119 0.119 0.119 2.418 3.515 2.418 3.515 2.418 3.515	2.464 2.466 0.365 0.225 0.225 0.226 0.203 2.298 0.226 0.203 2.298 0.226 0.203 0.203 0.205 0.203 0.205	0.341 4.264 4.536 0.451 4.592 10.053 6.769	2.874 6.875 0.432 0.296 0.469 2.483 0.099	hypothetical protein, truncated acetoni utilization protein, truncated late competence protein RecA regulator RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX beta-phosphoglucom RecX recX hypothetical protein tetrapyrrole methylase family protein aminoacylaesh-acyl-Lamino acid amidohydrolase/hippurate hydrolase controved hypothetical protein, MutT/mudX family protein tetrapyrrole methylase family protein aminoacylaesh-acyl-Lamino acid amidohydrolase/hippurate hydrolase controved hypothetical protein, MutT/mudX family protein mosodynaesh-acyl-Lamino acid hypothetical protein phosphotates, short chain dehydrogenase/reductase family conserved hypothetical protein, Huncated alcohd dehydrogenase I, truncated alcohd dehydrogenase I, truncated alcohd alcohydrogenase I, truncated bypothetical protein conserved hypothetics, truncated phosphatase, truncated phosphatase, truncated phosphatase, truncated phosphatase, truncated phosphatase, truncated phosphatase, truncated phosphatase, putative trapporter, putative phosphatase, alcohi exopolysaccharide biosynthesis protein acetoprice putative acetoprice truncater phosphatase protein protein aprotein protein aprotein protein aprotein protein aprotein bypothetical protein acetoprice bypothetical protein acetoprice bypothetical protein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein acetoprice bypothetical protein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein aprotein aprotein protein aprotein protein aprotein protein aprotein protein aprotein protein ap
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str03369 str03379 str0379 str0379 str0443 str04453 str04453 str04453 str04452 str0447 str0483 str0455 str0447 str0483 str0554 str0554 str06801 str05704 str05704 str0683 str06881 str0880 str0880 str0881 str0880 str0881 str0880 str0881 str0883 str0	recX metG colA - - - hipO1 - - adcA - - - - - - - - - - - - - - - - - - -	2.499 0.290 3.480 0.227 2.531 2.975 5.745 0.381 0.380 4.074 3.407 0.202 0.212	0.291 0.479 0.385 0.432 2.834 0.281	2.296 2.029 2.222 0.288 3.927 2.292 2.197 0.319 2.767 2.922 4.644 4.784 0.119 0.119 0.119 0.119 2.418 3.515 2.418 3.515 2.418 3.515	2.464 2.464 0.436 0.225 0.225 0.225 0.226 0.203 2.298 0.226 0.203 0.226 0.203 0.226 0.203 0.226 0.202 0.202 0.202 0.202 0.202 0.205 0.204 0.205 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.295 0.294 0.297 0.294	0.341 4.264 4.536 0.451 4.592 10.053 6.769	2.874 6.875 0.432 0.296 0.469 2.483 0.099	hypothetical protein, truncated acetoni utilization protein, truncated late competence protein RecA regulator RecX beta-Phosphoglucomises, putative generational enders, putative proteince protein, transcription factor methylizanetrases, putative hypothetical protein tetrapyrole methylase family protein aminoacylaes/AexAcyL-amino acid amidohydrolase/hippurate hydrolase corserved hypothetical protein, MutT/mudx family protein methylizanetrases, putative hypothetical protein tetrapyrole methylase family protein aminoacylaes/AexAcyL-amino acid amidohydrolase/hippurate hydrolase corserved hypothetical protein, MutT/mudx family protein hypothetical protein conserved hypothetical protein, DHF subfamily hypothetical protein conserved hypothetical protein, DHF subfamily hypothetical protein actorin reductase, thruncated alcohol dehydrogenase I, truncated alcohol dehydrogenase I, truncated alcohol adhydrogenase I, truncated hypothetical protein, truncated coxidoreductase, truncated hypothetical protein, truncated proteinical protein, truncated hypothetical protein, truncated hypothetical protein corserved hypothetics protein, acetyltransferase transporter, putative hypothetical protein corserved hypothetics protein acetorin reductase truncated hypothetical protein corserved hypothetics protein corserved hypothetics protein corserved hypothetics protein corserved hypothetics protein corserved hypothetics protein corserved hypothetics protein ABC transporter putative ABC transporter
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	cobQ	2.017						cobyric acid synthase
str1255 str1257	-				2.345			hypothetical protein
str1259 str1282		0.450			2.407		2,493	ABC transporter ATP binding protein ABC transporter ATP binding protein
str1202	pheT			2.178			2.435	phenylalanyl-tRNA synthetase beta subunit
str1307	-					6.168		hydrolase, haloacid dehalogenase-like family
str1308 str1319	bioY2			0.478			0.197	biotin synthase ABC transporter permease protein
str1320				0.353				hypothetical protein
str1321	-			0.217	0.264			hypothetical protein
str1324 str1330	-		0.369	0.217				ABC transporter ATP binding protein, truncated Na+-dependent transporter, putative
str1354	hipO2	0.210			0.291			aminoacylase/N-acyl-L-amino acid amidohydrolase/hippurate hydrolase
str1365 str1371				0.164	0.397 0.188			hypothetical protein oxidoreductase, aldo/keto reductase family
str1425	pknB			2.757	0.100			protein kinase
str1464	-		2.130	3.220	2.471			glutamine amidotransferase (class I), putative
str1480 str1496	1			3.039	0.330 0.451			polysaccharide/teichoic acid transporter, putative MutT/nudix family protein
str1522					2.083			hydrolase, haloacid dehalogenase-like family
str1566 str1605	-	3.679	3.507	2.108	3.248 2.125			hypothetical protein hypothetical protein
str1605	- hit	7.289	2.048		2.125			cell cycle regulation histidine triad (HIT) protein
str1621	÷	2.027						hypothetical protein
str1641 str1665	hlyX				0.105	0.497		hemolysin, putative hypothetical protein
str1666	-			2.046		0.437		ABC transporter ATP binding protein
str1696	-					0.461		hypothetical protein
str1715 str1723				0.359	0.381			hypothetical protein conserved hypothetical protein, Cof family
str1775					0.497	0.447		glucan-binding protein
str1802				0.000	0.173			hypothetical protein
str1809 str1840	jag -			2.008 0.440			0.411	conserved hypothetical protein, Jag protein hypothetical protein
str1847			0.290		0.168	7.326		permease, putative
str1848 str1855	-			0.306	0.337			phenylalanyl-tRNA synthetase homolog hypothetical protein, truncated
str1855 str1875	-			0.306	0.465			hypothetical protein, iruncated
str1948					0.329			hypothetical protein
str1951 str1965	-			2.814	0.302		2.381	hypothetical protein
str1903				2.014	0.459		2.301	acetyltransferase, GNAT family hypothetical protein
str1979	-				0.351			hypothetical protein
str1988 str2012					0.396 0.433	0.429		conserved hypothetical protein, MutT/nudix family peptidase
str2012	-				0.254			protease, putative
str2016	guaB				0.237			inositol-5-monophosphate dehydrogenase
Inorganic	ion transport a	und metabolis	m					
str0061	spxA				0.202	0.344		transcriptional regulator Spx
str0172 str0187	- adcB	0.200	0.356	0.446 0.208	0.308		0.420	dipeptide/oligopeptide ABC trasporter permease protein, truncated
str0265	trkA1	0.200	0.550	2.361	0.306			zinc ABC transporter permease protein potassium Trk transporter NAD+ binding protein
str0288	cbiM		0.439					cobalt transport protein CbiM
str0289 str0297	cbiQ		0.479 0.146		0.009	2.081		cobalt ABC transporter permease protein ABC transporter substrate binding protein
str0301	-	0.420	0.065		0.020	3.504		ABC transporter ATP binding protein
str0302	-	0.468	0.069		0.026	5.868		ABC transporter permease protein
str0308 str0310		0.304 0.234	0.200 0.111		0.217 0.195	3.809 11.303		ABC transporter ATP binding protein ABC transporter permease protein
str0351		0.201	0.111		0.461	11.000		cation transporter P-type ATPase, truncated
str0608	feoB				0.418			ferrous ion transport protein B
str0677 str0723	mntH dpr			0.349	0.344			manganese transport protein, NRAMP family peroxide resistance protein, non-heme iron-containing ferritin
str0724	fur			0.419				ferric transport regulator protein
str0745 str0840	- copB	2.146			0.210		11.473	hypothetical protein
		2 1 4 4		0.416	0.210			action transporting ATRass, connect transport
str0860	adcA	2.144		0.416	0.202		6.875	cation transporting ATPase, copper transport zinc ABC transporter substrate binding protein
str0874		2.144		0.416 2.661	0.202			cation transporting ATPase, copper transport zinc ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein
str0874 str0932	adcA	2.144			0.202		6.875	cation transporting ATPase, copper transport zinc ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein
str0874 str0932 str0943	adcA phnA -	2.144			0.202		6.875	cation transporting ATPase, cooper transport zinc ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter, substrate-binding protein, truncated
str0874 str0932 str0943 str1002 str1003	adcA phnA - pstC1 pstC2	2.144		2.661 2.201 2.090	0.202 2.277 0.353 2.209		6.875	cailon transporting ATPase, copper transport zinc ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter, substrate-binding protein, truncated phosphate ABC transporter permease protein phosphate ABC transporter permease protein
str0874 str0932 str0943 str1002 str1003 str1004	adcA phnA - pstC1 pstC2 pstB1	2.144		2.661	0.202 2.277 0.353 2.209 2.542		6.875	cation transporting ATPase, copper transport zin: ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter, substrate-binding protein, truncated phosphate ABC transporter permease protein phosphate ABC transporter permease protein phosphate ABC transporter permease protein
str0874 str0932 str0943 str1002 str1003 str1004 str1005 str1006	adcA phnA - pstC1 pstC2	2.144		2.661 2.201 2.090	0.202 2.277 0.353 2.209		6.875 2.371	cation transporting ATPase, copper transport zin: ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter, substrate-binding protein, truncated phosphate ABC transporter premease protein phosphate ABC transporter pre-holding protein phosphate ABC transporter ATP-binding protein phosphate ABC transporter ATP-binding protein phosphate ABC transporter ATP-binding protein
str0874 str0932 str0943 str1002 str1003 str1004 str1005 str1006 str1023	adcA phnA - pstC1 pstC2 pstB1 pstB2 phoU -	2.144		2.661 2.201 2.090 2.349	0.202 2.277 0.353 2.209 2.542 3.322		6.875 2.371 4.030	cátion transporting ATPase, coper transport zinc ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter permease protein phosphate ABC transporter ATP-binding protein phosphate ABC transporter ATP-binding protein phosphate ABC transporter ATP-binding protein phosphate ABC transporter ATP-binding protein phosphate Usake regulatory protein phosphate uptake regulatory protein
str0874 str0932 str0943 str1002 str1003 str1004 str1005 str1006 str1023 str1025	adcA phnA - pstC1 pstC2 pstB1 pstB2 phoU - fatB	2.144		2.661 2.201 2.090 2.349 4.336	0.202 2.277 0.353 2.209 2.542 3.322		6.875 2.371 4.030 3.752	cation transporting ATPase, copper transport zin: ABC transporter substrate binding protein conserved hypothetical protein, PhnA protein cation efflux protein ferrichrome ABC transporter permease protein phosphate ABC transporter permease protein phosphate ABC transporter primease protein phosphate ABC transporter ATP-binding protein freichrome ABC transporter ATP-binding protein
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Mixed culture transcriptome analysis

lot in CC tr0005 tr0017	pth -			0.464	0.401	0.414		peptidyl-tRNA hydrolase IS861, transposase (orf1), IS3 family, truncated
tr0021	mreD			2.118	0.340		2.015	rod shape-determining protein MreD
tr0030 tr0034	purC	2.742		0.271	0.098	0.318 0.483	3.644 2.288	phosphoribosylaminoimidazole-succinocarboxamide synthase phosphoribosylglycinamide formyltransferase
tr0034 tr0035	purN purH		2.176	0.473	0.480	0.483	2.288	phosphoribosylgiycinamide formyltransferase bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrol
r0035	-		2.170	0.473	0.358	0.4/1		IS861, transposase (orf2), IS3 family, truncated
r0043		2.382		0.468	0.204		2.457	hypothetical protein
r0044	-	2.446		0.493	0.347		2.469	hypothetical protein
r0057					0.466			3-methyladenine DNA glycosylase I, truncated
r0058 r0073	- rpsB			2.472	0.467			3-methyladenine DNA glycosylase I, truncated 30S ribosomal protein S2
r0082	ipsb			2.472	0.466			hypothetical protein
r0089					0.400	0.494		hypothetical protein
r0093	rpIM				0.314			50S ribosomal protein L13
r0094	rpsl				0.264			30S ribosomal protein S9
r0095		2.912			0.364			Integrase/recombinase, putative, truncated
tr0097 tr0098		2.912			0.224 0.394			hypothetical protein, putative bacteriocin lantibiotic biosynthesis protein, truncated
r0109				0.399	0.280			hypothetical protein, truncated
tr0111				0.127	0.216			hypothetical protein
r0116	dacB	2.764						D-alanyl-D-alanine-carboxypeptidase
tr0130	comX				0.327			transcriptional regulator, competence factor, RNA polymerase sigma factor
r0135 r0149					0.403		0.197	hypothetical protein 1,6-alpha-glucanhydrolase (dextranase), truncated
r0151	- def					0.418	0.197	peptide deformylase
r0153	msf				0.474	0.410		major facilitator superfamily transporter, efflux protein
r0154	rpsO			2.247				30S ribosomal protein S15
r0155	-				0.306	0.369		hypothetical protein
tr0156					0.387			hypothetical protein
tr0157 tr0161					0.456 3.432			hypothetical protein hypothetical protein
tr0162	mecA				0.197			adaptor protein
r0179	-			0.369				hypothetical protein
r0184			0.411					conserved hypothetical protein, peptide-efflux protein homolog
r0208		2.445						hypothetical protein
r0209					0.453			hypothetical protein
r0210 r0232					0.442	0.441		hypothetical protein hypothetical protein
r0232 r0240					2.214	0.441		acetyltransferase, GNAT family
r0241	pabC					0.497		aminodeoxychorismate lyase
r0251	-			0.380				hypothetical protein
r0261	scpB				5.715		0.437	segregation and condensation protein B
tr0263 tr0270	- plcR			2.162	6.288	0.468		hypothetical protein
tr0277	pick			2.102	0.200	0.400		transcriptional regulator urease cluster protein, truncated
tr0278	-				0.243			urease cluster protein, truncated
tr0279	-				0.215			urease cluster protein, truncated
tr0280	urel				0.242			urease accessory protein, putatuve transport protein urea amidohydrolase (urease) gamma subunit
tr0281	ureA		0.475		0.265			urea amidohydrolase (urease) gamma subunit urea amidohydrolase (urease) beta subunit
r0282 r0287	ureB ureD		0.473		0.270			urea amidonydrolase (urease) beta subunit urease accessory protein
tr0299		0.485	0.112		0.014	3.372		succinyl-diaminopimelic descuccinlyasadipeptidase, truncated
r0304		0.351	0.187		0.134	4.978		hypothetical protein
tr0319	-				0.205			hypothetical protein
tr0328				0.437		0.195		hypothetical protein
tr0330				0.424	2.291			hypothetical protein
tr0331 tr0332	manN manM				3.047 3.207			mannose PTS system component IID mannose PTS system component IIC
tr0354	-	0.072	0.057		0.181	10.544		hypothetical protein
tr0357	-				0.441			hypothetical protein
tr0365	-	2.315			3.391			acetoin utilization protein, truncated
tr0373					2.260			hypothetical protein
tr0394 tr0402	luxS	2.678	2.001	0.489 0.383				S-ribosylhomocysteinase PTS fructose-specific enzyme IIABC components, truncated
tr0402			2.001	0.390				PTS fructose-specific enzyme IIABC components, truncated
tr0404	-			0.476				PTS fructose-specific enzyme IIABC components, truncated
tr0410	-	3.762	2.578					hypothetical protein
tr0414	-				2.181			hypothetical protein
r0417	rplU				0.420			50S ribosomal protein L21
r0435	-			3.146				hypothetical protein
tr0441 tr0444				2.542	0.418			hypothetical protein truncated IS1193 transposase
r0444 r0446					0.410		2.867	surface immunogenic protein, truncated
r0448			3.014				2.007	hypothetical protein
r0456	prtM				0.266			protease maturation protein precursor
r0458					3.656			cell wall protein precursor, similar to choline binding protein, truncated
r0459					4.377			cell wall protein precursor, similar to choline binding protein, truncated
r0460 r0461		0.344			2.600			cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated
r0465	- argJ	0.044	0.473				0.357	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein
r0468	-			2.457				hypothetical protein
r0473					3.434			hypothetical protein
r0479	atpB				0.160			ATP synthase subunit A
tr0494	amtB	2.258		0.305	0.295			ammonium transporter, Amp/Mep/NrgA family
r0505 r0506	glyQ	2.258			2.642 2.551			glycyl-tRNA synthetase alpha subunit hypothetical protein
tr0506 tr0508					2.551 2.277			hypothetical protein
tr0510					0.496	0.377	0.361	hypothetical protein
tr0511							0.480	beta-glucoside-specific PTS system IIABC component, truncated
tr0514				a (0.263	0.398	beta-glucoside-specific PTS system IIABC component, truncated
tr0528				2.137				hypothetical protein
tr0530 tr0540	- queA			2.934 2.689	2.381			hypothetical protein S-adenosylmethionine:tRNA ribosyltransferase-isomerase
r0544	-			2.000	0.347		6.133	hypothetical protein
r0547				2.221			3.826	ABC transporter permease protein
r0550			0.415	0.355				hypothetical protein
r0558	-				2.164			hypothetical protein
r0564				0.410	0.435			conserved hypothetical protein, MutT/nudix family
0565				2.112	2.540			hypothetical protein
0571				2.381	2.519			hypothetical protein conserved hypothetical protein, putative hydrolase
r0573 r0574				3.267	3.822 2.352			conserved hypothetical protein, putative hydrolase hypothetical protein
r0574 r0578	- thyA			0.382	2.302			hypothetical protein thymidylate synthase
r0580	-	2.192		0.002				hypothetical protein
				2.700				hypothetical protein
r0585		0.459		3.311				hypothetical protein
r0586	-	0.001			0.278			hypothetical protein
r0586 r0591		3.094						hypothetical protein ferrous ion transport protein A
r0585 r0586 r0591 r0600	- fooA							
r0586 r0591	- feoA ark			0.388	0.297		0,483	dvcerate kinase, putative
r0586 r0591 r0600 r0607	- feoA grk -			0.388	0.297		0.483	encost ful transcriptional regulator-PBP synthesis, truncated exclusive transcriptional regulator-PBP synthesis, truncated exclusive exotoxin B, putative

str0660					0.444			hypothetical protein
str0664				2.086	8.452	0.139		hypothetical protein
str0670 str0672	-			2.086	3.332			hypothetical protein peptidase, U32 family
str0682				0.336	0.002			hypothetical protein
str0685			0.373			3.279		hypothetical protein
str0688	-			0.375				hypothetical protein
str0694 str0700					2.115			hypothetical protein
str0700 str0702	÷				3.929			hypothetical protein hypothetical protein
str0703					2.341			hypothetical protein
str0706				2.782				hypothetical protein
str0707				2.503	2.510			hypothetical protein
str0709		0.293		2.132	4.389			hypothetical protein hypothetical protein
str0710 str0714	- IemA			0.482	4.003 0.336			cytoplasmic membrane protein
str0730	-			0.402	3.087			hypothetical protein
str0738					2.084			hypothetical protein
str0744	·				0.433			truncated IS1193 transposase
str0747 str0756	apbE	4.266		2.442				lipoprotein involved thiamine biosynthesis hypothetical protein
str0757				2.352				hypothetical protein RAS-related protein
str0760	dltX			2.273				hypothetical protein, RAS-related protein component involved in D-alanylation of teichoic acids, putative
str0766	-				0.356			IS861, transposase (orf2), IS3 family, truncated
str0769				0.461				IS861, transposase (orf1), IS3 family, truncated
str0772 str0777		0.262	0.328	0.163 0.363	0.240			unknown protein, phage associated hypothetical protein, phage-plasmid associated
str0784				0.455				unknown protein, phage associated
str0793				0.181	0.193			sensor histidine kinase (homolog to ciaH Spn), truncated
str0794	·			0.166	0.215			sensor histidine kinase (homolog to ciaH Spn), truncated
str0798	rpsT				0.470	3.191	9.283	30S ribosomal protein S20
str0821 str0861	-				0.403 0.407			truncated IS1193 transposase hypothetical protein
str0862					2.969			hypothetical protein
str0890					2.385	4.078		hypothetical protein
str0891					4.269			transcriptional regulator, biotin repressor family
str0913				0.380				hypothetical protein
str0914 str0930				0.426	3.443			hypothetical protein hypothetical protein
str0939				0.229	3.443			hypothetical protein
str0944					0.355			hypothetical protein
str0951					0.408			hypothetical protein
str0965 str0969		0.254		0.254	3.351 2.788			hypothetical protein amidase, truncated
str0909				3.169	2.700			amidase, truncated
str0978				6.464	9.009			hypothetical protein
str0980				3.026	5.273			hypothetical protein
str0981					6.056			transcriptional regulator, AraC family, truncated
str0982 str1011				0.348	2.748 2.712			transcriptional regulator, AraC family, truncated hypothetical protein
str1011 str1013	- malQ				2.712	0.344		4-alpha-glucanotransferase
str1030	-			3.351		0.011		alkaline amylopullulanase, truncated
str1037				0.403				hypothetical protein
str1038		3.030		0.457				hypothetical protein
str1044 str1047		6.855			0.500		0.337	positive transcriptional regulator MutR family hypothetical protein
str1066		0.000			0.485		0.337	6-phospho-beta-glucosidase, truncated
str1078	epsK	0.400		3.770	3.925			exopolysaccharide gene claster protein
str1079	epsJ			4.121	3.543			exopolysaccharide polymerization protein
str1118 str1125		0.457		0.405	2.116			hypothetical protein, truncated
str1125 str1130		0.459		2.465	0.398			hypothetical protein IS657, transposase, IS200 family, truncated
str1130	- rpIT			2.408	0.390			50S ribosomal protein L20
str1140	sipB			4.471	5.585			signal peptidase I
str1151	-				7.041			hypothetical protein
str1153				0.425	4.952 2.875			hypothetical protein, acetyltransferase, truncated
str1156 str1165	- endA			0.425	2.875		10.932	hypothetical protein competence associated membrane nuclease
str1168	-				0.401			hypothetical protein
str1170					0.254			hypothetical protein
str1179	rpIS	0.461		2.098	0.179		5.261	50S ribosomal protein L19
str1184 str1191	-							
str1191				2.030	2 607			hypothetical protein
	2			2.000	2.607		0.215	hypothetical protein
str1193	-			2.030	2.770 3.263		0.215	hypothetical protein hypothetical protein
str1193 str1194	-			2.030	2.770 3.263 5.310		0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein
str1193 str1194 str1195	-				2.770 3.263		0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209	- - - - hstH			0.462	2.770 3.263 5.310 3.742		0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein histone-like DNA-binding protein
str1193 str1194 str1195	- - - hstH -				2.770 3.263 5.310 3.742 2.776 0.494	2.102	0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227	- - - hstH -				2.770 3.263 5.310 3.742 2.776 0.494 0.461	2.102	0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein histone-tike DMA-birding protein hypothetical protein hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1231	- - - hstH - -				2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893	2.102	0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1231 str1237	- - - hstH - - -				2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 2.599	2.102		hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1231	- - hstH - - - -	2.824			2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893	2.102	0.215	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1231 str1237 str1239 str1240 str1241	- - hstH - - - - -				2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 2.599 3.413 3.357 3.632	2.102		hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1217 str1231 str1237 str1239 str1241 str1241	- - hstH - - - - - -				2.770 3.263 5.310 3.742 2.776 0.494 0.494 0.494 2.893 2.599 3.413 3.357 3.632 2.750	2.102		hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein, ChA family
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1237 str1239 str1240 str1240 str1258	- - hstH - - - - - -				2.770 3.263 5.310 3.742 2.776 0.494 0.494 0.461 2.893 2.599 3.413 3.357 3.632 2.750 3.419	2.102		hypothetical protein hypothetical protein surface-associated protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1237 str1239 str1240 str1241 str1250 str1258 str1285	- - hstH - - - - - - - - - - - - - - - - - - -				2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 3.413 3.357 3.652 2.750 3.419 0.096	2.102		hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein, GrAf family
str1193 str1194 str1195 str1209 str1210 str12219 str1227 str1231 str1237 str1230 str1240 str1240 str1240 str1258 str1258 str1285 str1286	- - hstH - - - - - - - - - - - - - - - - - - -			0.462	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 3.413 3.357 3.652 2.750 3.419 0.096 0.153 0.344	2.102		hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str12219 str1227 str1237 str1237 str1239 str1240 str1241 str1258 str1283 str1285 str1285 str1286 str1290	- - hstH - - - - - - - - - - - - - - - - - - -			0.462 3.007 3.339	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 2.599 3.413 3.357 3.632 2.750 3.419 0.096 0.153 0.344 3.510	2.102	0.484	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1227 str1231 str1231 str1237 str1239 str1240 str1240 str1241 str1258 str1285 str1285 str1285 str1285 str1285 str1280 str1291	- - hstH - - - - - - - - - - - - - - - - - - -			0.462 3.007 3.339 4.090	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 3.413 3.357 3.652 2.750 3.419 0.096 0.153 0.344	2.102	0.484	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1231 str1239 str1241 str1250 str1268 str1283 str1285 str1286 str1280 str1290 str1293	· · · · ·			0.462 3.007 3.339 4.090 2.032	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 2.599 3.413 3.357 3.632 2.750 3.419 0.096 0.153 0.344 3.510		0.484	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1227 str1231 str1231 str1237 str1239 str1240 str1240 str1241 str1258 str1285 str1285 str1285 str1285 str1285 str1280 str1291	- - hstH - - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.339 4.090	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 2.599 3.413 3.357 3.632 2.750 3.419 0.096 0.153 0.344 3.510 3.030	2.102 23.396 19.004	0.484	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1200 str1219 str12219 str12219 str12217 str1231 str1231 str1231 str1241 str1250 str1245 str1283 str1285 str1286 str1291 str1291 str1293 str1314 str1314	· · · · ·	2.824	0.379	0.462 3.007 3.339 4.090 2.032 2.021	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 3.413 3.357 3.632 2.750 3.419 0.096 0.153 0.344 3.510 3.030 0.131 0.306	23.396 19.004 25.795	0.484 2.009	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str12210 str12210 str12217 str12237 str12237 str12239 str1240 str1241 str1258 str1285 str1286 str1285 str1285 str1290 str1293 str13131 str1315 str1315	- - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.339 4.090 2.032	2.770 3.263 5.310 3.742 2.776 0.494 0.494 2.899 2.899 2.899 2.899 2.893 3.313 3.357 3.632 2.750 3.632 2.750 0.953 0.153 3.419 3.630 0.153 3.030	23.396 19.004 25.795 0.124	0.484 2.009 0.357	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein ABC transport permase protein
str1193 str1194 str1195 str1200 str1210 str1219 str12219 str12217 str1231 str1231 str1231 str1241 str1256 str1283 str1285 str13855 str13855 str13855 str13855 str13855 str13855 str13855 str13855 str1	- - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.339 4.090 2.032 2.021	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.893 3.457 3.652 2.750 0.441 3.457 3.652 2.750 0.444 3.510 3.303 0.344 3.650 0.344 3.650 0.344	23.396 19.004 25.795	0.484 2.009	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str12210 str12210 str12217 str12237 str12237 str12239 str1240 str1241 str1258 str1285 str1286 str1285 str1285 str1290 str1293 str13131 str1315 str1315	- - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.339 4.090 2.032 2.021	2.770 3.263 5.310 3.742 2.776 0.494 0.494 2.899 2.899 2.899 2.899 2.893 3.313 3.357 3.632 2.750 3.632 2.750 0.953 0.153 3.419 3.630 0.153 3.030	23.396 19.004 25.795 0.124	0.484 2.009 0.357	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein ABC transporte promase protein hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1237 str1237 str1237 str1239 str1240 str1241 str1250 str1241 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1335 str1315 str1315 str1335 str1345 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str1355 str13555 str13555 str13555 str135555 str13555555555555555555555555555555555555	- - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.339 4.090 2.021 0.385	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.993 3.413 7.593 3.352 2.759 3.3413 3.352 2.759 0.153 3.304 0.153 3.030 0.131 0.304 3.3030 0.131 0.330 0.330 2.494 0.252 2.850	23.396 19.004 25.795 0.124	0.484 2.009 0.357 0.421	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1210 str1211 str1227 str1237 str1237 str1237 str1240 str1240 str1240 str1241 str1285 str1285 str1285 str1285 str1283 str1285 str1283 str1283 str1314 str1315 str1332 str1334 str1334 str1332 str1332 str1334 str1344 str1345 str1332 str1332 str1348 str134	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499	0.379	0.462 3.007 3.339 4.090 2.021 0.385 0.165 0.293	2.770 3.263 5.310 3.742 2.776 0.464 0.461 0.461 2.803 2.803 3.542 3.562 3.575 0.341 3.567 3.652 3.750 0.153 0.414 3.510 3.030 0.153 0.306 3.300 0.306 3.300 0.306 3.300 0.306 3.300 0.326 2.255 2.8555 2.8555 2.8555 2.85555 2.85555 2.85555555555	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein
str1193 str1194 str1195 str1209 str1210 str1219 str1227 str1237 str1237 str1239 str1240 str1240 str1241 str1250 str1241 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str1335 str1335 str1335 str1335 str1334 str1349 str134	- - - - - - - - - - - - - - - - - - -	2.824	0.379	0.462 3.007 3.309 2.032 2.021 0.385 0.165 0.165 0.490	2.770 3.263 5.310 3.742 2.776 0.494 0.461 2.993 3.413 7.593 3.352 2.759 3.3413 3.352 2.759 0.153 3.304 0.153 3.030 0.131 0.304 3.3030 0.131 0.330 0.330 2.494 0.252 2.850	23.396 19.004 25.795 0.124	0.484 2.009 0.357 0.421	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein histona-tiko DMA-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothe
str1193 str1194 str1195 str1210 str1210 str1210 str1211 str1227 str1237 str1237 str1238 str1285 str1385 str1385 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1386 str1385 str138	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499	0.379	0.462 3.007 3.339 4.090 2.022 2.021 0.385 0.165 0.293 0.490 0.364	2.770 3.263 3.742 2.760 0.461 2.693 3.413 2.699 3.413 3.572 2.750 0.264 3.413 3.572 2.750 0.544 3.510 3.131 0.096 0.153 0.344 3.510 3.330 0.344 0.434 0.252 2.850 0.225	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protei
str1193 str1194 str1195 str1209 str1210 str1210 str12210 str12210 str12210 str12231 str1231 str1231 str1233 str1241 str1258 str1242 str1285 str1285 str1285 str1285 str1285 str1285 str1285 str13135 str1314 str1315 s	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499	0.379	0.462 3.007 3.309 2.032 2.021 0.385 0.165 0.165 0.490	2.770 3.263 5.310 3.742 2.776 4.484 0.494 0.494 2.893 2.599 3.413 3.357 3.632 2.750 3.419 0.344 0.344 0.344 0.3510 3.030 0.131 0.306 0.131 0.306 0.131 0.366 0.255 0.255 0.222 0.312	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421 0.438	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein histona-tiko DMA-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothe
str1193 str1194 str1195 str1210 str1210 str1210 str12210 str12210 str12210 str12210 str12210 str1223 str1233 str1235 str1286 str1286 str1283 str1285 str1286 str1283 str1285 str1286 str1289 str1314 s	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.022 2.021 0.385 0.165 0.293 0.490 0.364	2.770 3.263 3.742 2.760 0.461 2.693 3.413 2.699 3.413 3.572 2.750 0.264 3.413 3.572 2.750 0.544 3.510 3.131 0.096 0.153 0.344 3.510 3.330 0.344 0.434 0.252 2.850 0.225	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421 0.438	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protei
str1193 str1194 str1195 str1210 str1210 str1210 str1210 str12210 str12210 str12210 str12230 str1231 str1231 str12230 str1241 str12255 str12255 str12255 str12255 str12255 str12255 str12255 str12255 str1235 str1235 str1235 str1235 str1355 str13555	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.022 0.262 0.285 0.485 0.293 0.490 0.384 0.491	2.770 3.263 3.742 2.763 4.742 4.744 0.461 2.893 3.413 3.557 2.363 2.693 3.413 3.557 2.363 2.693 0.419 0.753 0.344 3.510 3.300 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.330 0.131 0.334 0.334 0.334 0.335 0.344 0.345 0.355 0.345 0.355 0.345 0.3557 0.355 0.355 0.355 0.35570000000000000000000000000000000000	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421 0.438	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protei
str1193 str1194 str1195 str1209 str12019 str12219 str12219 str12231 str12231 str12231 str12230 str1240 str1241 str12255 str1286 str1286 str1285 str1286 str1286 str1287 str1281 str1333 str1334 str1345 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1334 str1345 str1334 str1345 str134	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.022 0.262 0.285 0.485 0.293 0.490 0.384 0.491	2.770 3.263 3.742 2.760 4.744 0.461 2.893 2.599 3.413 3.552 2.760 2.760 2.760 3.419 0.096 0.153 0.344 3.610 3.030 0.341 0.361 0.331 0.390 2.494 0.452 2.850 0.332 0.3330 0.344 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.452 0.334 0.454 0.454 0.454 0.454 0.454 0.454 0.454 0.454 0.454 0.454 0.454 0.455 0.344 0.455 0.244 0.455 0.244 0.255 0.244 0.255 0.244 0.255 0.244 0.255 0.244 0.255 0.244 0.255 0.244 0.255 0.244 0.255 0.245 0.255 0.244 0.255 0.245 0.255 0.245 0.255 0.245 0.255 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.255 0.254 0.2550000000000	23.396 19.004 25.795 0.124 0.092 2.721	0.484 2.009 0.357 0.421 0.438 0.399 0.473	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protei
str1193 str1194 str1195 str1209 str1201 str1210 str12231 str1231 str1231 str1231 str1231 str1232 str1241 str1255 str1240 str12285 str1286 str1286 str1286 str1287 str1333 str1334 str1335 str1348 str1348 str1386 str1486 str1	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.022 0.262 0.285 0.485 0.293 0.490 0.384 0.491	2.770 3.263 3.742 2.763 4.742 4.744 0.461 2.893 3.413 3.557 2.363 2.693 3.413 3.557 2.363 2.693 0.419 0.753 0.344 3.510 3.300 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.330 0.131 0.334 0.334 0.334 0.335 0.344 0.345 0.355 0.345 0.355 0.345 0.3557 0.355 0.355 0.355 0.35570000000000000000000000000000000000	23.396 19.004 25.795 0.124 0.092	0.484 2.009 0.357 0.421 0.438	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protei
str1193 str1194 str1195 str1209 str1210 str1210 str1210 str12210 str12210 str12210 str12210 str12230 str12230 str12230 str12230 str12285 str1385 str14	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.021 0.385 0.293 0.295 0.293 0.490 0.384 0.191 0.344 2.943 3.037	2.770 3.263 3.742 2.763 4.742 4.744 0.461 2.893 3.413 3.557 2.363 2.693 3.413 3.557 2.363 2.693 0.419 0.753 0.344 3.510 3.300 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.330 0.131 0.334 0.334 0.334 0.335 0.344 0.345 0.355 0.345 0.355 0.345 0.3557 0.355 0.355 0.355 0.35570000000000000000000000000000000000	23.396 19.004 25.795 0.124 0.092 2.721	0.484 2.009 0.357 0.421 0.438 0.399 0.473	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein histona-tike DNA-kinding protein hypothetical protein hypothetical protein hypothe
str1193 str1194 str1195 str1209 str1201 str1210 str12231 str1231 str1231 str1231 str1231 str1232 str1241 str1255 str1240 str12285 str1286 str1286 str1286 str1287 str1333 str1334 str1335 str1348 str1348 str1386 str1486 str1	- - - - - - - - - - - - - - - - - - -	2.824 0.448 0.499		0.462 3.007 3.339 4.090 2.022 2.021 0.385 0.165 0.293 0.490 0.364 0.191 0.344 2.943	2.770 3.263 3.742 2.763 4.742 4.744 0.461 2.893 3.413 3.557 2.363 2.693 3.413 3.557 2.363 2.693 0.419 0.753 0.344 3.510 3.300 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.304 0.131 0.330 0.131 0.334 0.334 0.334 0.335 0.344 0.345 0.355 0.345 0.355 0.345 0.3557 0.355 0.355 0.355 0.35570000000000000000000000000000000000	23.396 19.004 25.795 0.124 0.092 2.721	0.484 2.009 0.357 0.421 0.438 0.399 0.473	hypothetical protein hypothetical protein surface-associated protein cshA precursor, truncated hypothetical protein hypothetical protei

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str1424 str1437		2.160		2.247				potassium channel protein, truncated ABC transporter permease protein
str1437 str1450	- oxlT	3.031		0.260	0.021	0.220	3.256	oxalate:formate antiporter
str1462	-				2.054			hypothetical protein
str1475	-	0.485		2.260				hypothetical protein
str1477 str1487				2.998 2.168				glycosyl transferase, truncated hypothetical protein
str1499	-			2.100	0.325			hypothetical protein
str1500	-				0.336			hypothetical protein
str1507	-				0.357	0.480		hypothetical protein
str1511 str1518	2				2.078	0.480		positive transcriptional regulator MutR family hypothetical protein
str1528	-		0.494	3.211	0.162		2.194	acetyltransferase, GNAT family
str1548	rpsP			2.165				30S ribosomal protein S16
str1552	-				3.974			ISSth2, transposase, IS5 family, truncated
str1565 str1602		2.107			4.173	0.396		peptidoglycan GlcNAc deacetylase, truncated hypothetical protein
str1604	ilvD1	2.107			0.249	0.550		dihydroxy-acid dehydratase
str1608					0.288			ABC transporter permease protein
str1611	-	5.489						hypothetical protein
str1628 str1630	-	0.187 0.176		2.164		6.350 8.857		hypothetical protein
str1630		0.182		2.079		10.418		6-phospho-beta-glucosidase, truncated 6-phospho-beta-glucosidase, truncated
str1632	msrA2	0.285	0.488		0.457	6.990		methionine sulfoxide reductase A
str1639	-			0.217				hypothetical protein
str1658	cah	15.750	3.729			0.181 0.443	0.312	carbonate dehydratase
str1659 str1662		7.936	3.818	2.825	2.967	0.443	0.396	hypothetical protein plasmid mobilization protein, truncated
str1663	int3			2.808	2.307	0.353		integrase/recombinase plasmid associated, putative
str1671	gla				0.208			glycerol uptake facilitator protein
str1672	pepXP	3.292			2.770	0.446		x-prolyl-dipeptidyl aminopeptidase
str1685 str1688	blpK blpC			0.398 0.324	0.303			pore-forming peptide, putative bacteriocin signal peptide, putative
str1689	-			0.324	0.303			peptide ABC transporter, truncated
str1690	-				0.331			peptide ABC transporter accessory protein, truncated
str1712	-			0.353	0.298			hypothetical protein
str1718	-				0.189			hypothetical protein
str1719 str1724	- ansB	2.075			0.238			hypothetical protein L-asparaginase
str1724	-	2.010					0.414	hypothetical protein
str1735	scrB				2.720			sucrose-6-phosphate hydrolase
str1743	-			0.344	0.333			hypothetical protein
str1746 str1747	-	0.294		0.411				hypothetical protein hypothetical protein
str1750				2.012				hypothetical protein
str1752	rpsR			2.287	0.335		2.272	30S ribosomal protein S18
str1756	-					0.379		hypothetical protein
str1759	-			0.457				hypothetical protein
str1760 str1764				0.464	0.489			hypothetical protein hypothetical protein
str1776	gnlA				0.253			glutamine synthetase
str1782	pgk				0.201			phosphoglycerate kinase
str1791	rpsL			2.786				30S ribosomal protein S12
str1808 str1816	rpmH			2.121	0.181	0.411		50S ribosomal protein L34
str1817	- rpIA			3.112	0.437	0.411		oligopeptide ABC transporter substrate-binding protein, truncated 50S ribosomal protein L1
str1818	rplK			3.358	0.274			50S ribosomal protein L11
str1820	-					0.480		hypothetical protein
str1829 str1841	-			0.469 0.461			0.436	formate-nitrate transporter, truncated
str1843				0.461	0.351		0.430	hypothetical protein hypothetical protein
str1850	-				0.242			hypothetical protein
str1854	-			0.370				hypothetical protein
str1859	-			0.190				hypothetical protein
str1861 str1866				0.250				hypothetical protein hypothetical protein
str1874				0.217	0.371			dihydroxy-acid dehydratase, truncated
str1876	asp				0.388			alkaline-shock protein
str1883	-			0.235	0.395	0.380		alcohol-acetaldehyde dehydrogenase, truncated
str1886 str1887			2.530 2.083	0.158 0.119	0.403 0.451		0.443	trehalose-6-phosphate hydrolase, truncated trehalose-6-phosphate hydrolase, truncated
str1888		5.878	2.455	0.101	0.475	0.218	0.460	trehalose-6-phosphate hydrolase, truncated
str1889	-			0.072				PTS trehalose-specific IIBC component, truncated
str1890	-	10.738	2.192	0.077	0.286			PTS trehalose-specific IIBC component, truncated
str1891 str1894		7.187 2.074	2.023	0.096 0.343	0.261			PTS trehalose-specific IIBC component, truncated hypothetical protein
str1894 str1895		2.0/4		0.407				hypothetical protein
str1901				0.440	0.402			glutamatecysteine ligase, putative, truncated
str1902				0.359		149.748		glutamatecysteine ligase, putative, truncated
str1903 str1920	- rpsH			0.394	0.401 0.479			glutamatecysteine ligase, putative, truncated 30S ribosomal protein S8
str1920 str1924	rpsm				0.479			50S ribosomal protein L14
str1926	rpmC			2.502	2.100			50S ribosomal protein L29
str1929	rpIV			2.364	a ·			50S ribosomal protein L22
				2.645 2.239	0.429 0.335			50S ribosomal protein L4 50S ribosomal protein L3
str1933	rpID				0.000		0.407	50S ribosomal protein L3
	rpID rpIC						3.167	multidrug-efflux transporter, putative
str1933 str1934 str1943 str1950	rpID rpIC pmrB -				0.423		3.167	multidrug-efflux transporter, putative positive transcriptional regulator MutR family, truncated
str1933 str1934 str1943 str1950 str1953	rpID rpIC				0.060		3.167	multidrug-efflux transporter, putative positive transcriptional regulator MutR family, truncated replication initiator protein
str1933 str1934 str1943 str1950 str1953 str1954	rpID rpIC pmrB - rip -				0.060 0.399		3.167	multidrug-efflux transporter, putative positive transcriptional regulator MutR family, truncated replication initiator protein hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1954 str1955	rpID rpIC pmrB -			0.380	0.060 0.399 0.287		3.167	multidrug-efflux transporter, putative positive transcriptional regulator MutR family, truncated replication initiator protein hypothetical protein integrase/recombinase, phage associated hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1954 str1956 str1959	rpID rpIC pmrB - rip -				0.060 0.399 0.287 0.140 0.254		3.167	multidrug-efflux transporter, putative positive transportional regulator MutR family, truncated reglication initiator protein hypothetical protein integrase/ircecmbinase, phage associated hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1955 str1956 str1959 str1960	rpID rpIC pmrB - rip -			0.380	0.060 0.399 0.287 0.140 0.254 0.278			multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein integrase/recombinase, phage associated hypothetical protein Hypothetical protein Holidiay juncion resolvase-like protein
str1933 str1934 str1943 str1950 str1953 str1954 str1955 str1956 str1959 str1960 str1964	rpID rpIC pmrB - rip -				0.060 0.399 0.287 0.140 0.254 0.278 2.058		2.913	multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein integrase/recombinase, phage associated hypothetical protein Holiday junction resolvase-like protein Hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1955 str1956 str1959 str1960	rpID rpIC pmrB - rip -			0.380	0.060 0.399 0.287 0.140 0.254 0.278			multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein integrase/recombinase, phage associated hypothetical protein Hypothetical protein Holidiay juncion resolvase-like protein
str1933 str1934 str1943 str1950 str1953 str1955 str1956 str1956 str1950 str1960 str1964 str1970 str1976	rpID rpIC pmrB - rip -			0.380	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321	0.435		multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein hypothetical protein hypothetical protein Hypothetical protein Hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1955 str1955 str1956 str1959 str1960 str1964 str1970 str1970 str1983	rpID rpIC pmrB - rip -			0.380	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381	0.435		multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein trypothetical protein trypothetical protein Mypothetical protein Holidiay junction resofwase-tike protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1955 str1956 str1959 str1960 str1960 str1960 str1960 str1970 str1976 str1983 str1987 str1990	rpID rpIC pmrB - rip -			0.380	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381	0.435		multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein integrase/recombinase, phage associated hypothetical protein Hypothetical protein Holliday juncion resolvase-like protein Hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1933 str1934 str1943 str1950 str1953 str1955 str1955 str1956 str1959 str1960 str1964 str1970 str1970 str1983	rpID rpIC pmrB - rip -			0.380 3.817 0.487	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381	0.435		multidrug-efflux transporter, putative positive trans-profiloral regulator MuR family, truncated replication initiator protein hypothetical protein
str1933 str1934 str1943 str1953 str1954 str1955 str1956 str1956 str1959 str1966 str1969 str1960 str1976 str1970 str1970 str1983 str1983 str1991 str1991 str1991 str1992	rpID rpIC pmrB - rip -			0.380 3.817 0.487 0.436	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434	0.437		multidrug-efflux transporter, putative positive trans-priorional regulator MuR family, truncated replication initiator protein hypothetical protein hypothetical protein typothetical protein hypothetical protein
str1933 str1934 str1953 str1953 str1955 str1955 str1956 str1956 str1956 str1956 str1960 str1960 str1960 str1976 str1987 str1987 str1987 str1989 str1999 str1999 str1991 str1992 str2005	rpID rpIC pmrB - rip - int4 - - - - - - - - - - - - -			0.380 3.817 0.487 0.436 0.406 0.443	0.060 0.399 0.287 0.140 0.254 0.254 0.258 0.321 0.381 0.262 0.163 0.214 0.214 0.434			multidrug-efflux transporter, putative positive trans-priorional regulator MuR family, truncated replication initiator protein Integrase/recombinase, phage associated hypothetical protein Multidray junction resolvase-like protein Hypothetical protein
str1933 str1934 str1943 str1953 str1954 str1955 str1956 str1956 str1959 str1966 str1969 str1960 str1976 str1970 str1970 str1983 str1983 str1991 str1991 str1991 str1992	rpID rpIC pmrB - rip - int4 - - - - - - - - - - - - -			0.380 3.817 0.487 0.436 0.406	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434	0.437		multidrug-efflux transporter, putative positive trans-priorional regulator MuR family, truncated replication initiator protein hypothetical protein hypothetical protein typothetical protein hypothetical protein
str1933 str1934 str1943 str1950 str1955 str1955 str1956 str1959 str1995 str1997 str1997 str1997 str1997 str1997 str1997 str1997 str1992 str2004 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2002 str2004 str2005 str2002 str2005 str205 str2005	rpID rpIC pmrB - rip - int4 - - - - - - - - - - - - - - - - - - -	nd metabolism	ı	0.380 3.817 0.487 0.436 0.406 0.443 0.420	0.060 0.339 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434 0.068 0.347	0.437 0.485		multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein
str1933 str1934 str1943 str1943 str1953 str1955 str1955 str1955 str1955 str1959 str1960 str1965 str1975 str1983 str1987 str1983 str1990 str1992 str2004 str2005 str2022	rpID rpIC pmrB - rip - rp - - - - - - - - - - - - - - - - -	nd metabolism	1	0.380 3.817 0.487 0.436 0.406 0.443 0.420 0.424	0.060 0.339 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434 0.668 0.347 0.202	0.437 0.485 0.283	2.913	multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein integrase/recombinase, phage associated hypothetical protein Multidray junction resolvase-like protein hypothetical protein
str1933 str1934 str1943 str1953 str1955 str1955 str1955 str1955 str1956 str1985 str1985 str1986 str1986 str1986 str1986 str1987 str1989 str1989 str1992 str2004 str2002 str2004	rpID rpIC pmrB - rip - int4 - - - - - - - - - - - - - - - - - - -	nd metabolism	1	0.380 3.817 0.487 0.436 0.443 0.420 0.420 0.424 0.400	0.060 0.399 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434 0.668 0.347 0.202 0.310	0.437 0.485 0.283 0.478	2.913	multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein
str1933 str1934 str1943 str1953 str1955 str1955 str1955 str1955 str1956 str1956 str1987 str1987 str1987 str1987 str1983 str1987 str1982 str2004 str2002 str2004 str2002 str2004	rpID rpIC pmrB - rip - int4 - - - - - - - - - - - - - - - - - - -		1	0.380 3.817 0.487 0.436 0.406 0.443 0.420 0.424	0.060 0.339 0.287 0.140 0.254 0.278 2.058 0.321 0.381 0.262 0.163 0.214 0.434 0.668 0.347 0.202	0.437 0.485 0.283	2.913	multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetic
str1933 str1934 str1943 str1953 str1955 str1955 str1956 str1956 str1956 str1956 str1960 str1960 str1960 str1960 str1987 str1987 str1987 str1991 str1990 str1991 str1990 str1990 str1991 str1992 str2004 str2002 str200	rpID rpIC pmmB - rip - - - - - - - - - - - - - - - - - - -	4.899	2.561	0.380 3.817 0.487 0.436 0.406 0.443 0.420 0.424 0.420 0.452	0.060 0.399 0.287 0.140 0.254 0.278 0.258 0.258 0.321 0.321 0.321 0.321 0.321 0.321 0.347 0.262 0.163 0.214 0.347 0.268 0.347 0.244 0.347	0.437 0.485 0.283 0.478 0.491	2.913 2.594 2.604 2.604 2.407	multidrug-efflux transporter, putative positive trans-policional regulator MuR family, truncated replication initiator protein hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypotheti
str1933 str1934 str1943 str1953 str1955 str1955 str1956 str1956 str1956 str19864 str1987 str1985 str19	rpID rpIC pmmB - rip - int4 - - - - - - - - - - - - - - - - - - -	4.899 5.768	2.561 4.046	0.380 3.817 0.487 0.436 0.406 0.443 0.420 0.424 0.420 0.452	0.060 0.399 0.287 0.140 0.254 0.278 0.381 0.381 0.262 0.381 0.262 0.163 0.214 0.434 0.668 0.344 0.347 0.340 0.340 0.340 0.341 0.242 0.310 0.341 0.447 0.447 0.147	0.437 0.485 0.283 0.478 0.491	2.913 2.594 2.604 2.570 2.407 2.515	multidrug-efflux transporter, putative positive transcriptional regulator MuR family, truncated replication initiator protein hypothetical protein
str1933 str1934 str1943 str1953 str1955 str1955 str1956 str1956 str1956 str1956 str1960 str1960 str1960 str1960 str1987 str1987 str1987 str1991 str1990 str1991 str1990 str1990 str1991 str1992 str2004 str2002 str200	rpID rpIC pmmB - rip - - - - - - - - - - - - - - - - - - -	4.899	2.561	0.380 3.817 0.487 0.436 0.406 0.443 0.420 0.424 0.420 0.452	0.060 0.399 0.287 0.140 0.254 0.278 0.258 0.258 0.321 0.321 0.321 0.321 0.321 0.341 0.344 0.434 0.434 0.434 0.347 0.202 0.347	0.437 0.485 0.283 0.478 0.491	2.913 2.594 2.604 2.604 2.407	multidrug-efflux transporter, putative positive trans-policional regulator MuR family, truncated replication initiator protein hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypotheti

str0045	purB1	2.228	2.080		0.374			adenylosuccinate lyase
str0134 str0139	pyrG	4.852	2.078		0.321			CTP synthetase cyclo-nucleotide phosphodiesterase, truncated
str0141						0.395		cyclo-nucleotide phosphodiesterase, truncated
str0142 str0144	-	3.740	2.152	3.002		0.407	2.012	cyclo-nucleotide phosphodiesterase, truncated hypothetical protein
str0144 str0256	nrdl -			3.002	2.923		0.485	nypotnetical protein putative deoxyribonucleotide triphosphate pyrophosphatase/unknown domain fusion protein
str0438	pyrH			2.164				uridylate kinase
str0489 str0523	tmk pyrR	3.269			0.397 0.270			thymidylate kinase pyrimidine regulatory protein PyrR
str0526	carA				2.121	0.445		carbamoyl-phosphate synthase small subunit
str0527	carB				2.145	0.428		carbamoyl-phosphate synthase large subunit
str0551 str0566	- pfs		0.353	2,902	0.221			phosphorylase, Pnp/Udp family, putative 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
str0750	add			2.002	0.472			adenosine deaminase
str0751	tdk			0.389	0.409		2.355	thymidine kinase
str0791 str0803	fhs -			0.389	0.137 2.317		2.300	formate-tetrahydrofolate ligase pyrimidine-nucleoside phosphorylase, truncated
str0804	-				2.471			pyrimidine-nucleoside phosphorylase, truncated
str0805	-				2.644		0.404	deoxyribose-phosphate aldolase, truncated
str0806 str0807	- cdd				2.846 3.090		0.484	deoxyribose-phosphate aldolase, truncated cytidine deaminase
str0886	guaA				2.237			bifunctional GMP synthase/glutamine amidotransferase protein
str0941	-			0.460	0.258	0.279		phosphorylase, Pnp/Udp family
str0967 str0979	pyrF			0.460	3.842	0.279		orotidine 5'-phosphate decarboxylase 5'-nucleotidase, putative
str1113	deoD	0.482			2.455			purine nucleoside phosphorylase (family 1)
str1114	gat	0.350			2.457			glutamine amidotransferase
str1117 str1207	punA pyrDa	0.376		2.401				purine nucleoside phosphorylase dihydroorotate dehydrogenase
str1223	apt				0.329			adenine phosphoribosyltransferase
str1260	udk			3.567	2.305		4,742	uridine kinase
str1270 str1331	nrdE			0.360	0.366		4.742	ribonucleotide-diphosphate reductase alpha subunit cytidine/deoxycytidylate deaminase family protein, putative
str1339	-			0.391				nucleobase cation symporter for xanthine. truncated
str1341 str1610	- hit	7.289	2.048	0.500				nucleobase:cation symporter for xanthine, truncated cell cycle regulation histidine triad (HIT) protein
str1610 str1844	-	7.289	2.048	0.497	0.236			cytidine/deoxycytidylate deaminase family protein, putative
str1913	adk	0.494		4.704	0.459	0.479		adenylate kinase
str1941	flaR			0.040	0.482		0.004	topology modulation protein
str1963 str2016	nrdD guaB			3.618	0.237		3.391	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase
								······································
Posttrans str0119	lational modi grpE	fication, prote	n turnover, chaj 2.033	perones 0.444			0.483	heat shock protein, chaperonin
str0120	dnaK		2.033	0.404			0.438	molecular chaperone DnaK
str0121	dnaJ				2.787		0.440	heat shock protein, chaperonin
str0132 str0203	tig groES	2.176		0.377	0.095	0.448		trigger factor co-chaperonin GroES
str0203	groEL			0.351			0.465	chaperonin GroEL
str0284	ureE				0.368			urease accessory protein
str0285 str0356	ureF clpP				0.475	0.386		urease accessory protein ATP-dependent Clp protease proteolytic subunit
str0515	ppiA				0.293	2.041	2.835	peptidyl-prolyl cis-trans isomerase
str0602	clpE	3.441						ATP-dependent Clp protease
str0715 str0722	htpX piID			0.468 0.335				heat shock protein HtpX prepilin peptidase type IV
str0749	-	3.842		0.555	0.204			glutathione S-transferase family
str0827	-			2.601	0.264		2.887	hypothetical protein, coenzyme PQQ synthesis homologue
str0990 str1269	tpx nrdH		0.352	3.370 3.082	0.294 0.233	8.235	6.174	thiol peroxidase glutaredoxin
str1614	clpL			0.188	2.162		0.114	ATP-dependent proteinase ATP-binding subunit
str1640	pfIA	4.059			0.469	0.176		pyruvate-formate lyase activating enzyme
str1803 str1805	trxA1 bta				0.129 0.277			thioredoxin bacteriocin transport accessory protein, putative
str1846	-		0.171		0.286	6.616		transcription regulator, putative
str1849	trxA2				0.340			thioredoxin
str1885 str1966	pepO nrdG			2.377	0.407		2.641	endopeptidase O anaerobic ribonucleotide reductase activator
str2024	htrA			0.350	0.187		2.041	exported serine protease
Secondar	v metaboliter	e hioeunthoeie	, transport and	cataboliem				
str0029	acpP1	22.301	, transport and t	0.476	0.367			acyl carrier protein
str0384	acpP2				0.470			acyl carrier protein
str0763 str0909	dltC	0.380	0.432		2.281	4.592		D-alaninepoly(phosphoribitol) ligase subunit 2 acetoin reductase, truncated
str0910		0.000	0102	2.767		10.053		acetoin reductase, truncated
str0924	aldB				3.226			alpha-acetolactate decarboxylase
str0929 str1634	- entB			0.342	0.226			oxidoreductase, short chain dehydrogenase/reductase family pyrazinamidase/nicotinamidase, putative
								· · · · · · · · · · · · · · · · · · ·
Signal tra str0112	nsduction me	echanisms			0.126		2.319	hypothetical protein
str0152		2.401					2.010	transcriptional regulator, putative
str0159		0.001	0.055	3.273	2.047	0.405		amino acid (glutamine) ABC transporter substrate binding protein/permease protein
str0296 str0317	- rr01	0.361	0.056		0.082 0.291	6.942		amino acid ABC transporter substrate binding protein, putative response regulator (homolog to csrR/covR Spy)
str0318	hk01				0.291			sensor histidine kinase (homolog to csrS/covS Spy)
str0401	-			0.324				PTS fructose-specific enzyme IIABC components, truncated
str0447 str0543	phoH rr02				0.261 0.279			phosphate starvation-induced protein response regulator
str0665	-			0.421				hypothetical protein
str0729	typA				2.601	0.406		GTP-binding protein TypA/BipA (tyrosine phosphorylated protein A)
str0792 str0795				0.186 0.146	0.154 0.261			response regulator (homolog to ciaR Spn), truncated sensor histidine kinase (homolog to ciaH Spn), truncated
str0877						0.367	0.321	amino acid (dutamine) ABC transporter, substrate binding protein
str0908 str0974	-	0.435	0.273	2.771	2.366	3.666 0.297		ABC transporter substrate binding protein
str0974 str0975	2			2.771 3.287	2.366 4.384	0.297		ABC transporter substrate binding protein, truncated ABC transporter substrate binding protein, truncated
str1175				0.207	0.220			hypothetical protein
str1325	rr06		2.554		4.326			response regulator (homolog to RR11 Spn)
	hk06			0.236	2.469 2.060			sensor histidine kinase (homolog to HK11 Spn) response regulator (homolog to RR08 Spn) uncoupled, truncated
str1326 str1380				0.253			0.415	response regulator (homolog to RR08 Spn) uncoupled, truncated
str1380 str1381	·					0.419		response regulator (homolog to RR03 Spn)
str1380 str1381 str1420	- rr08					0.387		sensor histidine kinase (homolog to HK03 Spn) protein kinase
str1380 str1381 str1420 str1421	hk08			2.757				
str1380 str1381 str1420 str1421 str1425 str1425	- rr08 hk08 pknB pppL			2.757 2.297				phosphoprotein phosphatase
str1380 str1381 str1420 str1421 str1425 str1426 str1579	hk08 pknB	0.305	0.158	2.297 2.084	0.236	12.993		phosphoprotein phosphatase amino acid (glutamine) ABC transporter substrate binding protein
str1380 str1381 str1420 str1421 str1425 str1426 str1579 str1637 str1654	hk08 pknB	0.305	0.158	2.297	0.236	12.993		phosphoprotein phosphatase amiro acid (glutamine) ABC transporter substrate binding protein hypothetical protein ABC transporter substrate-binding protein, amino acid
str1380 str1381 str1420 str1421 str1425 str1426 str1579 str1657 str1654 str1948	hk08 pknB	0.305		2.297 2.084 0.217 2.320	0.331 0.329	12.993		phosphoprotein phosphatase amino acid (glutamine) ABC transporter substrate binding protein hypothetical protein ABC transporter substrate-binding protein, amino acid hypothetical protein
str1380 str1381 str1420 str1421 str1425 str1426 str1579 str1637 str1654	hk08 pknB	0.305		2.297 2.084 0.217	0.331	12.993		phosphoprotein phosphatase amiro acid (glutamine) ABC transporter substrate binding protein hypothetical protein ABC transporter substrate-binding protein, amino acid

Transcrip str0006								
5110000	trcF					0.489		transcription repair coupling factor
str0065	-				0.374			transcriptional regulator. MarR family, truncated
str0096 str0118	- hrcA				0.126	0.408	0.485	transcriptional regulator, putative, truncated heat-inducible transcription repressor
str0133	rpoE				0.153	0.361	0.405	DNA-directed RNA polymerase subunit delta
str0185	adcR			0.394				zinc transport transcriptional repressor
str0219	-			2.855	0.004			transcriptional regulator, DeoR family
str0242 str0317	greA rr01				2.364 0.291			transcription elongation factor GreA response regulator (homolog to csrR/covR Spy)
str0341	nusA			2.871				transcription elongation factor NusA
str0342	-			4.082				hypothetical protein
str0381 str0399	- fruR			0.475	0.498			transcriptional regulator, MarR family transcriptional repressor
str0452	-	0.366	0.205	0.475		9.072		transcriptional regulator, LysR family
str0543	rr02				0.279			response regulator
str0549	-				0.377			transcriptional repressor, putative
str0615 str0625	- ror		2.126	2.092				transcriptional antiterminator (BgIG family), truncated exoribonuclease R
str0630	ссрА			0.489				catabolite control protein
str0649	-			2.296	7.315			negative transcriptional regualtor-PBP synthesis, truncated
str0663 str0665	tex			2.434	4.710			transcriptional regulator, putative hypothetical protein
str0689				0.421	2.093			restriction-modification system regulatory protein, putative
str0792				0.186	0.154			response regulator (homolog to ciaR Spn), truncated
str0813	dinG	0.459		2.941				ATP-dependent DNA helicase
str0895	-				10.016		2.077	transcriptional regulator
str0916 str0931					3.830		2.077	transcriptional regulator transcriptional regulator, TetR family
str0950	fbp		2.039		0.000			fibronectin-binding protein-like protein A
str1214	- '				2.503			transcriptional repressor protein, putative
str1287 str1296	-			2.523 2.876	5.487		3.974	transcriptional regulator, putative ribonuclease III
str1296 str1325	rncS rr06		2.554	2.876	5.487 4.326			ribonuclease III response regulator (homolog to RR11 Spn)
str1366	-			0.315				conserved hypothetical protein, Rrf2 family protein
str1380	-			0.236	2.060		a ···-	response regulator (homolog to RR08 Spn) uncoupled, truncated
str1381 str1420	- rr08			0.253		0.419	0.415	response regulator (homolog to RR08 Spn) uncoupled, truncated
str1420 str1425	pknB			2.757		0.419		response regulator (homolog to RR03 Spn) protein kinase
str1435	-	2.459						transcriptional regulator, GntR family, putative
str1488	rpoD			2.319				RNA polymerase sigma factor
str1568 str1586	rheA			2.454 0.370	0.314			ATP-dependent RNA helicase negative transcriptional regulator - copper transport operon
str1586 str1600	copY -			0.370	0.314	0.359		transcriptional regulator, MerR family
str1699	rheB		2.174					ATP-dependent RNA helicase
str1725	recG						0.483	ATP-dependent DNA helicase
str1733 str1736	scrK			0.484	4.534	0.417	0.465	fructokinase sucrose regulon regulatory protein, truncated
str1777	gnIR				0.212			transcriptional regulator, repressor of the glutamine synthetase, MerR family
str1892	-		2.642	0.422				trehalose operon transcriptional repressor GntR family, truncated
str1908	rpoA				0.296			DNA-directed RNA polymerase alpha subunit
str1948 str1989					0.329			hypothetical protein hypothetical protein
str1995					0.426			transcriptional regulator, TetR/AcrR family
str2025	spoJ			0.378	0.241			chromosome segregation protein
Tranelatio	n riboeoms	al structure and	hiogenesis					
str_r01	11, 110030116	ai structure anu	2.649	0.487	0.402			
str_r03			2.292	0.465	0.375			
str_r04			2.526	0.376				
str_r05 str_r09				0.570	0.458			
		0.397	0.004	0.298	0.464			
str t01		0.397	2.224	0.298 0.459	0.464 0.364			
str_t01 str_t02		0.397	2.224	0.298	0.464 0.364 0.186 0.192			
str_t01 str_t02 str_t03			2.224	0.298	0.464 0.364 0.186 0.192 0.333		2.839	
str_t01 str_t02 str_t03 str_t05			2.224	0.298	0.464 0.364 0.186 0.192 0.333 0.148		2.839	
str_t01 str_t02 str_t03 str_t05 str_t06			2.224	0.298	0.464 0.364 0.186 0.192 0.333 0.148 0.343		2.839	
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08		0.415	2.224	0.298	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.189		2.839	
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08 str_t09		0.415	2.224	0.298 0.459	0.464 0.364 0.186 0.192 0.333 0.148 0.343 0.268 0.189 0.142			
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08 str_t09 str_t10		0.415 0.316 0.467		0.298 0.459 0.470	0.464 0.364 0.186 0.192 0.333 0.148 0.343 0.268 0.189 0.142 0.077			
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08 str_t09 str_t10 str_t11		0.415	2.224 0.370	0.298 0.459	0.464 0.364 0.186 0.192 0.333 0.148 0.343 0.268 0.189 0.142 0.077 0.078			
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08 str_t10 str_t10 str_t11 str_t13 str_t14		0.415 0.316 0.467		0.298 0.459 0.470	0.464 0.364 0.192 0.333 0.192 0.343 0.268 0.189 0.142 0.077 0.078 0.195 0.370			
str_t01 str_t02 str_t03 str_t05 str_t05 str_t06 str_t07 str_t08 str_t09 str_t10 str_t11 str_t13 str_t14 str_t15		0.415 0.316 0.467		0.298 0.459 0.470 0.057 0.323	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.142 0.077 0.077 0.077 0.370 0.438		2.699	
str_t01 str_t02 str_t03 str_t05 str_t06 str_t06 str_t07 str_t08 str_t09 str_t10 str_t11 str_t13 str_t14 str_t15 str_t16		0.415 0.316 0.467 0.129	0.370	0.298 0.459 0.470 0.057 0.323 0.439	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.189 0.142 0.077 0.078 0.195 0.370 0.438 0.224			
str_t01 str_t02 str_t03 str_t05 str_t06 str_t07 str_t08 str_t09 str_t10 str_t11 str_t13 str_t14 str_t15 str_t16 str_t17		0.415 0.316 0.467		0.298 0.459 0.470 0.057 0.323	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.142 0.077 0.077 0.077 0.370 0.438		2.699	
str_101 str_103 str_103 str_105 str_106 str_107 str_109 str_110 str_111 str_113 str_114 str_115 str_116 str_117 str_118		0.415 0.316 0.467 0.129 0.306	0.370	0.298 0.459 0.470 0.057 0.323 0.439 0.465 0.474	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.142 0.077 0.0778 0.370 0.438 0.224 0.224 0.224		2.699	
str_101 str_102 str_103 str_105 str_105 str_106 str_107 str_108 str_109 str_110 str_113 str_114 str_114 str_114 str_116 str_117 str_118		0.415 0.316 0.467 0.129	0.370	0.298 0.459 0.470 0.057 0.323 0.439 0.465	0.464 0.364 0.192 0.333 0.148 0.343 0.268 0.189 0.142 0.077 0.0778 0.195 0.370 0.438 0.224 0.226 0.172 0.243 0.185		2.699	
str_101 str_103 str_103 str_105 str_105 str_105 str_107 str_108 str_107 str_110 str_111 str_113 str_114 str_115 str_116 str_117 str_118 str_112 str_117		0.415 0.316 0.467 0.129 0.306	0.370	0.298 0.459 0.470 0.057 0.323 0.439 0.465 0.474	0.464 0.364 0.186 0.192 0.333 0.148 0.343 0.268 0.149 0.142 0.077 0.0778 0.195 0.370 0.438 0.224 0.226 0.185 0.185 0.198		2.699	
str_101 str_103 str_103 str_105 str_105 str_107 str_108 str_107 str_110 str_111 str_114 str_114 str_115 str_114 str_117 str_118 str_123 str_127		0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370	0.298 0.459 0.470 0.057 0.323 0.439 0.465 0.474 0.413	0.464 0.364 0.186 0.192 0.333 0.148 0.248 0.189 0.189 0.189 0.189 0.370 0.438 0.224 0.226 0.172 0.243 0.185		2.699	
str_101 str_103 str_103 str_105 str_105 str_105 str_107 str_108 str_109 str_110 str_113 str_114 str_114 str_115 str_116 str_117 str_123 str_123 str_123		0.415 0.316 0.467 0.129 0.306 0.447	0.370 0.404	0.298 0.459 0.459 0.470 0.057 0.323 0.439 0.465 0.474 0.413 0.479 0.444	0.464 0.364 0.196 0.192 0.333 0.148 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.488 0.1077 0.078 0.197 0.438 0.224 0.2444 0.24440000000000		2.699	
str_101 str_103 str_103 str_105 str_105 str_105 str_107 str_108 str_110 str_111 str_114 str_113 str_114 str_115 str_116 str_117 str_1123 str_123 str_123 str_123 str_124		0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370	0.298 0.459 0.459 0.470 0.057 0.323 0.439 0.465 0.474 0.413 0.479	0.464 0.364 0.196 0.192 0.333 0.148 0.333 0.268 0.489 0.482 0.433 0.438 0.195 0.370 0.077 0.077 0.077 0.077 0.077 0.077 0.195 0.370 0.438 0.438 0.438 0.224 0.438 0.226 0.172 0.243 0.195 0.244 0.185 0.4380 0.4380 0.4380 0.43800000000000000000000000000000000000		2.699	
str_101 str_103 str_103 str_105 str_105 str_105 str_107 str_108 str_107 str_108 str_113 str_113 str_114 str_114 str_115 str_116 str_117 str_116 str_117 str_127 str_127 str_127 str_127 str_130 str_144 str_152 str_155		0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370 0.404	0.298 0.459 0.470 0.057 0.323 0.439 0.465 0.473 0.443 0.479 0.444 0.278	0.464 0.364 0.196 0.192 0.333 0.148 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.343 0.488 0.1077 0.078 0.197 0.438 0.224 0.2444 0.2444 0.2444 0.2444 0.24440000000000		2.699	
str_101 str_103 str_103 str_105 str_106 str_107 str_107 str_109 str_109 str_111 str_113 str_114 str_114 str_115 str_114 str_115 str_1123 str_127 str_123 str_127 str_123 str_125 str_155 str_155 str_155 str_105		0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370 0.404	0.298 0.459 0.459 0.470 0.057 0.323 0.439 0.465 0.474 0.413 0.479 0.444	0.464 0.364 0.196 0.192 0.333 0.148 0.333 0.268 0.189 0.142 0.077 0.428 0.195 0.195 0.424 0.270 0.424 0.272 0.424 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.195 0.198 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.192 0.244 0.192 0.192 0.192 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.244 0.192 0.243 0.192 0.243 0.192 0.243 0.195 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.243 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.243 0.195 0.244 0.257		2.699	conserved hypothetical protein, S4 domain protein
str_101 str_103 str_103 str_105 str_106 str_107 str_108 str_109 str_110 str_113 str_113 str_113 str_114 str_115 str_114 str_117 str_118 str_117 str_118 str_127 str_128 str_127 str_128 str_127 str_154 str_159 str0007	argS	0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370 0.404	0.298 0.459 0.470 0.057 0.323 0.435 0.463 0.474 0.413 0.479 0.444 0.278 0.346	0.464 0.364 0.186 0.192 0.333 0.148 0.268 0.189 0.142 0.077 0.189 0.370 0.370 0.370 0.370 0.370 0.370 0.374 0.268 0.264 0.274 0.274 0.274 0.275 0.257		2.699	arginyl-tRNA synthetase
str_101 str_103 str_103 str_106 str_106 str_107 str_107 str_107 str_110 str_111 str_113 str_114 str_115 str_114 str_115 str_114 str_115 str_114 str_115 str_114 str_115 str_114 str_115str_115 str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115 str_115str_115str_115 str_115str_115 str_115str_115str_115 str_115str_115str_115 str_115str_115str_115 str_115str_115str_115 str_115str_115 str_115str_115str_115 str_115str_115str_115 str_115str_115str_115str_115str_115str_11	- argS pnpA	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426	0.370 0.404 0.421	0.298 0.459 0.470 0.057 0.323 0.435 0.463 0.474 0.413 0.479 0.444 0.278 0.346	0.464 0.364 0.196 0.192 0.333 0.148 0.333 0.268 0.189 0.142 0.077 0.428 0.195 0.195 0.424 0.270 0.424 0.272 0.424 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.192 0.244 0.195 0.198 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.244 0.192 0.192 0.192 0.244 0.192 0.192 0.192 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.243 0.244 0.192 0.243 0.192 0.243 0.192 0.243 0.195 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.243 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.195 0.243 0.195 0.243 0.195 0.244 0.257		2.699	arginyl-tRNA synthetase polynucleotide phosphorylase, (PNPase)
str_101 str_103 str_103 str_106 str_106 str_106 str_100 str_110 str_111 str_114 str_115 str_115 str_116 str_116 str_116 str_116 str_117 str_127 str_127 str_134 str_144 str_146 str_154 str_159 str0007 str00211		0.415 0.316 0.467 0.129 0.306 0.447 0.280	0.370 0.404	0.298 0.459 0.470 0.057 0.323 0.435 0.463 0.474 0.413 0.479 0.444 0.278 0.346	0.464 0.364 0.186 0.192 0.333 0.148 0.268 0.189 0.142 0.077 0.189 0.370 0.370 0.370 0.370 0.370 0.370 0.374 0.268 0.264 0.274 0.274 0.274 0.275 0.257		2.699	arginyl-tRNA synthetase polynucleotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucvi-IRNA synthetase
str_101 str_103 str_103 str_105 str_106 str_106 str_107 str_110 str_111 str_113 str_113 str_114 str_114 str_114 str_116 str_116 str_117 str_117 str_113 str_117 str_118 str_123 str_146 str_154 str_155 str_154 str_254 str_2554 str_2554 str_25555555	pnpA -	0.415 0.467 0.129 0.306 0.447 0.280 0.426	0.370 0.404 0.421	0.298 0.459 0.470 0.057 0.339 0.465 0.474 0.413 0.479 0.444 0.479 0.444 0.479 0.444 0.478 0.445	0.464 0.364 0.186 0.192 0.333 0.148 0.268 0.189 0.142 0.077 0.189 0.370 0.370 0.370 0.370 0.370 0.370 0.374 0.268 0.264 0.274 0.274 0.274 0.275 0.257		2.699	arginyl-IRNA synthetase polynucleotide phosphorylase, (PNPase) hbosomal large subunit pseudouridine synthase, RluD subfamily leucyl-IRNA synthetase rithrsomal large subunit reservatouridine synthase B
str_102 str_102 str_103 str_105 str_106 str_108 str_107 str_110 str_110 str_111 str_113 str_114 str_115 str_115 str_116 str_117 str_118 str_117 str_118 str_127 str_127 str_128 str_155str_155 str_155 str_155 str_155str_155 str_155str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155str_155 str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155str_155 str_155str_155str_15	pnpA - leuS rluB -	0.415 0.467 0.129 0.306 0.447 0.280 0.426	0.370 0.404 0.421	0.298 0.459 0.459 0.470 0.470 0.470 0.465 0.474 0.413 0.479 0.444 0.413 0.479 0.444 0.445	0.464 0.364 0.364 0.192 0.33 0.23 0.23 0.243 0.243 0.243 0.243 0.769 0.142 0.679 0.442 0.442 0.272 0.443 0.224 0.224 0.224 0.243 0.224 0.243 0.357 0.357 2.825 0.383	0.299	2.699	arginyi-HRNA synthetase polynuckedide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-HRNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methyttmasferase, TmH rRNA methyttmasferase, TmH
str_101 str_102 str_103 str_105 str_105 str_106 str_106 str_107 str_111 str_113 str_111 str_113 str_113 str_114 str_115 str_116 str_116 str_116 str_117 str_123 str_123 str_1244 str_155 str_154 str_155str_155 str_155 str_155str_155 str_155 str_155str_155 str_155str_155 str_155str_155 str_155str_155 str_155 str_155str_155str_155 str_155str_155str_1	pnpA - leuS	0.415 0.467 0.129 0.306 0.447 0.280 0.426	0.370 0.404 0.421	0.298 0.459 0.459 0.470 0.323 0.436 0.474 0.474 0.479 0.444 0.479 0.444 0.479 0.444 0.478 0.445	0.464 0.364 0.364 0.192 0.333 0.148 0.448 0.448 0.448 0.448 0.448 0.448 0.448 0.448 0.477 0.078 0.438 0.438 0.438 0.226 0.438 0.226 0.438 0.486 0.486 0.486 0.486 0.487 0.285 0.383 7.165 4.154	0.298 0.334	2.699	arginy14RNA synthetase polynucleotide hospohorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucy14RNA synthetase hosomal large subunit pseudouridine synthase B rRNA methyltransferase, TmH family sey14RNA synthetase
str_102 str_102 str_103 str_103 str_103 str_107 str_108 str_107 str_108 str_110 str_111 str_113 str_113 str_113 str_114 str_114 str_114 str_117 str_118 str_117 str_118 str_127 str_127 str_128 str_125 str_135 str_144 str_155 str_155 str_1067 str_1067 str_0077str_0077 str_0077 str_0077 str_0077str_0077 str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0077str_0077 str_0	pnpA - leuS rluB -	0.415 0.467 0.129 0.306 0.447 0.280 0.426	0.370 0.404 0.421	0.298 0.459 0.459 0.459 0.450 0.450 0.474 0.473 0.479 0.444 0.278 0.346 0.346 0.346 0.346 0.346 0.346 0.346 0.346 0.445	0.464 0.364 0.364 0.192 0.33 0.23 0.23 0.243 0.243 0.243 0.243 0.769 0.142 0.679 0.442 0.442 0.272 0.443 0.224 0.224 0.224 0.243 0.224 0.243 0.357 0.357 2.825 0.383		2.699	arginy1-RNA synthetase polynucleotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucy4-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytiransferase, TrmH family seny1-RNA synthetase hypothetical protein
str_102 str_102 str_103 str_105 str_105 str_106 str_107 str_108 str_110 str_113 str_114 str_114 str_115 str_114 str_115 str_115 str_114 str_117 str_117 str_114 str_115 str_123 str_123 str_145 str_154 str_254str_254 str_25	pnpA - leuS rluB - serS -	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421	0.298 0.459 0.459 0.470 0.323 0.436 0.474 0.474 0.479 0.444 0.479 0.444 0.479 0.444 0.478 0.445	0.464 0.364 0.192 0.332 0.343 0.343 0.343 0.343 0.343 0.343 0.469 0.142 0.477 0.078 0.478 0.478 0.234 0.224 0.224 0.224 0.224 0.172 0.224 0.172 0.224 0.357 2.825 0.383 7.165 4.154 4.154 4.125	0.334	2.699	arginyi-IRNA synthetase polynuckotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytiransferase, TrmH family senyi-RNA synthetase hypothetical protein translation initiation factor IF-2 acety(transferase, GNAT family, truncated
str_101 str_102 str_103 str_105 str_105 str_106 str_107 str_108 str_110 str_111 str_113 str_114 str_115 str_117 str_11	pnpA - leuS rluB - serS - infB -	0.415 0.467 0.129 0.306 0.447 0.280 0.425 2.672 2.136	0.370 0.404 0.421	0.298 0.459 0.459 0.459 0.450 0.450 0.474 0.473 0.479 0.444 0.278 0.346 0.346 0.346 0.346 0.346 0.346 0.346 0.346 0.445	0.464 0.364 0.1962 0.333 0.148 0.192 0.333 0.148 0.189 0.189 0.189 0.189 0.198 0.77 0.077 0.077 0.078 0.370 0.438 0.224 0.224 0.243 0.244 0.226 0.243 0.287 0.383 7.165 2.825 0.383	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucy44RNA synthetase ribbscomal large subunit pseudouridine synthase B rRNA methytuansiderase, TimH family Phytophatical protein translation nitiation factor IF-2 acetyftransferase, GNXT family, truncated acetyftransferase, GNXT family, truncated
str.,101 str.,102 str.,103 str.,105 str.,105 str.,105 str.,105 str.,105 str.,105 str.,105 str.,105 str.,105 str.,105 str.,114 str.,115 str.,114 str.,115 str	pnpA - leuS rluB - serS - infB	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421	0.298 0.459 0.459 0.457 0.323 0.465 0.474 0.444 0.279 0.444 0.246 0.445 2.164 4.484 2.554 3.451	0.464 0.364 0.364 0.192 0.333 0.343 0.343 0.343 0.343 0.343 0.443 0.463 0.777 0.0778 0.778 0.478 0.473 0.473 0.434 0.433 0.433 0.433 0.434 0.435 0.433 0.434 0.435 0.445 0.4550000000000	0.334	2.699	arginyi-IRNA synthetase polynuckotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytiransferase, Tirrit family seryi-IRNA synthetase hypothetical protein translation initiation factor IF-2 cactlytiransferase, GNAT family, truncated acety(transferase, GNAT family, truncated methionien-=RNA ligase
str_u01 str_u02 str_u02 str_u05 str_u05 str_u05 str_u05 str_u05 str_u05 str_u05 str_u05 str_u05 str_u1	pnpA - leuS rluB - serS - infB - metG -	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421	0.298 0.459 0.459 0.457 0.323 0.439 0.465 0.474 0.413 0.479 0.444 0.278 0.346 0.346 0.346 0.346 0.346 0.445 2.164 4.484 2.554 3.451	0.464 0.364 0.364 0.192 0.32 0.32 0.343 0.243 0.243 0.243 0.243 0.472 0.475 0.375 0.375 0.375 0.375 0.365 0.	0.334	2.699	arginyi-IRNA synthetase polynuckotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytransferase, Term Hamily seryi-RNA synthetase hypothetical protein translation initiation factor IF-2 cactlyttransferase, GNAT family, truncated activitransferase, GNAT family, truncated activitransferase, GNAT family, truncated activitransferase, GNAT family, truncated activitransferase, GNAT family, truncated methionien–ENA ligase
str_ub1 str_ub2 str_ub2 str_ub3 str_ub5 str_ub6 str_ub6 str_ub1 str_ub	pnpA - leuS rluB - serS - infB - metG - valS tuf	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421	0.298 0.459 0.459 0.459 0.450 0.474 0.433 0.479 0.444 0.278 0.34600000000000000000000000000000000000	0.464 0.364 0.192 0.192 0.33 0.234 0.243 0.243 0.243 0.243 0.248 0.192 0.478 0.478 0.478 0.422 0.276 0.195 0.424 0.226 0.175 0.226 0.195 0.357 2.825 0.383 7.165 4.154 2.125 0.247 8.255 0.383	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucy14RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytransferase, TmH family sery1-RNA synthetase hypothetical pototion factor IP-2 transition nitiation (NAIT family, truncated acetytitransferase, GNAT family, truncated methonine-IRNA ligase acetytitransferase, GNAT family valy1-RNA synthetase leonagion factor Tu
str_012 str_02 str_03 str_05 str_065 str_065 str_065 str_065 str_065 str_07 str_085 str_085 s	pnpA - leuS rluB - serS - infB - metG - valS tuf glyS	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421 2.662	0.298 0.459 0.459 0.465 0.473 0.465 0.474 0.445 0.479 0.444 0.479 0.444 0.479 0.444 0.479 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.459	0.464 0.364 0.364 0.192 0.32 0.32 0.343 0.243 0.243 0.243 0.243 0.472 0.475 0.375 0.375 0.375 0.375 0.365 0.	0.334	2.699	arginyi-IRNA synthetase polynuckontide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA. Nay mittaka eucyi-RNA. Nay mittaka RNA methytitansferase, TimH family seyni-RNA synthetase hypothetical protein translation nitiation factor IF-2 acetytitransferase, GNAT family, truncated acetytitransferase, GNAT family, truncated methicinine -IRNA ligate methicinine -IRNA ligate with the synthetase elongation factor Tu gyoyrHRNA synthetase beta subunit
str_u01 str_u02 str_u03 str_u05 str_u0	pnpA - leuS rluB - serS - infB - - - valS tuf glyS rpIJ	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421 2.662	0.298 0.459 0.459 0.470 0.057 0.323 0.439 0.454 0.473 0.444 0.278 0.346 0.445 0.346 0.445 2.164 4.484 2.554 3.451 2.785 3.588 2.070	0.464 0.364 0.192 0.192 0.33 0.234 0.243 0.243 0.243 0.243 0.248 0.192 0.478 0.478 0.478 0.422 0.276 0.195 0.424 0.226 0.175 0.226 0.195 0.357 2.825 0.383 7.165 4.154 2.125 0.247 8.255 0.383	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucy4rRNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytransferase, TrmH family sery1-RNA synthetase hypothetical protein translation initiation factor IF-2 casetytimasferase, GNAT family, truncated methonine-IRNA ligase acetytimasferase, GNAT family, truncated encetyticase, GNAT family, truncated encetyticase, GNAT family, truncated encetyticase, GNAT family, valy1-RNA synthetase beta subunit glogation factor Tu glycy14RNA synthetase beta subunit 505 ribosomal protein L10
str_u01 str_u02 str_u03 str_u05 str_u0	pnpA - leuS rluB - serS - infB - metG - valS tuf glyS	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421 2.662	0.298 0.459 0.459 0.465 0.473 0.465 0.474 0.445 0.479 0.444 0.479 0.444 0.479 0.444 0.479 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.459	0.464 0.364 0.192 0.192 0.33 0.234 0.243 0.243 0.243 0.243 0.248 0.192 0.478 0.478 0.478 0.422 0.276 0.195 0.424 0.226 0.175 0.226 0.195 0.357 2.825 0.383 7.165 4.154 2.125 0.247 8.255 0.383	0.334	2.699	arginyi-IRNA synthetase polynuckeotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA kynthetase nbosomal large subunit pseudouridine synthase B mosomal large subunit pseudouridine synthase B sonyi-RNA synthetase hypothetical protein translation initiation factor IF-2 acetytiransferase, GNAT family, truncated acetytiransferase, GNAT family, truncated acetytiransferase, GNAT family, truncated acetytiransferase, GNAT family vali-RNA synthetase devices and the subunit SGS ribosomal protein L70.12
str_u01 str_u02 str_u03 str_u05 str_u0	pripA - leuS rluB - serS - metG - valS tuf glyS rpIJ rpIJ rpIJ rpIJ rpIJ rpIA	0.415 0.467 0.129 0.306 0.426 0.426 0.426 2.672 2.136 2.571 2.415	0.370 0.404 0.421 2.662 2.359	0.298 0.459 0.459 0.457 0.323 0.436 0.465 0.474 0.465 0.474 0.465 0.474 0.444 0.278 0.444 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.455 0.445 0.455 0.445 0.445 0.475 0.445 0.475 0.445 0.475 0.445 0.475 0.475 0.475 0.445 0.4750	0.464 0.364 0.192 0.334 0.148 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.443 0.442 0.477 0.438 0.438 0.438 0.434 0.424 0.487 0.486 0.487 0.2857 0.383 7.165 4.154 2.125 0.383 7.165	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucy44RNA synthetase theoxy44RNA synthetase mbscomal large subunit pseudouridine synthase B mbscomal large subunit pseudouridine synthase B mbscomal large subunit pseudouridine synthase suby44RNA synthetase. Tim Hamily hypothetical protein translation nitiation factor IF-2 acetyftransferase, GNAT family, truncated acetyftransferase, GNAT family, truncated acetyftransferase, GNAT family valy44RNA synthetase leiongation factor Tu glycy14RNA synthetase bale subunit bSG ritioscimal protein JT1 12 htmorny44RNA synthetase
str_u01 str_u02 str_u03 str_u03 str_u05 str_u0	pnpA - leuS rluB - serS - infB - - valS tuf glyS rpIJ rpIL thrS rpsA lysS	0.415 0.316 0.467 0.129 0.306 0.447 0.280 0.426 2.672 2.136	0.370 0.404 0.421 2.662	0.298 0.459 0.459 0.457 0.323 0.439 0.465 0.474 0.413 0.479 0.444 0.413 0.479 0.444 0.445 0.445 2.164 4.484 2.554 3.451 2.785 3.588 2.070 5.859 2.075 2.612	0.464 0.364 0.364 0.192 0.333 0.343 0.343 0.343 0.343 0.343 0.463 0.142 0.77 0.077 0.077 0.077 0.077 0.433 0.343 0.343 0.226 0.333 0.226 0.333 0.226 0.357 7.165 2.825 0.383 7.165 4.154 4.2125 0.266 4.433 4.433 4.584	0.334	2.699	arginyi-IRNA synthetase polynucketide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytiansferase, TMT family seryi-RNA synthetase hypothetical protein translation initiation factor IF-2 acetytitransferase, GNAT family, truncated acetytitransferase, GNAT family, truncated metrionion-erRNA ligaze acation family and the bela subunit by Gyr-RNA synthetase elongation factor Tu gyr-YRAN synthetase belase acation factor factor SSS finosomal protein 1/2/12 htmoryi-RINA synthetase 305 finosomal protein S1 htmoryi-RINA synthetase
str_ub1 str_ub2 str_ub2 str_ub3 str_ub5 str_ub6 str_ub5 str_ub5 str_ub1 str_ub	pnpA - leuS rluB - serS - infB - valS tuf glyS rpIJ rpIJ rpIJ rpIJ rpIJ ileS	0.415 0.467 0.129 0.306 0.426 0.426 0.426 2.672 2.136 2.571 2.415	0.370 0.404 0.421 2.662 2.359	0.298 0.459 0.459 0.457 0.323 0.436 0.465 0.474 0.465 0.474 0.465 0.474 0.444 0.278 0.444 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.445 0.455 0.445 0.455 0.445 0.445 0.475 0.445 0.475 0.445 0.475 0.445 0.475 0.475 0.475 0.445 0.4750	0.464 0.364 0.364 0.162 0.192 0.33 0.243 0.243 0.243 0.268 0.142 0.077 0.077 0.375 0.365 0.27600000000000000000000000000000000000	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucy44RNA synthetase nbosomal large subunit pseudouridine synthase B rRNA methytransferase, TimH family by pothatical protein translation initiation factor IF-2 acetytransferase, GNAT family, truncated acetytransferase, GNAT family, truncated acetytransferase, GNAT family, truncated acetytransferase, GNAT family, valv4RNA synthetase leingation factor Tu glogy14RNA synthetase bota subunit Sigs inbosoma protein 10 to 30 mbosoma protein 11 ysy4-IRNA synthetase isolacy14RNA synthetase isolacy14RNA synthetase
str_u01 str_u02 str_u03 str_u03 str_u05 str_u0	pnpA - leuS rluB - serS - infB - valS tuf glyS rpIJ rpsA lysS ileS iles rpmE	0.415 0.467 0.129 0.306 0.426 0.426 0.426 2.672 2.136 2.571 2.415	0.370 0.404 0.421 2.662 2.359	0.298 0.459 0.459 0.457 0.323 0.439 0.465 0.474 0.413 0.479 0.444 0.413 0.479 0.444 0.445 0.445 2.164 4.484 2.554 3.451 2.785 3.588 2.070 5.859 2.075 2.612	0.464 0.364 0.364 0.192 0.333 0.343 0.343 0.343 0.343 0.343 0.463 0.142 0.77 0.077 0.077 0.077 0.077 0.373 0.343 0.343 0.226 0.333 0.226 0.333 0.226 0.357 7.165 2.825 0.383 7.165 4.154 4.2125 0.266 4.433 4.438 4.584	0.334	2.699	arginyi-IRNA synthetase polynucketide phosphorylase, (PNPase) ribosomal large subunit pseudouridine synthase, RluD subfamily leucyi-RNA synthetase ribosomal large subunit pseudouridine synthase B rRNA methytiansferase, TMT family seryi-RNA synthetase hypothetical protein translation initiation factor IF-2 acetytitransferase, GNAT family, truncated acetytitransferase, GNAT family, truncated metrionion-erRNA ligaze acation family and the bela subunit by Gyr-RNA synthetase elongation factor Tu gyr-YRAN synthetase elongation factor Tu gyr-YRAN synthetase fibosomal protein 1/2/12 htmoryi-RINA synthetase 305 ribosomal protein S1 hypothetase
str_u01 str_u02 str_u03 str_u03 str_u05 str_u0	pnpA - leuS rluB - serS - infB - valS tuf glyS rpIJ rpIJ rpIJ rpIJ rpIJ ileS	0.415 0.467 0.129 0.306 0.426 0.426 0.426 2.672 2.136 2.571 2.415	0.370 0.404 0.421 2.662 2.359	0.298 0.459 0.459 0.457 0.323 0.439 0.465 0.474 0.413 0.479 0.444 0.413 0.479 0.444 0.445 0.445 2.164 4.484 2.554 3.451 2.785 3.588 2.070 5.859 2.075 2.612	0.464 0.364 0.364 0.192 0.333 0.343 0.343 0.343 0.343 0.343 0.462 0.168 0.142 0.77 0.078 0.433 0.433 0.433 0.226 0.333 0.226 0.333 0.226 0.333 0.226 0.357 7.165 2.825 0.383 7.165 4.154 4.2125 0.264 4.584 4.584 4.584	0.334 0.441 0.498	2.699	arginyi-IRNA synthetase polynuckeotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RLD subfamily leucyi-RRNA synthetase decyi-RRNA synthetase rRNA methyltransferase, TrmH family seryi-RRNA synthetase hypothetical protein translation hitatori FI-2 acetyftransferase, GNAT family, truncated acetyftransferase, GNAT family, sentymer and the synthetase for the synthetase beta subunit 50s fribosomal protein L10 50s fribosomal protein L11 sols fribosomal protein 51s fribosomal protein 51s fribosomal protein 50s fribosom
str_ubi1 str_ubi2 str	pnpA - leuS rluB - serS - infB - - wetG - valS tuf glyS rplJ thrS rpsA lies rpmE prfA	0.415 0.467 0.129 0.306 0.426 0.426 0.426 2.672 2.136 2.571 2.415	0.370 0.404 0.421 2.662 2.359	0.298 0.459 0.459 0.459 0.457 0.323 0.439 0.439 0.439 0.474 0.473 0.474 0.473 0.474 0.473 0.474 0.478 0.346 0.3670	0.464 0.364 0.364 0.192 0.192 0.33 0.288 0.288 0.788 0.788 0.788 0.798 0.797 0.077 0.078 0.198 0.420 0.777 0.278 0.226 0.772 0.243 0.226 0.772 0.243 0.226 0.357 2.825 0.383 7.165 4.154 2.125 0.287 0.383 7.165 4.584 4.584 3.756 0.266 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.270 0.260 0.270 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260 0.270 0.260	0.334	2.699	arginy14RNA synthetase polynucleotide phosphorylase, (PNPase) nbosomal large subunit pseudouridine synthase, RluD subfamily leucy44RNA synthetase nbosomal large subunit pseudouridine synthase B rRNA methytransferase, TimH family bypothatical protein translation initiation factor IF-2 acetytransferase, GNAT family, truncated acetytransferase, GNAT family, truncated acetytransferase, GNAT family, truncated acetytransferase, GNAT family, valv44RNA synthetase leingation factor Tu glvgv14RNA synthetase SGS rhosomal protein 110 SGS rhosomal protein 120 SGS rhosomal protein 131 pspt/deAna release factor 1

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str1000			2.521				rRNA methyltransferase, putative
str1133	rpml		3.648				50S ribosomal protein L35
str1134	infC		3.801	0.481			translation initiation factor IF-3
str1146	prfB		0.001	0.355			peptide chain release factor 2
str1177	miaA			0.223			tRNA delta(2)-isopentenvlpvrophosphate transferase
str1292	pheT		2.178	0.225			phenylalanyl-tRNA synthetase beta subunit
str1294	pheS		2.226				phenylalanyl-tRNA synthetase alpha subunit
str1428	fmt		2.353				methionyl-tRNA formyltransferase
str1420	rosU		2.196	0.354			30S ribosomal protein S21
str1505	rsuA2		2.130	0.381			ribosomal small subunit pseudouridine synthase A
str1559	-			0.479			acetyltransferase, GNAT family
str1568	rheA		2.454	0.473			ATP-dependent RNA helicase
str1574	prfC		2.600				peptide chain release factor 3
str1625	gatB	3.336	2.000				aspartyl/glutamyl-tRNA amidotransferase subunit B
str1625	gatC	3.330	2.131	0.431			asparty/glutamyl-tRNA amidotransferase subunit C
str1699	rheB	2.174	2.131	0.431			ATP-dependent RNA helicase
str1754	rosF	2.174	2.760	0.350		2.605	30S ribosomal protein S6
str1754 str1790	rpse		2.760	0.350		2.605	30S ribosomal protein S6 30S ribosomal protein S7
str1806	tgt		3.090	0.367			queuine tRNA-ribosyltransferase
str1844	iyi		0.497	0.236			
	- tvrS		2.520				cytidine/deoxycytidylate deaminase family protein, putative
str1870 str1907	rpIQ		2.520	0.418 0.346			tyrosyl-tRNA synthetase 50S ribosomal protein L17
str1907 str1909				0.293			30S ribosomal protein £17
	rpsK						
str1910	rpsM			0.268			30S ribosomal protein S13
str1911	rpmJ			0.278			50S ribosomal protein L36
str1912	infA		0.007	0.221			translation initiation factor IF-1
str1919	rpIF		2.307				50S ribosomal protein L6
str1921	rpsN		2.100				30S ribosomal protein S14
str1922	rpIE			0.480			50S ribosomal protein L5
str1925	rpsQ			0.442			30S ribosomal protein S17
str1927	rpIP			0.492			50S ribosomal protein L16
str1928	rpsC		2.036				30S ribosomal protein S3
str1930	rpsS			0.393			30S ribosomal protein S19
str1931	rplB		2.228	0.471			50S ribosomal protein L2
str1932	rpIW		2.218	0.385			50S ribosomal protein L23
str1935	rpsJ		2.301	0.282			30S ribosomal protein S10
str1958	rpmB		2.708				50S ribosomal protein L28
str1969	aspS			0.487			aspartyl-tRNA synthetase
str1971	hisS			0.486		2.120	histidyl-tRNA synthetase
str1974	rpmF		2.440	0.209		2.013	50S ribosomal protein L32
str1975	rpmGB		2.868	0.211			50S ribosomal protein L33
str1997	rpsD		2.011				30S ribosomal protein S4
str2003	trmU			0.387	0.337		tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
str2018	trpS			0.354			tryptophanyl-tRNA synthetase

Supplementary Table 3. Significant (≥2-fold FDR≤0.05) differential expression of *L. bulgaricus* genes between mixed and mono-cultures and between cultures supplemented with formic acid and cultures without any supplement, per functional category. Values represent ratios between the first and the second condition. Columns 3-6 contain ratios of mixed cultures over by mono-cultures in the first exponential phase (3.5 h), reduced growth phase (5.5 h), second exponential phase (8 h) and stationary phase (12 h), respectively. Columns 7 and 8 contain ratios of a culture supplemented with formic acid over one without supplement in the early exponential phase and mid exponential phase, respectively.

			Mixed cu	lture over		Formic	acid over			
			mono	culture		n	one			
Locus ID	Locus	1st exp.	Transition	2nd exp.	Stationary	1st exp.	2nd exp.	Product		
20003 10	20003	phase	phase	phase	phase	phase	phase			
Amino acid tra	ansport and	metabolism								
LBUL 0065	TesA				0.402			Lysophospholipase L1 and related esterase		
LBUL 0084	SerA		3.717			0.262		Phosphoglycerate dehydrogenase and related dehydrogenase		
LBUL_0089	MetA		0.390		0.212			Homoserine trans-succinylase		
LBUL 0112	TvrR				0.476			Transcriptional regulator of aromatic amino acids metabolism		
LBUL 0129	LívG		2,794					ABC-type branched-chain amino acid transport systems ATPase component		
LBUL 0145	HisM			5,749				ABC-type amino acid transport system permease component		
LBUL_0156	PrsA	2.071		0.441		0.312	0.433	Phosphoribosylpyrophosphate synthetase		
LBUL 0161	CarB		0.475					Carbamoylphosphate synthase large subunit (split gene in MJ)		
LBUL 0165	DAP2		0.138					Dipeptidyl aminopeptidase/acylaminoacyl-peptidase		
LBUL 0176	HisJ				0.438			ABC-type amino acid transport/signal transduction systems periplasmic component/domain		
LBUL 0177	GInQ	0.331	0.347	2.596				ABC-type polar amino acid transport system ATPase component		
LBUL 0178	OpuBB	0.294	0.350	2.695				ABC-type proline/glycine betaine transport systems permease component		
LBUL 0179	OpuBB	0.153	0.186				3.599	ABC-type proline/glycine betaine transport systems permease component		
LBUL_0180	OppA				0.249			ABC-type oligopeptide transport system periplasmic component		
LBUL 0184	CarB			0.350				Carbamovlphosphate synthase large subunit (split gene in MJ)		
LBUL 0211	MetH		0.372					Methionine synthase I cobalamin-binding domain		
LBUL_0214	HisM	0.229	0.117		0.140			ABC-type amino acid transport system permease component		
LBUL_0215	HisM	0.202	0.155		0.117			ABC-type amino acid transport system permease component		
LBUL 0216	GInQ	0.386	0.055		0.159			ABC-type polar amino acid transport system ATPase component		
LBUL_0217	HisJ	0.412	0.171		0.224			ABC-type amino acid transport/signal transduction systems periplasmic component/domain		
LBUL_0225	ArgE				0.144			Acetylomithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylase		
LBUL_0233	OppA			2.226		0.251		ABC-type oligopeptide transport system periplasmic component		
LBUL 0235	OppA				2,491		0.251	ABC-type oligopeptide transport system periplasmic component		
LBUL 0238	DopD				2.013			ABC-type dipeptide/oligopeptide/nickel transport system ATPase component		
LBUL_0239	DppF				3,705			ABC-type dipeptide/oligopeptide/nickel transport system ATPase component		
LBUL 0241	PepC					0.398	0.479	Aminopeptidase C		
LBUL 0242	PepC		2.070					Aminopeptidase C		
LBUL_0251	GltB	2.639				0.290	0.458	Glutamate synthase domain 2		
LBUL_0252	PabA	2.315						Anthranilate/para-aminobenzoate synthase component II		
LBUL 0256	OpuBA		0.347	6.884				ABC-type proline/glycine betaine transport systems ATPase components		
LBUL 0261	HisJ	0.421	0.335	2.825	0.088			ABC-type amine giving being transport signal transduction systems periplasmic component/domain		
LBUL_0262	GInQ	0.380	0.268		0.077			ABC-type polar amino acid transport system ATPase component		
LBUL 0263	HisM	0.357	0.268		0.085			ABC-type amino acid transport system permease component		
LBUL 0273	AnsB			0.186				L-asparaginase/ Glu-tRNAGIn amidotransferase subunit D		
LBUL_0303	CysE		0.392		2.057		0.432	Serine acetyltransferase		
LBUL_0326	PepD			2.960				Di- and tripeptidase		
LBUL_0399	ARO8		2.272	0.487				Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR		
								family) and their eukaryotic orthologs		
LBUL 0427	SerB		3.059					Phosphoserine phosphatase		
LBUL_0431	BrnQ		0.241					Branched-chain amino acid permease		
LBUL 0445	DppF		0.333					ABC-type dipeptide/oligopeptide/nickel transport system ATPase component		
LBUL 0457	DppD		0.368		6.995			ABC-type dipeptide/oligopeptide/nickel transport system ATPase component		
LBUL_0479	ProV			0.430				ABC-type proline/glycine betaine transport system ATPase component		

LBUL_0480	PrsA				0.202			Phosphoribosylpyrophosphate synthetase
LBUL_0481 LBUL_0488	PotE CsdB	0.273	0.210	0.224				Amino acid transporter Selenocysteine lyase
LBUL_0496	PepP		0.492	0.224	2.524			Xaa-Pro aminopeptidase
LBUL_0500	DAP2		0.293					Dipeptidyl aminopeptidase/acylaminoacyl-peptidase
LBUL_0506 LBUL_0529	MetH SdaC		0.349	2.661	4.576			Methionine synthase I cobalamin-binding domain Amino acid permease
LBUL_0548	GltD				0.425			NADPH-dependent glutamate synthase beta chain and related oxidoreductase
LBUL_0550 LBUL_0553	LivG DmpA		2.433 2.448	0.243	0.098			ABC-type branched-chain amino acid transport systems ATPase component
LBUL_0553	SerB		2.448	0.284	2.538			L-aminopeptidase/D-esterase Phosphoserine phosphatase
LBUL_0572 LBUL_0578	PotA		0.448		2.000			ABC-type spermidine/putrescine transport systems ATPase components
LBUL_0579	PotB	0.442	0.396					ABC-type spermidine/putrescine transport system permease component I
LBUL_0580 LBUL_0581	PotC PotD		0.268 0.402					ABC-type spermidine/putrescine transport system permease component II Spermidine/putrescine-binding periplasmic protein
LBUL_0585	SerB	2.582	0.102	0.484				Phosphoserine phosphatase
LBUL_0589	SerB	0.358						Phosphoserine phosphatase
LBUL_0646 LBUL_0663	EutJ EutJ		0.383		0.459 3.612			Ethanolamine utilization protein possible chaperonin Ethanolamine utilization protein possible chaperonin
LBUL_0686	NifS	0.402	0.328		5.142			Cysteine sulfinate desulfinase/cysteine desulfurase
LBUL_0688	ArgG		2.445		8.246			Argininosuccinate synthase
LBUL_0717 LBUL_0726	OppA DadA		0.254	0.047	0.130	4.189	3.051	ABC-type oligopeptide transport system periplasmic component Glycine/D-amino acid oxidase (deaminating)
LBUL_0737	AR08		4,440	3.248	0.065	0.125	3.031	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR
								family) and their eukaryotic orthologs
LBUL_0812 LBUL_0823	HisZ GcvH		0.288	0.211	6.877 0.345		2.227	ATP phosphoribosyltransferase involved in histidine biosynthesis Glycine cleavage system H protein (lipoate-binding)
LBUL_0825	CarB		0.295	0.132	0.391		2.221	Carbamoylphosphate synthase large subunit (split gene in MJ)
LBUL_0869	PotC	0.300						ABC-type spermidine/putrescine transport system permease component II
LBUL_0870	GInQ PotA		0.216		0.363			ABC-type polar amino acid transport system ATPase component
LBUL_0882 LBUL_0883	PotA		0.350		5.201			ABC-type spermidine/putrescine transport systems ATPase components ABC-type spermidine/putrescine transport systems ATPase components
LBUL_0895	SerB				2.029			Phosphoserine phosphatase
LBUL_0904	ThrB ThrB	0.222	0.179	0.456				Homoserine kinase
LBUL_0905 LBUL_0906	ThrB	0.232 0.156	0.157 0.171		3.061			Homoserine kinase Homoserine kinase
LBUL_0914	SerB		4.041	0.139	0.138			Phosphoserine phosphatase
LBUL_0917	SerA DAP2			0.343	4.671		0.498	Phosphoglycerate dehydrogenase and related dehydrogenase Dipeptidyl aminopeptidase/acylaminoacyl-peptidase
LBUL_0918 LBUL_0931	CarA	3.078			4.671	0.230		Dipeptidyi aminopeptidase/acytaminoacyi-peptidase Carbamoylphosphate synthase small subunit
LBUL_0932 LBUL_0933	CarB	2.215			0.059	0.369		Carbamovlphosphate synthase large subunit (split gene in MJ)
LBUL_0933	GcvR		0.270		0.117	0.322		Glycine cleavage system regulatory protein
LBUL_0961 LBUL_0975	ArgE CarA		0.270	16.246	10.350			Acetylomithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylase Carbamoylphosphate synthase small subunit
LBUL_0989	PotA	0.408			4.992			ABC-type spermidine/putrescine transport systems ATPase components
LBUL_1067	SerA	0.410			3.027			Phosphoglycerate dehydrogenase and related dehydrogenase
LBUL_1069 LBUL_1070	OpuBA PotA			7.779 7.598				ABC-type proline/glycine betaine transport systems ATPase components ABC-type spermidine/putrescine transport systems ATPase components
LBUL_1096	ProA		0.123	0.177				Gamma-glutamyl phosphate reductase
LBUL_1103 LBUL_1110	MalY	0.301			40.440			Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities
LBUL_1110	AsnA PepD	0.089	0.141		10.118 8.033			Asparagine synthetase A Di- and tripeptidase
LBUL_1126 LBUL_1138	DadA			2.770				Glycine/D-amino acid oxidase (deaminating)
LBUL_1157 LBUL_1180	SerB COG0436	0.432		0.328		7.961 0.224	0.290	Phosphoserine phosphatase
LBUL_1180	GltD			0.412		0.224		Aspartate/tyrosine/aromatic aminotransferase NADPH-dependent glutamate synthase beta chain and related oxidoreductase
LBUL_1189 LBUL_1204	PotA			62.155				ABC-type spermidine/putrescine transport systems ATPase components
LBUL_1213	GlnQ HisM			2.998	4.248			ABC-type polar amino acid transport system ATPase component
LBUL_1214 LBUL_1219	IIVE				4.248		0.225	ABC-type amino acid transport system permease component Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
LBUL_1227	EutJ	0.367	0.479					Ethanolamine utilization protein possible chaperonin
LBUL_1231	MetF	0.393	0.371		0.000			5 10-methylenetetrahydrofolate reductase
LBUL_1232 LBUL_1235	MetE CysK	0.488 9.381	3.000	23.087	2.229 2.835			Methionine synthase II (cobalamin-independent) Cysteine synthase
LBUL_1236	MetC	6.367	2.770	13.936	4.313			Cystathionine beta-lyase/cystathionine gamma-synthase
LBUL_1241	ArgK HIS2			3.477	4.074			Putative periplasmic protein kinase ArgK and related GTPase of G3E family
LBUL_1246 LBUL_1257	Asd				4.074		3.733	Histidinol phosphatase and related hydrolase of the PHP family Aspartate-semialdehyde dehydrogenase
LBUL_1261 LBUL_1267	DppF	0.137						ABC-type dipeptide/oligopeptide/nickel transport system ATPase component
LBUL_1267	HisJ	0.201	0.345 0.366					ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_1285 LBUL_1288	ArgK DdpA		0.366					Putative periplasmic protein kinase ArgK and related GTPase of G3E family ABC-type dipeptide transport system periplasmic component
LBUL_1289	DdpA	0.383		2.321	0.356			ABC-type dipeptide transport system periplasmic component
LBUL_1291	DppB	0.330	0.229	2.883	0.179 0.193			ABC-type dipeptide/oligopeptide/nickel transport systems permease components
LBUL_1292 LBUL_1293	DppD DppD	0.324	0.262	2.588 2.768	0.193			ABC-type dipeptide/oligopeptide/nickel transport system ATPase component ABC-type dipeptide/oligopeptide/nickel transport system ATPase component
LBUL_1308	EutQ			0.462				
LBUL_1330 LBUL_1334	CarB AsnB		0.339					Ethanolamine utilization protein
LDUL_1334			0.333		0.063		2 314	Ethanolamine utilization protein Carbamoylphosphate synthase large subunit (split gene in MJ)
LBUL_1336	HisH		0.371 0.442		0.052 0.039		2.314	Ethanolamine utilization protein Carbamoyiphosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferase
LBUL_1339	ArgH		0.371		0.052 0.039 0.165	0.332	2.314	Ethanolamine utilization protein Carbamoylohophate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferase Argininosuccinate lyase
LBUL_1339 LBUL_1340	ArgH CarB	0.491	0.371 0.442		0.052 0.039 0.165 0.105	0.332 0.303	2.314	Ethanolamine utilization protein Carbamoyi/bosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferase Argininosuccinate lyase Carbamoyi/bosphate synthase large subunit (spit gene in MJ)
LBUL_1339 LBUL_1340 LBUL_1353	ArgH CarB MetA CysK	0.491	0.371 0.442 0.233 0.157	0.356	0.052 0.039 0.165	0.332 0.303	2.314	Ethanolamine utilization protein Carbamoyiphosphate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferrase Argininosuccinate lyase Carbamoyiphosphate synthase large subunit (split gene in MJ) Homoserine trans-succinylase Cysteline synthase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1368	ArgH CarB MetA CysK GInA	0.491	0.371 0.442 0.233	0.356 0.328	0.052 0.039 0.165 0.105 0.081	0.332 0.303		Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine+hydrolyzing) Glutamine aminosucinate lyase Argininosucinate lyase Carbamory/hosphate synthase large subunit (split gene in MJ) Cysteine synthase Glutamine synthase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1368	ArgH CarB MetA CysK	0.491	0.371 0.442 0.233 0.157		0.052 0.039 0.165 0.105 0.081	0.332 0.303	2.314 2.350	Ethanolamine utilization protein Carbamoyiphosphate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferrase Argininosuccinate lyase Carbamoyiphosphate synthase large subunit (split gene in MJ) Homoserine trans-succinylase Cysteline synthase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1368 LBUL_1423 LBUL_1423 LBUL_1426 LBUL_1466	ArgH CarB MetA CysK GInA PrsA AroK GItD		0.371 0.442 0.233 0.157 0.345	0.328	0.052 0.039 0.165 0.105 0.081	0.332 0.303		Ethanolamine utilization protein Carbamoyihopshate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferrase Argininosuccinate lyase Carbamoyihopshate synthase large subunit (split gene in MJ) Homoserine trans-succinylase Cysteline synthase Glutamine synthese Brildmate kinase Shildmate kinase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1354 LBUL_1368 LBUL_1368 LBUL_1423 LBUL_1426 LBUL_1466 LBUL_1474	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP	0.491	0.371 0.442 0.233 0.157 0.345 0.364	0.328	0.052 0.039 0.165 0.105 0.081	0.332 0.303		Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine+hydrolyzing) Glutamine amidoransferrase Argininosuccinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Hosphare ny transcom/yase Glutamine synthetase Phosphoribos/yburyophosphate synthetase Shikimate kinase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro aminopertidase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1368 LBUL_1423 LBUL_1423 LBUL_1426 LBUL_1466	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP ArgA		0.371 0.442 0.233 0.157 0.345 0.364	0.328	0.052 0.039 0.165 0.105 0.081	0.332 0.303		Ethanolamine utilization protein Carbamoyihosphate synthase large subunit (split gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidotransferase Argininosuccinate lyase Carbamoyihosphate synthase large subunit (split gene in MJ) Homoserine trans-succinylase Cysteline synthase Glutamine synthese Glutamine synthese Shikimate kinase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro aminopeptidase
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1354 LBUL_1368 LBUL_1423 LBUL_1426 LBUL_1474 LBUL_1474 LBUL_1474	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP	2.063	0.371 0.442 0.233 0.157 0.345 0.364	0.328	0.052 0.039 0.165 0.105 0.081	0.332 0.303	2.350	Ethanolamine utilization protein Cardamoiyhoksphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrolyzing) Gutamine amicotransferase Cardamoyhoksphate synthase large subunit (spit gene in MJ) Homozerine trans-succinylase Cysteine synthase Gutamine synthese Phosphonibos/grycophosphate synthese Phosphonibos/grycophosphate synthese Shiimate kinase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase transfort system ATPase component Transcriptional regulators containing a DNA-binding HTH domai and an aminotransferase domain (MocR
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1423 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1502 LBUL_1562 LBUL_1563	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP ArgA DppD ARO8	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363	0.052 0.039 0.165 0.105 0.081	0.332 0.303	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine aminosucinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Homoserine trans-succinylase Cysteine synthese Glucamine synthese Glucamine synthese Glucamine synthese Hollamate synthase beta chain and related oxidoreductase Xaa-Pto aminoperitidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pto aminoperitidase Nacerty/glutamate synthase and related actylitransferase ASC-type diperite/olioppoptidickied transport System ATPase component Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR Family) and their eukaryotic orthologs
LBUL_1339 LBUL_1340 LBUL_1353 LBUL_1353 LBUL_1358 LBUL_1358 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1502 LBUL_1563 LBUL_1561 LBUL_1581	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP ArgA DppD	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600	0.052 0.039 0.165 0.105 0.081	0.332 0.303	2.350	Ethanolamine utilization protein Cardamory/bhosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrolyzing) Gutamine amicotransferase Adamory/bhosphate) ysithase large subunit (spit gene in MJ) Homoserine trans-succinylase Cysteine synthase Gutamine synthase Gutamine synthase Phosphonibos/typrophosphate synthetase Phosphonibos/typrophosphate synthetase Shilimate kinase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADP-hogendent gutamate synthase hogen transport system ATPase component Transcriptionaling a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
LBUL_1330 LBUL_1340 LBUL_1353 LBUL_1353 LBUL_1354 LBUL_1358 LBUL_1358 LBUL_1426 LBUL_1426 LBUL_1466 LBUL_1462 LBUL_1562 LBUL_1563 LBUL_1581 LBUL_1581	ArgH CarB MetA CysK GInA PrsA AroK GIID PepP ArgA DppD ARO8 CarB ProA DppF	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670	0.052 0.039 0.165 0.105 0.081 0.034	0.332 0.303	2.350	Ethanolamine utilization protein Cardamory/bhosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrolyzing) Gutamine amicotransferase Acadamory/bhosphate synthase large subunit (spit gene in MJ) Homoserine trans-succinylase Cysteine synthase Gutamine synthase Gutamine synthase Shikimate kinase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related oxidoreductase AsB-Orpot dipeptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipopptide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipotide/clipot
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1474 LBUL_1562 LBUL_1563 LBUL_1567 LBUL_1588 LBUL_1588 LBUL_1588	ArgH CarB MetA CysK GInA PrsA AroK GItD PepP ArgA DppD ARO8 CarB ProA DppF PepC	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670 0.454	0.052 0.039 0.165 0.105 0.081 0.034 0.034	0.332 0.303	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine aminosucinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Homoserine trans-succinylase Cysteine synthese Glutamine synthese Glutamine synthese Shifumate kinase Shifumate kinase ASC-type diopendendulaminate synthase bata chain and related oxidoreductase NaC-type diopendendulaminate synthase bata chain and related oxidoreductase NaC-type diopendendulaminate synthase and related activities accomponent Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR Family) and their eukaryotic orthologo Carbamory/hosphate synthase large subunit (spit gene in MJ) Gamma-glutamy/hosphate reductase ABC-type diopeptide/oliopoptide/hickel transport system ATPase component ABC-type diopeptide/oliopoptide/hickel transport system ATPase component ABC-type diopeptide/oliopoptide/hickel transport system ATPase component
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1474 LBUL_1562 LBUL_1563 LBUL_1567 LBUL_1588 LBUL_1588 LBUL_1588	ArgH CarB MetA CysK GlnA PrsA AroK GltD PepP ArgA DppD ARO8 CarB ProA DppF PepC ArgE ThrB	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670	0.052 0.039 0.165 0.105 0.081 0.034	0.332	2.350	Ethanolamine utilization protein Cardamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrolydra)) Gutamine and/otransforase Cardamory/hosphate synthase large subunit (spit gene in MJ) Amore free trans - succinylase Cysteine synthase Gutamine synthase Gutamine synthase Gutamine synthase Shiimate kinase NADPH-dependent gutamine synthase beta chain and related oxidoreductase NADPH-dependent gutamiate synthase beta chain and related oxidoreductase NADPH-dependent gutamiate synthase beta chain and related oxidoreductase NADPH-dependent gutamiate synthase beta chain and related oxidoreductase NADPH-dependent gutamine and related acetyltransferase ABC-type dipeptide/dipepptide/hickel transport system ATPase component Transcriptional synthase are large subunit (spit gene in MJ) Gamma-gutamy (hosphate reductase ABC-type dipeptide/dipeptide/hickel transport system ATPase component ABC-type dipeptide/dipeptide/hickel transport system ATPase component ABC-type dipeptide/dipeptide/hickel transport system ATPase component ABC-type dipeptide/dipeptide/dipetickel transport system ATPase component ABC-type dipeptide/dipeptide/dipetickel transport system ATPase component ABC-type dipeptide/dipetickel transport system ATPase component ABC-type dipeptide/dipetickel transport system ATPase component ABC-type dipeptide/dipetickel transport system ATPase component ABC-type dipetide/dipetickel/dises/Succinyl-diaminopimelate desuccinylase and related deacylase Homoserine kinase
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1428 LBUL_1428 LBUL_1428 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1563 LBUL_1563 LBUL_1564 LBUL_1588 LBUL_1588 LBUL_1619 LBUL_1619 LBUL_1619	ArgH CarB MetA CysK GinA PrsA AroK GilD PepP ArgA DppD ArgA DppD ArgA DppF ProA DppF PepC ArgE ThrB LdcC	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670 0.454 0.248	0.052 0.165 0.165 0.105 0.081 0.034	0.332 0.303	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine+hydrolyzing) Glutamine amidoransferase Argininosuccinate lyase Carbamory/hosphates synthase large subunit (spit gene in MJ) Hospitaline synthase Glutamine synthase Glutamine synthase MapPH-dependent glutamate synthese NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro anjhoopptidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro anjhoopptidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro anjhoopptidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pro anjhoopptidase Na-BC-type dipedice)idoppetidickel transport system ATPase component Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and there leakarydic orthologs Carbamory/phosphate synthase large subunit (spit gene in MJ) Gamma-glutamate Jhosphate reductase Aminoppetidase C Avaety/omithine decardylase/Sucury-diaminopimelate desuccinylase and related deacylase Homoserine kinase
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1428 LBUL_1428 LBUL_1428 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1563 LBUL_1563 LBUL_1564 LBUL_1588 LBUL_1588 LBUL_1619 LBUL_1619 LBUL_1619	ArgH CarB MetA CysK GinA PrsA AroK GIID PepP ArgA DppD ARO8 CarB ProA DppF PepC ArgE ThrB LdcC LYS9	2.063	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670 0.454 0.248	0.052 0.039 0.165 0.105 0.034 0.034 0.034 0.034	0.332	2.350	Ethanolamine utilization protein Cardamorylohosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrolydrag) Gutamine anitotransferase Cardamorylohosphate synthase large subunit (spit gene in MJ) Homozerine trans-succinylase Cysteine synthase Gutamine synthase Gutamine synthase Shikimate kinase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADP-transcriptional regulators containing a DNA-binding HTH domain and a aminotransferase domain (MocR family) and their eukaryotic orthologs Carbamorylohosphate synthase targe subunit (spit gene in MJ) Gamma-gutamy (phosphate reductase ABC-type dipeptide/clicoppotide/incket transport system ATPase component ABC-type dipeptide/clicoppotide/incket transport system ATPase component ABC-type dipeptide/clicoppotide/incket transport system ATPase component ABC-type dipeptide/clicoppotide/incket transport system ATPase component Aminopeptidase/Gucappatide/clicket transport system ATPase component Aminoperities de adviseae/Succinyl-diaminopimelate desuccinylase and related deacylase Saccharonite de devidyrogenase and related protein
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1460 LBUL_1460 LBUL_1602 LBUL_1603 LBUL_1663 LBUL_1681 LBUL_161 LBUL_161 LBUL_161 LBUL_161 LBUL_1630 LBUL_1640 LBUL_1640 LBUL_1640 LBUL_1641	ArgH CarB MetA CysK GinA PrsA Arok GitD PrepP ArgA DppP PepD ARO8 CarB ProA ARO8 CarB ProA DppF PepC ThrB LdcC LYS9 AnspC SdB	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.364 0.500	0.328 0.402 0.363 3.600 3.670 0.454 0.248	0.052 0.039 0.165 0.108 0.081 0.034 0.034 0.034 0.442 2.248 0.386 0.121 0.185 2.204	0.332	2.350	Ethanolamine utilization protein Cardamory/bhosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrodyzing) Gluramine aminoschinate lyase Agaminoschinate lyase Momoscine trans succinylase Cysteine synthase Glutamine synthase Glutamine synthase Shilimate kinase NADPH-dependent glutamate synthase beta chain and related oxidoreductase NADPH-dependent glutamate synthase beta chain and related oxidoreductase NADP-transcriptional related accity/transformase NADP-trybe dispensional related accity/transformase NADP-trybe dispensional gas synthesis and the synthase beta chain and related oxidoreductase Sacharonylo hosphate synthase targe subunit (spit gene in MJ) Gamma-glutamy (hosphate reductase ABC-type dispension) and an aminotransferase domain (MocR Tamity) phosphate reductase ABC-type dispension) and the subs soft system ATPase component Amicopeptidase Carbamorylohosphate synthase desubs targe subunit (spit gene in MJ) Gamma-glutamy (hosphate reductase Hornoserine kinase Hornoserine kinase Hornoserine kinase Sacharonyne and enastylase/Succinyl-diaminopimelate desuccinylase and related deacylase Hornoserine kinase Selencoysteine lyses
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1466 LBUL_1502 LBUL_1502 LBUL_1563 LBUL_1563 LBUL_1588 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1689 LBUL_1689 LBUL_1689	ArgH CarB MetA CysK GinA Arok GinD Prep Papp Arok GinD PepP Arok Arok CarB DppD ARO8 CarB DppD ARO8 CarB DppD Arok Aros CarB Aros Aros CarB Aros Aros CarB Aros Aros Aros Aros Aros Aros Aros Aros	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.364 0.500 0.459	0.328 0.402 0.363 3.600 3.670 0.454 0.248 0.381	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.034 0.034 0.034 0.386 0.386 0.386 0.386 0.321 0.185 2.204 7.298	0.332	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine amidoransferase Argininosuccinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Homoserine trans-succinylase Glutamine amidor subunit (spit gene in MJ) Homoserine trans-succinylase Glutamine amidor subunit (spit gene in MJ) Homoserine trans-succinylase Asphrotic synthese and related acetyltransferase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pto aminopeptidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xaa-Pto aminopeptidase NADPH-dependent glutamate synthase beta chain and related oxidoreductase Xab-Type dipeptide/oliopoptide/inickel transport system ATPase component Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs Carbamory/hosphate synthase large subunit (spit gene in MJ) Gamma-glutase Carbylase/Succinyl-diaminopimelate desuccinylase and related deacylase Homoserine kinase Aglo-type dipeptide/dilopoptide/nickel transport system ATPase component Aminopeptidase Gamma-glutase Carbylase/Succinyl-diaminopimelate desuccinylase and related deacylase Homoserine kinase Saccharopine dehydrogenase and related protein Gamma-glutanet-deh-chain amino acid transport system ATPase component ABC-type brached-chain amino acid transport system ATPase component Anginenelysine/nether/diaminopimelate desuccinylase and related deacylase Homoserine kinase Selenocysteine lyase
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1460 LBUL_1502 LBUL_1503 LBUL_1563 LBUL_1563 LBUL_1614 LBUL_1	ArgH CarB MetA CysK GinA PrsA Arok GitD PrepP ArgA DppP PepD ARO8 CarB ProA ARO8 CarB ProA DppF PepC ThrB LdcC LYS9 AnspC SdB	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.364 0.500 0.459	0.328 0.402 0.363 3.600 3.670 0.454 0.248	0.052 0.039 0.165 0.108 0.081 0.034 0.034 0.034 0.442 2.248 0.386 0.121 0.185 2.204	0.332	2.350	Ethanolamine utilization protein Cardamory/bhosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine hydrodyzing) Gluramine aminosuccinate lyase Argininosuccinate lyase Argininosuccinate lyase Momerserine trans-succinylase Ovatame synthase Ovatame synthase Ovatame synthase Ovatame synthase Ovatame synthase Shikimate kinase NADPH-dependent glutamate synthase beta chain and related oxidoreductase NADPH-dependent glutamate synthase and related acaylitransferasa NaDPH-dependent glutamate synthase targe subunit (spit PH domain and a aminotransferase domain (MocR family) and their eukaryotic orthologs Cartamory/bhosphate synthase flore glucons (spit gene in MJ) Gamma-glutamy phosphate reductase Homoserine kinase Homoserine kinase Homoserine kinase Acaylinel/spit continitre decarboxylase Homoserine kinase ABC-type branched-chain amino acid transport systems ATPase component ABC-type branched-chain amino acid transport systems ATPase component ABC-type branched-chain amino acid transport systems ATPase component ABC-type branched-chain amino acid transport systems ATPase component
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1562 LBUL_1562 LBUL_1562 LBUL_1564 LBUL_1588 LBUL_1694 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1669 LBUL_1	ArgH CarB MetA CysK GinA ArgA ArgA CarB ProA ArgA DppD ArgA DppD CarB ProA ProA PepC ArgB LtYS9 AnsP CsdB LtYS9 AnsP CsdB LtYS9 AnsP	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.364 0.500 0.459	0.328 0.402 0.363 3.670 0.454 0.248 0.381 0.272 0.156	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.034 0.034 0.034 0.386 0.386 0.386 0.386 0.386 0.321	0.332	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine+hydrolyzing) Glutamine aminosuchinate lyzae Argininosucchinate lyzae Argininosucchinate lyzae Cysterine synthase Cysterine synthasynthase Cysterine synthase Cysterine synthas
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1424 LBUL_152 LBUL_1567 LBUL_1567 LBUL_1561 LBUL_1581 LBUL_1581 LBUL_1630 LBUL_1630 LBUL_1630 LBUL_1630 LBUL_1634 LBUL_1734 LBUL_17	ArgH CarB MetA CysK GinA PrsA AroK GitD PepP ArgA ArgA ArgA ArgA DppD BrpA ProA AROB CarB ProA AROB CarB ProA ArgE ThrB LdcC CatB CarB DppF PepC ArgB ArgB ArgB ArgB ArgB ArgB ArgB ArgB	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.345 0.364 0.500 0.459 0.324	0.328 0.402 0.363 3.600 3.670 0.454 0.248 0.381	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.442 2.248 0.386 0.386 0.321 0.185 2.204 7.298 0.323 3.998	0.332	2.350	Ethanolamine utilization protein Cardamoiyhohosphate synthase large subunit (spit gene in MJ) Asparagine synthase (dutamine-hydrolyding) Gutamine amolybhosphate synthase large subunit (spit gene in MJ) Aromozerine trans-succinylase Cysteine synthase Gutamine synthase Gutamine synthase Gutamine synthase Shimitak kinase Phosphonibos/yprophosphate synthetase Shimitak kinase NADPH-dependent gutamate synthase beta chain and related oxidoreductase NADPH-dependent gutamate synthase beta chain and related acrylarse ABC-type dipeptide/dipopptide/nickel transport system ATPase component Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs Carbamoiyhosphate synthase large subunit (spit gene in MJ) Gamma-gutamy phosphate reductase ABC-type dipeptide/dilopoptide/nickel transport system ATPase component ABC-type dipeptide/dilopoptide/nickel transport system ATPase component ABC-type playel/delois/opptide/dilokel transport system ATPase component ABC-type playel/delois/opptide/dilokel transport system ATPase component ABC-type playel acrylitase? Succharopine tervitase and related portein Gamma-aminobutyrate permease and related protein Gamma-aminobutyrate permease and related protein Gamma-aminobutyrate permease and related protein GAC-type play annine add transport system ATPase component ABC-type playel annine add transport system ATPase component ABC-type playel annine add transport system ATPase component ABC-type playel system ATPase component
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1423 LBUL_1423 LBUL_1423 LBUL_1422 LBUL_1423 LBUL_1562 LBUL_1563 LBUL_1563 LBUL_1564 LBUL_1581 LBUL_1581 LBUL_1581 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1624 LBUL_1751 LBUL_1752 LBUL_1762 LBUL_1762 LBUL_1762 LBUL_1762	ArgH CarB MetA CysK GinA ArgA ArgA CarB ProA ArgA DppD ArgA DppD CarB ProA ProA PepC ArgB LtYS9 AnsP CsdB LtYS9 AnsP CsdB LtYS9 AnsP	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.345 0.364 0.500 0.459 0.324	0.328 0.402 0.363 3.670 0.454 0.248 0.381 0.272 0.156	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.034 0.034 0.386 0.121 0.185 2.204 0.185 2.208	0.332	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine+hydrolyzing) Glutamine aminosuchinate lyzae Argininosucchinate lyzae Argininosucchinate lyzae Cysterine synthase Cysterine synthasynthase Cysterine synthase Cysterine synthas
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1562 LBUL_1562 LBUL_1567 LBUL_1567 LBUL_1581 LBUL_1681 LBUL_1681 LBUL_1681 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1772 LBUL_1773	Argh CarB MetA CysK GinA PrsA Arok GilD PepP PrsA ArgA DppD DppF CarB DppF Thits LivG DatA DppF TesA ArgB LivG DpF DpF TesA ArgB DppF TesA ArgA DppF TesA ArgA DppF TesA ArgA DppF TesA ArgA DppF DpF DatA	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.364 0.364 0.459 0.459 0.324 0.365 0.158	0.328 0.402 0.363 3.600 3.670 0.454 0.248 0.381 0.272 0.156 5.544 2.745	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.442 2.248 0.386 0.386 0.321 0.185 2.204 7.298 0.323 3.998	0.332	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine and distransferrase Argininosuccinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Hospital synthesise Phosphorbosylpyrophosphate synthese Shikimate kinase NADPH-dependent glutamate synthese beta chain and related oxidoreductase Xaa-Pro anjhoopptidase NADPH-dependent glutamate synthase bata chain and related oxidoreductase Xaa-Pro anjhoopptidase Na-BC-type dipedife/dioppoptidahickel transport system ATPase component ABC-type dipedicalipoptidahickel transport system ATPase component Amorphitase C Astrophitase C Astrophit
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1428 LBUL_1428 LBUL_1428 LBUL_1426 LBUL_1562 LBUL_1562 LBUL_1562 LBUL_1562 LBUL_1563 LBUL_1564 LBUL_1588 LBUL_1588 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1619 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1626 LBUL_1753 LBUL_1	Argh Carb Carb Cysk Gina Arok Gina Arok Gilb Pepp Dipb Dipb Dipb Dipb Dipb Dipb Dipb Di	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.345 0.500 0.459 0.324 0.365 0.324	0.328 0.402 0.363 3.600 3.670 0.454 0.248 0.381 0.272 0.156 5.544	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.034 0.442 2.248 0.386 0.321 0.121 0.185 2.204 7.298 0.323 3.998 2.425	0.332	2.350	Ethanolamine utilization protein Cardamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine aminosuchinate lyase Anginicosuchinate lyase Anginicosuchinate lyase Anginicosuchinate lyase Cysteline synthase Glutamine synthase Glutamine synthase Cysteline synthase Glutamine synthase Shikimate kinase NADPH-dependent glutamate synthase beta chain and related oxidoreductase NADPH-dependent glutamate synthase beta chain and related synthase NaDPH-dependent glutamate synthase beta chain and related synthase NaDPH-dependent glutamate synthase beta chain and related synthase Carbamory/hosphates synthase glutase Carbamory/hosphates synthase glutase Carbamory/hosphates synthase glutase containing a DNA-binding HTH domain and a aminotransferase domain (MocR Tamily) phosphate reductase ABC-type plotedeolicopoptidenticket transport system ATPase component ABC-type branched-chain amino acid transport system STPase component Ab-
LBUL_1330 LBUL_1340 LBUL_1354 LBUL_1354 LBUL_1354 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1562 LBUL_1562 LBUL_1567 LBUL_1567 LBUL_1581 LBUL_1681 LBUL_1681 LBUL_1681 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1693 LBUL_1772 LBUL_1773	Argh CarB MetA CysK GinA PrsA Arok GilD PepP PrsA ArgA DppD DppF CarB DppF Thits LivG DatA DppF TesA ArgB LivG DpF DpF TesA ArgB DppF TesA ArgA DppF TesA ArgA DppF TesA ArgA DppF TesA ArgA DppF DpF DatA	2.063 0.212 0.247	0.371 0.442 0.233 0.157 0.345 0.364 0.364 0.459 0.459 0.324 0.365 0.158	0.328 0.402 0.363 3.600 3.670 0.454 0.248 0.381 0.272 0.156 5.544 2.745	0.052 0.039 0.165 0.105 0.081 0.034 0.034 0.442 2.248 0.386 0.321 0.121 0.185 2.204 7.298 0.323 3.998 2.425	0.332	2.350	Ethanolamine utilization protein Carbamory/hosphate synthase large subunit (spit gene in MJ) Asparagine synthase (glutamine-hydrolyzing) Glutamine and distransferrase Argininosuccinate lyase Carbamory/hosphate synthase large subunit (spit gene in MJ) Hospital synthesise Phosphorbosylpyrophosphate synthese Shikimate kinase NADPH-dependent glutamate synthese beta chain and related oxidoreductase Xaa-Pro anjhoopptidase NADPH-dependent glutamate synthase bata chain and related oxidoreductase Xaa-Pro anjhoopptidase Na-BC-type dipedife/dioppoptidahickel transport system ATPase component ABC-type dipedicalipoptidahickel transport system ATPase component Amorphitase C Astrophitase C Astrophit

LBUL_1885 LBUL_1890	SerB COG4126			0.499	2.236			Phosphoserine phosphatase Hydantoin racemase
LBUL_1909 LBUL_1930	PepD AspA			0.263	0.016	0.254	3.051	Dipeptidase Aspartate ammonia-lyase
LBUL 1942	HisH				3.898	0.234		Glutamine amidotransferase
LBUL_1950 LBUL_1954	CarB PrsA	0.368	0.393	2.979	5.512		7.197	Carbamoylphosphate synthase large subunit (split gene in MJ) Phosphoribosylpyrophosphate synthetase
LBUL_1955	TrpA		0.206	2.592	0.417			Tryptophan synthase alpha chain
LBUL_1959 LBUL_1961	RhaT SerB		0.206		0.417			Permease of the drug/metabolite transporter (DMT) superfamily Phosphoserine phosphatase
LBUL_2003 LBUL_2004	GInQ LivH		0.416	2.851 3.269				ABC-type polar amino acid transport system ATPase component Branched-chain amino acid ABC-type transport system permease components
LBUL_2005	LivH	0.300	0.241	3.352		4.057		Branched-chain amino acid ABC-type transport system permease components
LBUL_2020 LBUL_2034	GInQ IIvB	0.419	0.253		11.093	4.257		ABC-type polar amino acid transport system ATPase component Thiamine pyrophosphate-requiring protein
Carbohydrate	transport and	metabolism						
LBUL_0033 LBUL_0039	RbsK COG0702	3.297	15.670	2.484 2.025	0.249			Sugar kinase ribokinase family Predicted nucleoside-diphosphate-sugar epimerase
LBUL 0099	NagC	0.363	0.354	2.025	2.571			Transcriptional regulator/sugar kinase
LBUL_0129 LBUL_0145	TagH UgpA		2.794	5.749				ABC-type polysaccharide/polyol phosphate transport system ATPase component ABC-type sugar transport systems permease components
LBUL_0173	PtsN	0.004	0.047	0.212	0.441			Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
LBUL_0177 LBUL_0215	MalK MalG	0.331 0.202	0.347 0.155	2.596	0.117			ABC-type sugar transport systems ATPase components ABC-type maltose transport systems permease component
LBUL_0216 LBUL_0238	MalK MalK	0.386	0.055		0.159 2.013			ABC-type sugar transport systems ATPase components ABC-type sugar transport systems ATPase components
LBUL_0239	MalK	0.004	0.005		3.705			ABC-type sugar transport systems ATPase components 2-keto-3-deoxy-6-phosphogluconate aldolase
LBUL_0246 LBUL_0251	Eda NanE	0.221 2.639	0.285		0.053	0.290	0.458	Putative N-acetylmannosamine-6-phosphate epimerase
LBUL_0256 LBUL_0262	MalK MalK	0.380	0.347 0.268	6.884	0.077			ABC-type sugar transport systems ATPase components ABC-type sugar transport systems ATPase components
LBUL_0263 LBUL_0266	UgpA GlpR	0.357 0.318	0.268		0.085			ABC-type sugar transport systems permease components Transcriptional regulators of sugar metabolism
LBUL_0303	GlgC	0.310	0.392		2.057		0.432	ADP-glucose pyrophosphorylase
LBUL_0326 LBUL_0327	FrvX NanE		0.461	2.960				Cellulase M and related protein Putative N-acetylmannosamine-6-phosphate epimerase
LBUL_0399	GlpR		2.272	0.487				Transcriptional regulators of sugar metabolism
LBUL_0445 LBUL_0498	MgIA GlgC		0.448		5.087			ABC-type sugar transport system ATPase component ADP-glucose pyrophosphorylase
LBUL_0532 LBUL_0550	WcaG MgIA		0.451 2.433	0.243	0.098			Nucleoside-diphosphate-sugar epimerase ABC-type sugar transport system ATPase component
LBUL_0578	MalK	0.442	0.448					ABC-type sugar transport systems ATPase components
LBUL_0579 LBUL_0580	UgpA UgpE	0.442	0.396 0.268					ABC-type sugar transport systems permease components ABC-type sugar transport system permease component
LBUL_0581 LBUL_0585	UgpB NagD	2.582	0.402	0.484				ABC-type sugar transport system periplasmic component Predicted sugar phosphatase of the HAD superfamily
LBUL_0674	COG1819	0.499	0.220	0.404				Glycosyl transferase related to UDP-glucuronosyltransferase
LBUL_0676 LBUL_0821	XylB WcaG		0.434 0.318	0.258	0.196			Sugar (pentulose and hexulose) kinase Nucleoside-diphosphate-sugar epimerase
LBUL_0869 LBUL_0870	UgpE MalK	0.300			0.363			ABC-type sugar transport system permease component ABC-type sugar transport systems ATPase components
LBUL_0882	MalK		0.216					ABC-type sugar transport systems ATPase components
LBUL_0883 LBUL_0904	MalK GalK		0.350 0.179	0.456	5.201			ABC-type sugar transport systems ATPase components Galactokinase
LBUL_0905 LBUL_0906	GalK GalK	0.232	0.157		3.061			Galactokinase Galactokinase
LBUL_0919	COG5309				4.804			Exo-beta-1 3-glucanase
LBUL_0989 LBUL_1069	MalK MalK	0.408		7.779	4.992			ABC-type sugar transport systems ATPase components ABC-type sugar transport systems ATPase components
LBUL_1070 LBUL_1148	MalK TagH	0.413	0.206	7.598 0.267				ABC-type sugar transport systems ATPase components ABC-type polysaccharide/polyol phosphate transport system ATPase component
LBUL_1204	MgIA MalK	0.110	0.200	62.155 2.998				ABC-type sugar transport system ATPase component
LBUL_1213 LBUL_1214	UgpA			2.998	4.248			ABC-type sugar transport systems ATPase components ABC-type sugar transport systems permease components
LBUL_1261 LBUL_1292	MalK MalK	0.137	0.262	2.588	0.193			ABC-type sugar transport systems ATPase components ABC-type sugar transport systems ATPase components
LBUL_1293	MalK	0.282	0.278	2.768	0.148			ABC-type sugar transport systems ATPase components
LBUL_1297 LBUL_1419	DAK1 Hit			0.284 0.375	0.412			Dihydroxyacetone kinase Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolase
LBUL_1422 LBUL_1562	SgbH MalK	0.212					2.359 0.162	3-hexulose-6-phosphate synthase and related protein ABC-type sugar transport systems ATPase components
LBUL_1588	MalK			0.381	0.442			ABC-type sugar transport systems ATPase components
LBUL_1630 LBUL_1639	GalK RbsB			31.959	0.121			Galactokinase ABC-type sugar transport system periplasmic component
LBUL_1652 LBUL_1658	UhpC UhpC	2.845	2.903		0.017	2.471 0.058		Sugar phosphate permease Sugar phosphate permease
LBUL_1664 LBUL_1693	WcaG MgIA	0.485			7.298			Nucleoside-diphosphate-sugar epimerase ABC-type sugar transport system ATPase component
LBUL_1700	MalK			0.272	0.323			ABC-type sugar transport systems ATPase components
LBUL_1710 LBUL_1772	GlgA MglA				5.122 2.425			Glycogen synthase ABC-type sugar transport system ATPase component
LBUL_1807	GlgA	0.393	0.294	2.498				Glycogen synthase
LBUL_1835 LBUL_1854	WcaG COG1819	0.00-		2.298				Nucleoside-diphosphate-sugar epimerase Glycosyl transferase related to UDP-glucuronosyltransferase
LBUL_1857 LBUL_1870	CapC COG2074	0.282	0.429					Capsular polysaccharide biosynthesis protein 2-phosphoglycerate kinase
LBUL_1959 LBUL_2001	RhaT RbsB	0.484	0.206		0.417			Permease of the drug/metabolite transporter (DMT) superfamily ABC-type sugar transport system periplasmic component
LBUL_2002	RbsB	0.404			0.308	0.330		ABC-type sugar transport system periplasmic component
LBUL_2003 LBUL_2004	MgIA AraH		0.416	2.851 3.269				ABC-type sugar transport system ATPase component Ribose/xylose/arabinose/galactoside ABC-type transport systems permease components
LBUL_2005 LBUL_2020	AraH MalK	0.300	0.241	3.352		4.257		Ribose/xylose/arabinose/galactoside ABC-type transport systems permease components ABC-type sugar transport systems ATPase components
LBUL_2034	COG3961	0.419	0.253		11.093			Pyruvate decarboxylase
Cell division a	nd chromosom	e partitionir	ng					
LBUL_0129 LBUL_0177	FtsE FtsE	0.331	2.794 0.347	2.596				Predicted ATPase involved in cell division Predicted ATPase involved in cell division
LBUL_0216	FtsE	0.386	0.055	2.000	0.159			Predicted ATPase involved in cell division
LBUL_0238 LBUL_0239	FtsE FtsE				2.013 3.705			Predicted ATPase involved in cell division Predicted ATPase involved in cell division
LBUL_0252 LBUL_0256	MesJ FtsE	2.315	0.347	6.884				Predicted ATPase of the PP-loop superfamily protein implicated in cell cycle control Predicted ATPase involved in cell division
LBUL_0262	FtsE	0.380	0.268	0.004	0.077			Predicted ATPase involved in cell division
LBUL_0320 LBUL_0322	COG2919 MesJ		0.398 0.484		0.260			Septum formation initiator Predicted ATPase of the PP-loop superfamily protein implicated in cell cycle control
LBUL_0445 LBUL_0529	FtsE FtsK		0.333 0.349	2.661				Predicted ATPase involved in cell division DNA segregation ATPase FtsK/SpolIIE and related protein
LBUL_0548	GidA				0.425			NAD/FAD-utilizing enzyme apparently involved in cell division
LBUL_0550 LBUL_0578	FtsE FtsE		2.433 0.448	0.243	0.098			Predicted ATPase involved in cell division Predicted ATPase involved in cell division
LBUL_0591	CrcB			6.545		2.785		Integral membrane protein possibly involved in chromosome condensation
LBUL_0646	MreB				0.459			Actin-like ATPase involved in cell morphogenesis

LBUL_0655 LBUL_0667 LBUL_0677 LBUL_0677 LBUL_0677 LBUL_0688 LBUL_0688 LBUL_0688 LBUL_0883 LBUL_0883 LBUL_0883 LBUL_0883 LBUL_0883 LBUL_1080 LBUL_1100 LBUL_1100 LBUL_1231 LBUL_1231 LBUL_1235 LBUL_1285 LBUL_2285 LBUL_2285 LBUL_2285 LBUL_2285 LBUL_2285 LBUL_285 LBUL_285 LBUL_195 LBU_295 LBU	Ezra Mrea Fisso Fi	0.408 0.367 0.137 0.324 0.282 0.212	0.383 0.434 2.445 0.382 0.216 0.350 0.350 0.356 0.366 0.366 0.366 0.366 0.3262 0.278	0.451 0.330 0.352 7.779 7.598 0.412 62.155 2.998 2.588 2.768 0.272 2.324 2.851	3.612 2.291 8.246 2.050 0.363 5.201 4.992 4.280 0.193 0.148 4.141 0.442 7.296 0.323 2.425	4.257	0.219 0.162 3.583	Negative regulator of septation ring formation Actin-like ATPase involved in cell morphogenesis Actin-like ATPase involved in cell division Predicate ATPase of the P4-loop superfamily protein implicated in cell cycle control Bacterial cell division membrane protein Predicate ATPase of the P4-loop superfamily protein implicated in cell cycle control Bacterial cell division Predicate ATPase involved in cell di
							0.000	от сот то сольту оплутно аррановну птотов и сов имзют
LBUL_0031 LBUL_0039 LBUL_0069 LBUL_0109 LBUL_0118 LBUL_0118 LBUL_0140 LBUL_0140 LBUL_0146 LBUL_0146 LBUL_0161 LBUL_0206 LBUL_0206 LBUL_0216 LBUL_0217 LBUL_0217	biogenesis, ou Acm RfaE COG0702 WcaA Prc TagH Spr COG4623 DdIA TagH DdIA MurE TagH COG4623 TagH TagH TagH TagH	0.331 0.181 0.480 0.386 0.412	15.670 2.794 0.404 0.475 0.347 0.150 0.335 0.055 0.171 0.347	2.484 2.025 5.749 2.596 0.350 2.028	3.249 0.249 40.987 8.677 0.159 0.224 2.013 3.705		0.131 0.415 0.297	Lyzozyme M1 (1 4-bata-N-acetylmuramidase) ADP-heptose synthase bifunctional sugar kinase/adenylyttransferase Predicide nucleoside-diphosphate-sugar epimerase Glycosyltransferase involved in cell wall biogenesis Periplasmic protease ABC-type polysaccharide/polyol phosphate transport system ATPase component Cell wall-associated hytdrolase (Invasion-associated protein) Predicate soluble lytic transglycosylase tused to an ABC-type animo acid-binding protein D-alanine-D-alanine ligase and related ATP-grasp protein ABC-type polysaccharide/polyol phosphate transport system ATPase component D-alanine-D-alanine ligase and related ATP-grasp protein Phosphoglycerol transferase and related at protein pase protein D-Alanine-D-alanine ligase and related ATP-grasp protein Phosphoglycerol transferase and related at protein subar protein D-Alanine-D-alase-charide/polyol phosphate transport system ATPase component ABC-type polysaccharide/polyol phosphate transport system ATPase component
LBUL_0256 LBUL_0261 LBUL_0262 LBUL_0303 LBUL_0404 LBUL_0404 LBUL_0445 LBUL_0451 LBUL_0493 LBUL_0498 LBUL_0498 LBUL_0506 LBUL_0532	COG4623 TagH GlmU LepA OCH1 TagH Murl WecB GalU LepA DItE	0.421 0.380 0.379	0.335 0.268 0.392 0.465 0.476 0.333 0.448 0.451	0.357	0.088 0.077 2.057 2.251 5.087 4.576		0.432 0.335	Predicial soluble lyic transpirozsylase fused to an ABC-type amino acid-binding protein ABC-type polysaccharide/polyol phosphate transport system ATPase component N-acetylglucosamine-1-phosphate undyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains) Membrane GTPase LepA Mannoyttransferase OCH1 ABC-type polysaccharide/polyol phosphate transport system ATPase component Glutamate racemase UDP-N-acetylglucosamine 2-epimerase UDP-N-acetylglucosamine 2-epimerase UDP-Glucose prophosphorylose Membrane GTPase LepA
LBUL_0546 LBUL_0577 LBUL_0578 LBUL_0623 LBUL_0661 LBUL_0664 LBUL_0671 LBUL_0672	Lgt MurB TagH MdoB MurE MurE MreC Ftsl Rfe	0.350 0.342 0.303	0.385 0.442 0.448 0.467 0.419 0.297 0.242	0.258	2.449 4.814 5.486			(D-alanine transfer protein) Prolipoprotein dacylgbroeytiransferase UDP-N-acetylmuramate dehydrogenase ABC-type oplysaccharide(polyd) phosphate transport system ATPase component Prosphoglycerol transferase and related protein alkaline phosphatase superfamily UDP-N-acetylmuramyl tipeptide synthase Cell shape-determining protein Cell division protein FISUpenicillin-binding protein 2 UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase
LBUL_0673 LBUL_0674 LBUL_0675 LBUL_0696 LBUL_0700 LBUL_0700 LBUL_0709 LBUL_0726 LBUL_0776 LBUL_0821	MurD MurG FtsQ LepA TagD Prc LepA Glf LepA DItE	0.499 0.448	0.382 0.220 0.332 0.332 3.587 0.278 0.318	2.430 0.047 0.258	2.251 2.191 2.182 2.301 2.048 0.130 3.234 0.196	4.189	3.051	UDP-N-acetylmuramoytellarine-D-glutamate ligase UDP-N-acetyljuocsamine LPS Nacetylgluocsamine transferase Cell division septal protein Membrane GTPase LepA Cytidylyttansferase Periplasmic protease Membrane GTPase LepA UDP-galactopyranose mutase Membrane GTPase LepA Short-chain detyrdiogenase involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid
LBUL_0825 LBUL_0870 LBUL_0883 LBUL_0919 LBUL_0929 LBUL_09990 LBUL_09990 LBUL_1060 LBUL_1060 LBUL_1070 LBUL_1073	DdlA TagH TagH MrcB LspA TagH LolE COG3264 TagH TagH COG1247	3.422 0.408 0.381	0.295 0.216 0.350 0.148	0.132 0.481 0.352 7.779 7.598 0.120	0.391 0.363 5.201 4.804 0.021 4.992 4.118	0.269		(D-alanine-basinine transfer protein) D-alanine-basinine ligase and related ATP-grasp protein ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component Membrane caracterized polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component Small-conductance mechanosensitive channel ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component
LBUL_1148 LBUL_1180 LBUL_1204 LBUL_1213 LBUL_1213 LBUL_1214 LBUL_1225 LBUL_1226 LBUL_1230 LBUL_1236 LBUL_1261 LBUL_1261 LBUL_1285	TagH WecE TagH COG4623 SrtA LepA RfaE WecE LepA TagH COG4623 TolA	0.413 0.341 6.367 0.137 0.201	0.206 0.269 2.770 0.345 0.366	0.267 62.155 2.998 13.936 3.477	4.248 4.575 4.313	0.224		ABC-type polysaccharide/polyd phosphate transport system ATPase component Predicide privious I phosphate-deependent enzyme apparentij involved in regulation of cell wall biogenesis ABC-type polysaccharide/polyd phosphate transport system ATPase component ABC-type polysaccharide/polyd phosphate transport system ATPase component ADP-teptoes organizase bilincitional sugar kinase/aden/yltransferase ADP-teptoes applicase) Membrane GTPase LapA ABC-type polyaccharide/polyd phosphate transport system ATPase component Predicad soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein Membrane GTPase LapA
LBUL_1286	COG3264		0.326					Small-conductance mechanosensitive channel

LBUL_1292	TagH	0.324	0.262	2.588	0.193			ABC-type polysaccharide/polyol phosphate transport system ATPase component
LBUL_1293 LBUL_1308	TagH Cfa	0.282	0.278	2.768 0.462	0.148			ABC-type polysaccharide/polyol phosphate transport system ATPase component Cyclopropane fatty acid synthase and related methyltransferase
LBUL_1330 LBUL_1334	DdIA GlmS		0.339 0.371		0.063		2.314	D-alanine-D-alanine ligase and related ATP-grasp protein Glucosamine 6-phosphate synthetase contains amidotransferase and phosphosugar isomerase domains
LBUL_1340 LBUL_1356	DdlA Cfa		0.301		0.105 0.051	0.303		D-alanine-D-alanine ligase and related ATP-grasp protein Cyclopropane fatty acid synthase and related methyltransferase
LBUL_1413	MurC		0.383	0.387	2.190			UDP-N-acetylmuramate-alanine ligase
LBUL_1515 LBUL_1542 LBUL_1562	COG3264 WcaA		0.376		3.376			Small-conductance mechanosensitive channel Glycosyltransferase involved in cell wall biogenesis
LBUL_1562 LBUL_1588	TagH TagH	0.212			0.442		0.162	ABC-type polysaccharide/polyol phosphate transport system ATPase component ABC-type polysaccharide/polyol phosphate transport system ATPase component
LBUL_1600	RfaJ GutQ			0.320	2.219			Lipopolysaccharide biosynthesis protein LPS:glycosyltransferase
LBUL_1618 LBUL_1664	GalE	0.485						Predicted sugar phosphate isomerase involved in capsule formation UDP-glucose 4-epimerase
LBUL_1667 LBUL_1691	Spr WecE		0.365	4.745	2.204			Cell wall-associated hydrolase (invasion-associated protein) Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis
LBUL_1693 LBUL_1700	TagH TagH			0.272	7.298 0.323			ABC-type polysaccharide/polyol phosphate transport system ATPase component ABC-type polysaccharide/polyol phosphate transport system ATPase component
LBUL_1707 LBUL_1709	MdoB RfaG		0.140	2.453	4.510 12.066			Phosphoglycerol transferase and related protein alkaline phosphatase superfamily Glycosyltransferase
LBUL_1710	RfaG		0.140	2.400	5.122			Glycosyltransferase
LBUL_1772 LBUL_1800	TagH TagD	0.210	0.119		2.425			ABC-type polysaccharide/polyol phosphate transport system ATPase component Cytidylyltransferase
LBUL_1801 LBUL_1807	COG3475 RfaG	0.236	0.154 0.294	2.304 2.498				LPS biosynthesis protein Glycosyltransferase
LBUL_1808	WcaA	0.472		3.024	2.394			Glycosyltransferase involved in cell wall biogenesis
LBUL_1810 LBUL_1812	Glf WcaJ	0.447		2.745	4.943 4.090			UDP-galactopyranose mutase Sugar transferase involved in lipopolysaccharide synthesis
LBUL_1835 LBUL_1843	RfbD COG1215	0.288	0.304	6.551				dTDP-4-dehydrorhamnose reductase Glycosyltransferase probably involved in cell wall biogenesis
LBUL_1848 LBUL_1853	WcaA OCH1	0.191	0.480 0.440					Glycosyltransferase involved in cell wall biogenesis Mannosyltransferase OCH1
LBUL_1854	MurG		0.440	2.298				UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
LBUL_1856 LBUL_1857	WcaJ CapC	0.319 0.282						Sugar transferase involved in lipopolysaccharide synthesis Capsular polysaccharide biosynthesis protein
LBUL_1866 LBUL_1890	Spr RacX		0.474	3.163	2.236			Cell wall-associated hydrolase (invasion-associated protein) Aspartate racemase
LBUL_1902	GidB DdIA		0.434				7.197	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell division D-alanine-D-alanine ligase and related ATP-grasp protein
LBUL_1950 LBUL_1984	DItB					0.421	1.191	Predicted membrane protein involved in D-alanine export
LBUL_2003 LBUL_2020	TagH TagH			2.851		4.257		ABC-type polysaccharide/polyol phosphate transport system ATPase component ABC-type polysaccharide/polyol phosphate transport system ATPase component
Cell motility a								
LBUL_0111 LBUL_0112	CheB Tar	0.373			0.476			Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain Methyl-accepting chemotaxis protein
LBUL_0140	FimV		0.404		8.677		0.297	Tfp pilus assembly protein FimV
LBUL_0197 LBUL_0412	FlgJ FlgJ				6.229 2.460			Muramidase (flagellum-specific) Muramidase (flagellum-specific)
LBUL_0515 LBUL_0535	MecA FlaH			0.451	0.471		0.359	Negative regulator of genetic competence sporulation and motility Predicted ATPase involved in biogenesis of flagella
LBUL_0610 LBUL_0612	PulE PulG	7.998	0.445	18.355				Type II secretory pathway ATPase PuIE/Tfp pilus assembly pathway ATPase PilB Type II secretory pathway pseudopilin PuIG
LBUL_0621 LBUL_0646	CheB PilM		0.445	0.403	0.459			Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain
LBUL_0663	PilM		0.383		3.612			Tfp pilus assembly protein ATPase PilM Tfp pilus assembly protein ATPase PilM
LBUL_0676 LBUL_0872	PilM CheB	0.378	0.434		2.434			Tfp pilus assembly protein ATPase PilM Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain
LBUL_1070	VirB11			7.598				Type IV secretory pathway VirB11 protein involved in flagella biosynthesis
I BUI 1282			0.358		4.280			Flagellar GTP-binding protein
LBUL_1282 LBUL_1285	FIhF FIhF		0.358 0.366	0.070	4.280			Flagellar GTP-binding protein Flagellar GTP-binding protein
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756	FIhF FlaH FIhB			2.872	4.280 4.797			Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagellar biogynthesis pathway component FlhB
LBUL_1282 LBUL_1285 LBUL_1601	FlhF FlaH	0.198 2.021		2.872 4.153		0.449	0.488	Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944	FlhF FlaH FlhB Tar	2.021	0.366			0.449	0.488	Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagellar biogynthesis pathway component FlhB Methyl-accepting chemotaxis protein Flagellar GTP-binding protein
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285	FIhF FIaH FIhB Tar FIhF	2.021	0.366			0.449	0.488	Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagelfar biosynthesis pathway component FihB Methyl-accepting chemotaxis protein Ragellar GTP-binding protein Histone chaperone involved in gene silencing
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285 LBUL_1474	FlhF FlaH FlhB Tar FlhF ructure and dyr COG5137 COG5406	2.021 namics	0.366	4.153		0.449	0.488	Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagellar biogynthesis pathway component FlhB Methyl-accepting chemotaxis protein Flagellar GTP-binding protein
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285 LBUL_1474 Coenzyme m LBUL_0033	FIhF FlaH FIhB Tar FIhF ructure and dyr COG5137 COG5406 etabolism PdxK	2.021 namics	0.366 2.121 0.366	4.153			0.488	Flageliar GTP-binding protein Flageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flageliar biosynthesis pathway component FlhB Methyl-accepting chemotaxis protein Flageliar GTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285 LBUL_1474 Coenzyme m LBUL_0033 LBUL_0084 LBUL_0129	FIhF FlaH FihB Tar FIhF COG5137 COG5406 etabolism PdxK LdhA FepC	2.021 namics	0.366 2.121 0.366 3.717 2.794	4.153 0.402	4.797	0.449	0.488	Flageliar GTP-binding protein Flageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flageliar biosynthesis pathway component FIhB Methyl-accepting chemotaxis protein Flageliar GTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase ABC-type coblamin/F64-sidenpohrees transport systems ATPase components
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285 LBUL_1474 Coenzyme m LBUL_0033 LBUL_0034 LBUL_0129 LBUL_0161	FIhF FlaH FlhB Tar FIhF vucture and dyr COG5137 COG5406 etabolism PdxK LdhA FepC RimK	2.021 namics 2.063	0.366 2.121 0.366 3.717 2.794 0.475	4.153 0.402 2.484	4.797		0.488	Flageliar GTP-binding protein Flageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagelia Flageliar biosynthesis pathway component Fh/B Hageliar biosynthesis pathway protein Flageliar GTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxanie kinase Lactate dehytogeness and related dehytogenese ABC-type cobatamin/FG3-siderophores transport systems ATPase components Glutathione synthase/Ribosomal protein ST
LBUL_1282 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1757 LBUL_1757 LBUL_1757 LBUL_1757 LBUL_1285 LBUL_1474 Coenzyme m LBUL_0033 LBUL_00184 LBUL_0161 LBUL_0161	FIhF FlaH FlhB Tar FIhF COG5137 COG5406 etabolism PdxK LdhA FepC RimK FepC FolB	2.021 namics 2.063 0.331	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430	4.153 0.402	4.797		0.488	Flagellar GTP-binding protein Pragellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Plagellar Disputchesis pathway component FINB Methyl-accepting chemotoxis protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxil/pyridoxine/pyridoxime kitase Ladau dehydrogenes/sub-silencing dehydrogenes Ladau dehydrogenes/sub-silencing dehydrogenes Citatatione synthase/Ribosomal protein S ABC-type cobalamin/F64-siderophores transport systems ATPase components Dilydroncepterin alcolase
LBUL_1282 LBUL_1285 LBUL_1285 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatins str LBUL_1285 LBUL_1285 LBUL_1285 LBUL_1285 LBUL_0033 LBUL_0033 LBUL_0033 LBUL_0034 LBUL_0161 LBUL_0176 LBUL_0208 LBUL_0209 LBUL_02010	FIhF FlaH FIhB Tar FIhF COG5137 COG5406 etabolism PdxK LdhA FepC RimK FepC RimK FolB FolE FolE	2.021 namics 2.063	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.347 0.335	4.153 0.402 2.484	4.797		0.488	Flageliar GTP-binding protein Prageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Predicted ATPase involved in biogenesis of flagella Plageliar Diversities pathway component FIhB Methyl-accepting chemotaxis protein Hageliar GTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase AC-Upe ocbalamin/F63-siderophores transport systems ATPase components ABC-Upe cobalamin/F63-siderophores transport systems ATPase components Dibridroncepterin alcolase GTP cyclohydrolase I Folylopolydiamate synthase
LBUL_1282 LBUL_1285 LBUL_1265 LBUL_1601 LBUL_1756 LBUL_1757 LBUL_1944 Chromatin str LBUL_1285 LBUL_1285 LBUL_1285 LBUL_0184 LBUL_0033 LBUL_0033 LBUL_0034 LBUL_0039 LBUL_0039 LBUL_0149 LBUL_0149 LBUL_0149 LBUL_0208 LBUL_0210 LBUL_0211 LBUL_0216	FIhF FlaH FlhB Tar FlhF FlhF COG5137 COG5137 COG5406 etabolism PdxK LdhA FepC RimK FepC RimK FoIB FoIB FoIC FoIP FepC	2.021 namics 2.063 0.331 0.386	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430 0.311	4.153 0.402 2.484	4.797 0.249 0.159		0.488	Flageliar GTP-binding protein Prageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Predicted ATPase involved in biogenesis of flagella Plageliar Diversities pathway component FIhB Methyl-accepting chemotaxis protein Plageliar CTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase ABC-type cobaminr F64adephores transport systems ATPase components BC-type cobaminr F64adephores transport systems ATPase components DGTP cyclohydrolase I DTP cyclohydrolase I DTP cyclohydrolase I DAC-type cobalaminr F64adelphores transport systems ATPase components DGTP cyclohydrolase I DTP cyclohydrolase I DTP cyclohydrolase I DAC-type cobalaminr F64adelprophores transport systems ATPase components DDV proteobalaminr F64adelprophores transport systems ATPase components
LBUL_1282 LBUL_1285 LBUL_1285 LBUL_1285 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1744 Coerzyme m LBUL_0034 LBUL_0024 LBUL_0161 LBUL_0208 LBUL_0210 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216	FINF FlaH FlnB Tar FINF vucture and dyr COG5137 COG5406 etabolism PdxK LdhA FepC RimK FepC RimK FepC FoIB FoIE FoIC FoIP	2.021 namics 2.063 0.331 0.386 0.480 0.386	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430 0.311 0.332	4.153 0.402 2.484	4.797 0.249		0.488	Flageliar GTP-binding protein Prageliar GTP-binding protein Prageliar GTP-binding protein Flageliar GTP-binding protein Flageliar GTP-binding protein Flageliar GTP-binding protein Histone chaperone involved in gene silencing Nucleoscome binding factor SPN SPT 16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase ABC-type coblamin/F64-siderophores transport systems ATPase components BAC-type coblamin/F64-siderophores transport systems ATPase components Dihydroneopterin aldolase GTP cyclohydrolase I Folylop/guitamate synthase Dihydroneopterin aldolase Dihydroneopterin aldolase Dihydroneopterin aldolase
LBUL_1282 LBUL_1285 LBUL_1285 LBUL_1285 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1756 LBUL_1744 Coerzyme m LBUL_0034 LBUL_0024 LBUL_0161 LBUL_0208 LBUL_0210 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216 LBUL_0216	FihF FiaH FihB Tar FihF COG5137 COG5137 COG5406 etabolism PdxK LdhA FepC RimK FepC RimK FepC FolB FolC FolP FepC FepC	2.021 namics 2.063 0.331 0.386 0.480	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430 0.311 0.332	4.153 0.402 2.484	4.797 0.249 0.159 2.013 3.705		0.488	Flagellar GTP-binding protein Pragellar GTP-binding protein Pradicted ATPase involved in biogenesis of flagella Pragellar Diversities pathway component FIHB Heighlar Diversities pathway component FIHB Heighlar Diversities pathway component FIHB Heighlar CTP-binding protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pridoxal/pridoxinal-pridoxinal protein S ABC-type coblamin/FG3-siderophores transport systems ATPase components Gittathione syntheser(Blocom) Birdyroteroate synthase Dihydroopteroate synthase Bi-C-type coblamin/FG3-siderophores transport systems ATPase components CFC cyclohydrolase I Folyloplyditatesimine synthase Dihydroopteroate synthase Dihydroopteroate synthase ABC-type coblamin/FG3-siderophores transport systems ATPase components ABC-type
LBUL [1282 LBUL [1282 LBUL [1601 LBUL [1601 LBUL [1767 LBUL [1747 Chromatin str LBUL [1747 Chromatin str LBUL [1747 Chromatin str LBUL [1747 Chromatin str LBUL [1767 LBUL [1285 LBUL [1767 LBUL [1767	FihF FiaH FihB Tar FihF COG5137 COG5406 etabolism PdxK LdhA FepC FoiB FoiC FoiB FoiC FoiB FoiC FoiB FoiC FoiC FoiC FoiC FoiC FoiC FoiC FoiC	2.021 namics 2.063 0.331 0.386 0.480 0.386	0.366 2.121 0.366 3.717 2.794 0.475 0.430 0.311 0.335 0.372 0.355	4.153 0.402 2.484 2.596	4.797 0.249 0.159 2.013 3.705 0.077		0.488	Flagellar GTP-binding protein Pragellar GTP-binding protein Pradicted ATPase involved in biogenesis of flagella Pragellar GTP-binding protein Hagellar GTP-binding protein Histone chaperone involved in gene silencing Nucleoscome binding factor Pridoxal/pridoxins/protein Pridoxal/pridoxins/protein Pridoxal/pridoxins/protein Pridoxal/pridoxins/pridoxins Statation Editory Statation Editory Pridoxal/pridoxins/pridoxins Radio Components ABC-type cobalamin/F63-siderophores transport systems ATPase components GTP cyclohydrolase I Folylop/gridoxining/pridox transport systems ATPase components BC-type cobalamin/F63-siderophores transport systems ATPase components BC-type cobalamin/F63-siderophores transport systems ATPase components ABC-type cobalamin/F63-siderophores transport systems ATPase components<
LBUL [1282 LBUL [1282 LBUL [160] LBUL [160] LBUL [161] LBUL [161]	FihF FiaH FinB Tar FihF COGS137 COGS406 COGS406 PdxK LdhA FepC FoiB FoiC FoiB FoiC FoiB FoiC FoiB FoiC FoiC FoiC FoiC FoiC FoiC FoiC FoiC	2.021 namics 2.063 0.331 0.386 0.480 0.386 2.315 0.380	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430 0.311 0.335 0.372 0.055 0.347 0.268 0.392	4.153 0.402 2.484 2.596 6.884	4.797 0.249 0.159 2.013 3.705 0.077 5.175 2.057		0.488	Flageliar GTP-binding protein Prageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagelia Predicted ATPase involved in biogenesis of flagelia Hageliar Diversities pathway component FIhB Methyl-accepting chemotoxis protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenots Citrathion synthase/Fibosomal protein S Dihydrogeniase and related dehydrogenots Citrathion synthase/Fibosomal protein S Dihydronopterin adolase GTP cyclohydrolase I Folylopyditamate synthase Dihydroperoste synthase ABC-type cobalamin/FG4-siderophores transport systems ATPase components Dihydroperoste synthase ABC-type cobalamin/FG4-siderophores transport systems ATPase components ABC-type cobalamin/FG4-siderophores transport systems ATPase components <td< td=""></td<>
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LBUL [1282 LBUL [1282 LBUL [160] LBUL [160] LBUL [160] LBUL [160] LBUL [160] LBUL [1944 Chromain str LBUL [1944 LBUL [194	FinF FiaH FinB Tar FinF CCG5137 CCG5406 etabolism PdxK LdnA FepC RimK FepC FepC FepC FepC FepC FepC FepC FepC	2.021 namics 2.063 0.331 0.386 0.480 0.386 2.315 0.380	0.366 2.121 0.366 3.717 2.794 0.475 0.430 0.430 0.430 0.332 0.372 0.055 0.347 0.268 0.392 0.329	4.153 0.402 2.484 2.596 6.884 2.217	4.797 0.249 0.159 2.013 3.705 0.077 5.175 2.057 4.203		0.432	Flageliar GTP-binding protein Prageliar GTP-binding protein Predicted ATPase involved in biogenesis of flagelia Prageliar GTP-binding protein Highlar Liboyan Component FINB Highlar Liboyan Component FINB Highlar Liboyan Component FINB Highlar Liboyan Component FINB Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pyridoxal/pyridoxamine kinase Lacatate dehytopomesa and related dehytoponese ABC-type cobatamin/F63siderophores transport systems ATPase components Glutathine synthase/Ribosomal protein SF Dihydroneptria alcolase GTP cyclohydrolase I Folyhophydiatamine synthase DBC-type cobatamin/F63siderophores transport systems ATPase components ABC-type cobatamin/F63siderophores transport systems ATPase compone
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LBUL [1282 LBUL [1282 LBUL [160] LBUL [160] LBUL [161] LBUL [161]	FilipFilipFilipFilipFilipFilipFilipFili	2.021 namics 2.063 0.331 0.386 0.480 0.386 2.315 0.380 0.308	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.430 0.335 0.355 0.355 0.355 0.347 0.268 0.392 0.329 0.329 0.333 0.368 0.195 2.433	4.153 0.402 2.484 2.596 6.884 2.217 0.487	4.797 0.249 0.159 2.013 3.705 0.077 5.175 2.057 4.203 0.483 0.480		0.432	Flagellar GTP-binding protein Flagellar GTP-binding protein Fragellar GTP-binding protein GTP-dicted ATPase involved in biogenesis of flagella Flagellar Disviputinesis pathway component FIhB Heltyl-accepting chemotoxis protein Histone chaperone involved in gene silencing Nucleosome binding factor SPN SPT16 subunit Pryridoxia/pryridoxine/pryridoxamine kinase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase ABC-type cobalaminF64-siderophores transport systems ATPase components ABC-type cobalaminF64-siderophores transp
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LBUL, 1282 LBUL, 1282 LBUL, 1282 LBUL, 1282 LBUL, 1287 LBUL, 1757 LBUL, 1757 LBUL, 1757 LBUL, 1757 LBUL, 1757 LBUL, 1757 LBUL, 1282 LBUL, 1282 LBUL, 1285 LBUL, 1285 LBUL, 1202 LBUL, 0024 LBUL, 0024 LBUL, 0228 LBUL, 0238 LBUL, 0238 LBUL, 0238 LBUL, 0238 LBUL, 0241 LBUL, 0256 LBUL, 0264 LBUL, 0274 LBUL, 0276 LBUL, 0276 LBUL, 0276 LBUL, 0477 LBUL, 0477 LBUL, 0479 LBUL, 0470 LBUL, 0471 LBUL, 0472 LB	FIInF FIInF FIInH FIInF FIInF FIInF FIInF FIInF FIInF FIInF Vectore and dyr Coostant COOStato COOStato COOStato Fool PddxK LdthA LdthA Fenc Fool Fool Fool Fool Fool Fool Fool Fool Coast BioF Cobl Fool Coast BioF Cobl Fool Fool Fool Fool Fool Fool Fool Fool Fool Fool Robl Fool Nade Fool Nade Fool Robl Fool Robl Fool Robl Fool Robl Bind Rind Bind Bind Sobl Fool </td <td>2.021 2.063 0.331 0.386 0.480 0.386 0.386 0.386 0.360 0.308 0.359</td> <td>0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.331 0.355 0.355 0.347 0.268 0.392 0.329 0.329 0.329 0.333 0.485 0.195 2.433 0.448 0.396 0.495 0.402 0.425 0.322</td> <td>4.153 0.402 2.484 2.596 6.884 2.217 0.487 0.243 0.243</td> <td>4.797 0.249 0.159 2.013 3.705 7.175 2.057 4.203 0.480 0.480 0.480 0.480 0.425 0.495 0.425 0.498 4.814 8.246 2.182 2.182 0.393 0.391 0.391 0.391</td> <td>0.262</td> <td>0.432 0.472</td> <td> Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagellar CTP-binding protein Methyl-accepting chemotaxis protein Flagellar CTP-binding protein Histone CTP-binding protein Histone CTP-binding protein Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF64-sideophores transport systems ATPase components ABC-type cobalaminF64-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components APC-type cobalaminF63-sideophores transport systems ATPase components APC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobal</td>	2.021 2.063 0.331 0.386 0.480 0.386 0.386 0.386 0.360 0.308 0.359	0.366 2.121 0.366 3.717 2.794 0.475 0.347 0.331 0.355 0.355 0.347 0.268 0.392 0.329 0.329 0.329 0.333 0.485 0.195 2.433 0.448 0.396 0.495 0.402 0.425 0.322	4.153 0.402 2.484 2.596 6.884 2.217 0.487 0.243 0.243	4.797 0.249 0.159 2.013 3.705 7.175 2.057 4.203 0.480 0.480 0.480 0.480 0.425 0.495 0.425 0.498 4.814 8.246 2.182 2.182 0.393 0.391 0.391 0.391	0.262	0.432 0.472	 Flagellar GTP-binding protein Flagellar GTP-binding protein Predicted ATPase involved in biogenesis of flagella Flagellar CTP-binding protein Methyl-accepting chemotaxis protein Flagellar CTP-binding protein Histone CTP-binding protein Histone CTP-binding protein Pyridoxal/pyridoxine/pyridoxamine kinase Lactate dehydrogenase and related dehydrogenase ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF64-sideophores transport systems ATPase components ABC-type cobalaminF64-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components APC-type cobalaminF63-sideophores transport systems ATPase components APC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobalaminF63-sideophores transport systems ATPase components ABC-type cobal

LBUL_090	COG1685		0.179	0.456				shikimate kinase
LBUL_090 LBUL_090	5 COG1685 5 COG1685	0.232 0.156	0.157 0.171		3.061			shikimate kinase shikimate kinase
LBUL_091	' LdhA			0.343			0.498	Lactate dehydrogenase and related dehydrogenase
LBUL_093 LBUL_097	PabA PabA	3.078		16.246	0.038	0.230		Anthranilate/para-aminobenzoate synthase component II Anthranilate/para-aminobenzoate synthase component II
LBUL_098	FepC	0.408			4.992			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_106	/ LdhA FepC	0.410		7.779	3.027			Lactate dehydrogenase and related dehydrogenase ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_106 LBUL_107 LBUL_108) FepC			7.598				ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_108	UbiE CobL	0.180	0.350 0.255		3.841			Methylase involved in ubiquinone/menaquinone biosynthesis Precorrin-6B methylase 2
LBUL_112 LBUL_113	3 THI4	0.100	0.255	2.770	3.041			Flavoprotein involved in thiazole biosynthesis
LBUL_118) BioF			0.412		0.224		7-keto-8-aminopelargonate synthetase
LBUL_118 LBUL_120	UbiH FepC			62.155				2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductase ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_121	8 FepC			2.998				ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_121 LBUL_123) IIVÉ) RibF				4.736 4.575		0.225	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase FAD synthase
LBUL_126	FepC	0.137						ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_128	5 CobT		0.366					Cobalamin biosynthesis protein CobT (nicotinate-mononucleotide:5 6-dimethylbenzimidazole phosphoribosyltransferase)
LBUL_129	P FepC	0.324	0.262	2.588	0.193			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_129	B FepC THI80	0.282	0.278	2.768 5.059	0.148			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_130 LBUL_130	CobL		4.434	0.462				Thiamine pyrophosphokinase Precorrin-6B methylase 2
LBUL_133) RimK		0.339		0.063			Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
LBUL_133 LBUL_133	3 ThiL 5 ThiL		0.334 0.453		0.045		2.116 2.397	Thiamine monophosphate kinase Thiamine monophosphate kinase
LBUL_133	6 PDX2		0.442		0.039		2.007	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis
LBUL_134 LBUL_135) LdhA 3 UbiG		0.301		0.105	0.303		Lactate dehydrogenase and related dehydrogenase 2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1 4-benzoquinol methylase
LBUL_137	5 COG0212	0.420	0.245		0.051			5-formyltetrahydrofolate cyclo-ligase
LBUL_140	5 CoaE			0.369				Dephospho-CoA kinase
LBUL_141: LBUL_146	B FolC 5 THI4		0.383 0.500	0.387	2.190			Folylpolyglutamate synthase Flavoprotein involved in thiazole biosynthesis
LBUL_146 LBUL_150	CobJ			0.482				Precorrin-3B methylase
LBUL_153 LBUL_156	P EeoC	4.058 0.212					0.162	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_156 LBUL_158	RimK			3.600				Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
LBUL_158 LBUL_163	FepC COG1685			0.381	0.442			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components shikimate kinase
LBUL_169	B FepC				7.298			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
LBUL_170 LBUL_177) FepC 2 ThiQ			0.272	0.323 2.425			ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components ABC-type thiamine transport system ATPase component
LBUL_180) CoaD	0.210	0.119					Phosphopantetheine adenylyltransferase
LBUL_181) HemY 3 LdhA		3.201	2.745 3.363	4.943			Protoporphyrinogen oxidase
LBUL_186 LBUL_190) CobB		0.321	2.324				Lactate dehydrogenase and related dehydrogenase Cobyrinic acid a c-diamide synthase
LBUL 190	2 CobL		0.434					Precorrin-6B methylase 2
LBUL_194 LBUL_195	2 CobB) RimK				3.898		7.197	Cobyrinic acid a c-diamide synthase Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
LBUL_195	5 ThiE			2.592				Thiamine monophosphate synthase
LBUL_200 LBUL_202 LBUL_203	B FepC FepC			2.851		4.257		ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components
1 0111 000	IIVB	0.419	0.253		11.093			Thiamine pyrophosphate-requiring protein
LBUL_203							0.500	
LBUL_203	5 UbiH	0.201					3.583	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductase
LBUL_203	5 UbiH m	0.201	0.000				3.583	
LBUL_203 Cytoskelete LBUL_066	5 UbiH 9n 8 COG5277	0.201	0.383	0.330	3.612		3.583	Actin and related protein
LBUL_203 Cytoskelete LBUL_066 LBUL_071	5 UbiH 9n 3 COG5277 2 CDC3	0.201	0.383	0.330			3.583	
LBUL_203 Cytoskelete LBUL_066 LBUL_071 Defense m	5 UbiH on 3 COG5277 2 CDC3 echanisms	0.201		0.330			3.583	Actin and related protein Septin family protein
LBUL_203 Cytoskelete LBUL_066 LBUL_071 Defense m LBUL_012 LBUL_017	5 UbiH 9 COG5277 2 CDC3 9 CcmA 7 SalX	0.331	2.794 0.347	2.596			3.583	Actin and related protein Septin family protein ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_012 LBUL_017 LBUL_017	5 UbiH 3 COG5277 2 CDC3 9 ccmA 7 SalX 3 SapC	0.331 0.294	2.794 0.347 0.350					Actin and related protein Septin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component
LBUL_203 Cytoskelete LBUL_066 LBUL_0712 Defense m LBUL_012 LBUL_017 LBUL_017 LBUL_017 LBUL_021	5 UbiH 90 93 COG5277 92 CDC3 94 94 95 CcmA 15 SalX 95 SalX 95 SalX	0.331	2.794 0.347	2.596	3.612 0.159		3.583	Actin and related protein Septin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system permeases component ABC-type antimicrobial peptide transport system Paraese component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_023	5 UbiH 90 13 COG5277 12 CDC3 13 14 14 15 15 15 15 15 15 15 15 15 15	0.331 0.294 0.153	2.794 0.347 0.350 0.186	2.596	3.612 0.159 2.013			Actin and related protein Septin family protein ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_023 LBUL_023 LBUL_023	5 UbiH 90 3 COG5277 2 CDC3 9 CcmA 7 SalX 3 SapC 9 SapC 9 SapC 3 SapF 5 LcnDR2	0.331 0.294 0.153	2.794 0.347 0.350 0.186 0.055	2.596 2.695 4.400	3.612 0.159			Actin and related protein Septin family protein ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_023 LBUL_023 LBUL_023 LBUL_023	5 UbiH 3 COG5277 2 CDC3 achanisms 9 CcmA 7 SalX 8 SapC 9 SapC 9 SapC 9 SapF 9 SapF 5 LcnDR2 5 MdB	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055	2.596 2.695	3.612 0.159 2.013 3.705			Actin and related protein Septin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component Lantbiotic modifying protein
LBUL_203 Cytoskelett LBUL_066 LBUL_077 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_023 LBUL_025 LBUL_025 LBUL_026	5 UbiH an COG5277 2 CDC3 achanisms CcmA 3 SapC 4 SapC 5 SalX 8 SapC 6 SapL 8 SapC 9 SapF 5 LonDR2 6 MdB 2 SalX	0.331 0.294 0.153	2.794 0.347 0.350 0.186 0.055 0.347 0.268	2.596 2.695 4.400	3.612 0.159 2.013			Actin and related protein Septin family protein ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component Lantibiotic modifying protein ABC-type antimicrobial peptide transport system ATPase component RBC-type antimicrobial peptide transport system ATPase component RBC-type antimicrobial peptide transport system ATPase component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_024 LBUL_022 LBUL_026 LBUL_026	5 UbiH an 3 COG5277 2 CDC3 2 achanisms 5 ComA 9 CcmA 5 7 SalX 3 8 SapC 5 9 SapC 5 9 SapD 5 9 SapF 5 5 MdlB SalX 2 Mirr 5 2 Mir 5	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055	2.596 2.695 4.400 6.884	3.612 0.159 2.013 3.705 0.077			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type mittinicrobial peptide transport system ATPase component Restriction endonuclease
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_023 LBUL_025 LBUL_025 LBUL_026 LBUL_044 LBUL_054	5 UbiH m 3 COG5277 2 CDC3 achanisms achanisms 0 CcmA 7 SalX SapC 8 SapC SapC 6 SapC SapC 6 SapC SapF 6 LonDR2 SalX 2 SalX SapC 3 BapC SapC 6 MdlB Z 2 SalX SapA 3 BapA Arr 6 CcmA SapA 9 HsdR HsdR	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333	2.596 2.695 4.400 6.884 0.373 0.095	0.159 2.013 3.705 0.077 0.450 0.085			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component ABC-type midling transport system ATPase component ABC-type antimicrobial petide transport system ATPase component Uncharacterized bacitracin resistance protein Type I site-specific restriction-modification system R (restriction) subunit and related helicase
LBUL_203 Cytoskelete LBUL_066 LBUL_071: Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_023 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_052 LBUL_052 LBUL_055 L	5 UbiH m 3 COG5277 2 CDC3 3 achanisms 9 CcmA 9 CcmA 7 SalX 3 SapC 3 SapC 4 SapC 5 SalX 5 SapD 3 SapC 5 LonDR2 MdlB 2 SalX 2 Mrr 5 CcmA 5 SalX 3 BacA 6 HsdR 0 CcmA 7 SalX 2 Mrr	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433	2.596 2.695 4.400 6.884 0.373	3.612 0.159 2.013 3.705 0.077 0.450			Actin and related protein Septin family protein ABC-type multidrug transport system ATPase component ABC-type artimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase component Cheracetarize backtracin resistance protein Type I site-specific restriction-modification system R (restriction) subunit and related helicase ABC-type multidrug transport system ATPase component Type I site-specific restriction-modification system R (restriction) subunit and related helicase ABC-type multidrug transport system ATPase component
LBUL_203 Cytoskelett LBUL_066 LBUL_071 Defense m LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_023 LBUL_025 LBUL_026 LBUL_054 LBUL_054 LBUL_054 LBUL_057 LB	5 UbiH n 3 COG5277 2 CDC3 CDC3 achanisms 0 CcmA 7 SalX SapC 3 SapC SapC 4 SalX SapC 5 SapC SapC 6 SapC SapC 5 SapC SapC 6 SapC SapC 2 SalX SapC 3 BapC SapC 4 BacA HsdR 5 CcmA CcmA	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333	2.596 2.695 4.400 6.884 0.373 0.095	0.159 2.013 3.705 0.077 0.450 0.085 0.098			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component BC-type antimicrobial peptide transport system ATPase component Macharaterized bactrach resistance protein Type I site-specific restriction-molification system R (restriction subunit and related helicase ABC-type multidrug transport system ATPase component ABC-type multidrug transport system ATPase component ABC-type multidrug transport system ATPase component
LBUL_203 Cytoskelet LBUL_066 LBUL_071 L	5 UbiH nn 3 COG5277 2 CDC3 achanisms 9 CcmA saba 7 SalX SapC 3 SapC SapC 5 SalX SapC 5 SapC SapC 5 SapC SapC 5 SapC SapC 6 SapC SapC 5 SapC SapC 6 SapC SapC 7 SapC SapC 8 BacA SapA 9 HsdR CcmA 8 CcmA CcmA 9 HsdM VanZ	0.331 0.294 0.153 0.386	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329	2.596 2.695 4.400 6.884 0.373 0.095 0.243	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC-type antimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase component Restriction endolf: restriction-modification system ATPase component ABC-type multidrug transport system ATPase component Type I restriction-modification system ATPase component ABC-type multidrug transport system ATPase component Type I restriction-modification system ATPase component ABC-type multidrug transport system ATPase component ABC-type multidrug transport system ATPase component ABC-type multidrug transport system ATPase component ABC-type ADBC-type
LBUL_203 Cytoskelet LBUL_066 LBUL_012 LBUL_012 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_025	j UbiH on a accharisms accharisms accast asapc assapc asapc b sapc b bcma b com	0.331 0.294 0.153 0.386 0.380 0.466	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296	0.159 2.013 3.705 0.077 0.450 0.085 0.098			Actin and related protein Septin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase component CBC-type multidrug transport system ATPase component Uncharacterized bacttrain resistance protein Type I site-specific restriction-modification system R(restriction) subunit and related helicase ABC-type multidrug transport system ATPase component CBC-type transitication resistance protein CBC-type transitication transferase subunit CBC-type transferase class C and other periodilin binding protein
LBUL_203 Cytoskelet LBUL_066 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_026 L	j UbiH m a COS5277 a CDC3 schanisms schanisms schanisms schanisms a SagC schanisms b SagF schanisms c ConsA schanisms b SagF schanisms c ConsA schanisms b BacA schanisms b ConsA schanisms c ConsA schanisms c ConsA schanisms d Yang C schanisms d HascR schanisms d HascR schanisms d AmpC schanisms	0.331 0.294 0.153 0.386 0.380 0.466	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470			Actin and related protein Sepin family protein ABC-type antinicrobial peptide transport system ATPase component ABC-type minificrobial peptide transport system ATPase component Type I testicion-modification system ATPase component ABC-type minificrobial peptide transport system ATPase component Type I testicion-the periodia transport system ATPase subnit Type I testicion-the system ATPase subnit ATD-type minification system ATPase subnit Type I testicion-the system ATPase subnit Type I testicion-the system ATPase subnit ATD-type minification system ATPase subnit ATD-type mi
LBUL_203 Cytoskelet LBUL_066 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_025 LBUL_025 LBUL_025 LBUL_025 LBUL_026 L	j UbiH m a COS5277 a CDC3 schanisms schanisms schanisms schanisms a SagC schanisms b SagF schanisms c ConsA schanisms b SagF schanisms c ConsA schanisms b BacA schanisms b ConsA schanisms c ConsA schanisms c ConsA schanisms d Yang C schanisms d HascR schanisms d HascR schanisms d AmpC schanisms	0.331 0.294 0.153 0.386 0.380 0.466	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441 0.216	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937			Actin and related protein Septin family protein ABC-type antiinicrobial peptide transport system ATPase component ABC-type antiinicrobial peptide transport system ATPase component Carbon and the transport system ATPase component Carbon and the transport system ATPase component ABC-type multidrug transport system ATPase componen
LBUL_203 Cytoskelet LBU_065 LBU_071 LBUL_071 LBU	UbiH in a COG5277 a CDC5 a Comparing a Comparing a CarnA a SapC a SapC a SapC b BacA b BacA b CarnA b CarnA b CarnA c CarnA c CarnA c CarnA c CarnA c CarnA c CarnA c <	0.331 0.294 0.153 0.386 0.380 0.466	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201			Actin and related protein Septin family protein ABC-type multiding transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component Carbon and the transport system ATPase component Carbon and the transport system ATPase component ABC-type multidrug
LBUL_203 Cytoskelet LBU_06 LBU_07 LBU	UbiH on a COS5277 a COS5277 a COS5277 a Costa a SagC a SagC a SagC a SagC a SagC a SagC b SagF c CcnA a SagC b SagF c CcnA a BacA b HsdR b HarpC c CcnA a AmpC c CcmA c CcmA i c c <td>0.331 0.294 0.153 0.386 0.386 0.466 0.208</td> <td>2.794 0.347 0.350 0.196 0.055 0.347 0.268 0.333 0.448 0.329 0.385 0.441 0.216 0.350</td> <td>2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296</td> <td>0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992</td> <td></td> <td></td> <td>Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component MC-type multiding transport system ATPase component MC-type multiding transport system ATPase component MC-type multiding transport system ATPase component ABC-type multiding transport system ATPase component Type I restriction-modification system ATPase component ABC-type multiding transport system ATPase component ABC-type multiding transpor</td>	0.331 0.294 0.153 0.386 0.386 0.466 0.208	2.794 0.347 0.350 0.196 0.055 0.347 0.268 0.333 0.448 0.329 0.385 0.441 0.216 0.350	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296	0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component MC-type multiding transport system ATPase component MC-type multiding transport system ATPase component MC-type multiding transport system ATPase component ABC-type multiding transport system ATPase component Type I restriction-modification system ATPase component ABC-type multiding transport system ATPase component ABC-type multiding transpor
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH m cOC63277 coc63277<	0.331 0.294 0.153 0.386 0.380 0.466	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441 0.216	2.596 2.695 4.400 6.884 0.373 0.243 0.243 0.214 7.779	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201			Actin and related protein Sepin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase component Macharaterized bactiracin resistance protein Type I restriction-modification system ATPase component ABC-type multidrug transport system ATPase component Type I restriction-modification system ATPase component ABC-type multidrug transport system ATPase component ABC-type nultidrug transport system ATPase component ABC-type nultidrug transport system ATPase component ABC-type antimicrobial peptide transport system
LBUL_203 Cytoskelet LBUL_062 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_021 LBUL_021 LBUL_022 LBUL_022 LBUL_022 LBUL_022 LBUL_022 LBUL_023 LBUL_023 LBUL_025 LBUL_05 LBUL_05 LBUL_05 LBUL_055 LBUL_055 LBUL	UbiH in a COG5277 a CDC05 a Company a SapC a SapC a SapC b SapC b SapC b SapC b SapC b SapF c SatX b BacnA b BacA b BacA b HodR c ComA c	0.331 0.294 0.153 0.386 0.386 0.466 0.208	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441 0.216 0.350 0.148	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296 0.214	0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992			Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBU_06 LBU_07 LBUL	UbiH on a COS5277 a COS5277 a CoS277 ascharisme Scharisme ascharisme Scharisme ascharisme Scark a SagC a SagC a SagC a SagC b SagC b SagF c ConsA b BaspF c Scark b BaspF c Scark b BaspF b ConA b ConA c ConA c ConA c ConA b SatX	0.331 0.294 0.153 0.386 0.386 0.466 0.208	2.794 0.347 0.350 0.196 0.055 0.347 0.268 0.333 0.448 0.329 0.385 0.441 0.216 0.350	2.596 2.695 4.400 6.884 0.373 0.295 0.243 0.296 0.214 7.779 7.598 3.468	0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992			Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH in a COG5277 a CDG5277 a CDG5277 b Comds a SapC b MdB b MdB b MdB	0.331 0.294 0.153 0.386 0.386 0.466 0.208	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.441 0.216 0.350 0.148	2.596 2.695 4.400 6.884 0.373 0.295 0.243 0.296 0.214 7.779 7.598 3.468 62.155	0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992			Actin and related protein Septin family protein ABC-type antimicrobial populé transport system ATPase component ABC-type multidrug transport system ATPase component Charbacture and transport system ATPase component ABC-type multidrug transport system ATPase subprise ABC-type multidrug transport system ATPase component Type I restriction-modification system ATPase component ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system permease component ABC
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH in a COG5277 a CDG5277 a CDG5277 a CACAsianisms a CapC a SapC a SapC a SapC a SapC a SapC b MdB	0.331 0.294 0.153 0.386 0.386 0.466 0.208	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 0.448 0.329 0.385 0.441 0.216 0.350 0.148 0.449	2.596 2.695 4.400 6.884 0.373 0.295 0.243 0.296 0.214 7.779 7.598 3.468	0.159 2.013 3.705 0.077 0.450 0.085 0.085 0.085 0.470 6.937 0.363 5.201 5.106 4.992			Actin and related protein Septin family protein ABC-type antimicrobial populé transport system ATPase component ABC-type antimicrobial populé transport system ATPase component Carbitotic modifying protein ABC-type multiding transport system ATPase component Chranacterize bactraria relastance protein Type I sels-specific restriction-modification system R (restriction) subunit and related helicase ABC-type multiding transport system ATPase component Type I restriction-modification system ATPase component ABC-type multiding transport system ATPase and permease component ABC-type multiding transport system ATPase and permease component ABC-type multiding transport system ATPase and permease component ABC-type antimicrobial populé transport syst
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	JbiH Jn COC3277 COC3277 COC3277 Coc3277 SapC March SapC SapC MdB MdB MdB MdB MdB SapC MdB MdB MdB SapC	0.331 0.294 0.153 0.386 0.466 0.208 0.408 0.381 0.4137	2.794 0.347 0.350 0.186 0.186 0.350 0.347 0.268 0.333 2.433 0.344 0.329 0.344 0.350 0.441 0.216 0.350 0.148 0.499 0.326	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998	3.612 0.159 2.013 3.705 0.450 0.085 0.088 0.470 6.937 0.363 5.106 4.992 4.118			Actin and related protein Septin family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component MC-type multiding transport system ATPase component MC-type multiding transport system ATPase component ABC-type multiding transport system ATPase and permease component ABC-type multiding
LBUL_203 Cytoskelet LBUL_062 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_072 L	UbiH in a COG5277 a COG5277 a Cod5277 a SapC b ComA a SapC b McmB c ComA a BacA b AmpC a HsdM b HsdM b ComA a ComA a ComA b McMB b MdB b MdB b MdB b MdB b MdB b SapE	0.331 0.234 0.153 0.386 0.386 0.466 0.466 0.208 0.408 0.381	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998 2.888	3.612 0.159 2.013 3.705 0.077 0.450 0.098 0.470 6.937 0.363 5.201 5.106 5.106 5.106 4.992 4.118			Actin and related protein Sepin family protein AC-type antimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase and permease component ABC-type antimicrobial peptide transport system ATPase and permease components ABC-type antimicrobial peptide transport system ATPase and permease components ABC-type antimicrobial peptide transport system ATPase and permease components ABC-type antimicrobial peptide transport system ATPase and per
LBUL_203 Cytoskelet LBUL_062 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_072 L	UbiH in a COG5277 a COG5277 a Cod5277 a SapC b ComA a SapC b McmB c ComA a BacA b AmpC a HsdM b HsdM b ComA a ComA a ComA b McMB b MdB b MdB b MdB b MdB b MdB b SapE	0.331 0.254 0.356 0.386 0.380 0.466 0.408 0.381 0.381	2.794 0.347 0.350 0.186 0.055 0.347 0.268 0.333 0.448 0.329 0.385 0.441 0.216 0.350 0.148 0.499 0.326 0.229	2.596 2.695 4.400 6.884 0.273 0.295 0.243 0.296 0.214 7.779 7.598 3.468 62.185 2.998 2.883	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118			Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_072 L	UbiH in a COG5277 a COG5277 a Cod5277 a SapC b ComA a SapC b McmB c ComA a BacA b AmpC a HsdM b HsdM b ComA a ComA a ComA b McMB b MdB b MdB b MdB b MdB b MdB b SapE	0.331 0.234 0.153 0.386 0.386 0.466 0.466 0.208 0.408 0.381	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998 2.888	3.612 0.159 2.013 3.705 0.077 0.450 0.098 0.470 6.937 0.363 5.201 5.106 5.106 5.106 4.992 4.118		3.599	Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_071 LBUL_072 L	UbiH in	0.331 0.294 0.153 0.386 0.386 0.466 0.408 0.381 0.408 0.381 0.137 0.381 0.228	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.373 0.243 0.243 0.243 0.243 0.243 0.243 0.214 7.779 7.598 3.468 62.155 2.998 2.898 2.588 2.588	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.193 0.183 0.179		3.599	Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_012 LBUL_012 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_021 LBUL_022 L	UbiH in a COG5277 a COG5277 a Codcardisme a CarnA a SapC a SapC a SapC a SapC a SapC b SapF b ComA b ComA c	0.331 0.234 0.153 0.386 0.386 0.466 0.466 0.208 0.408 0.381	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.373 0.243 0.243 0.243 0.243 0.243 0.243 0.214 7.779 7.598 3.468 62.155 2.998 2.898 2.588 2.588	3.612 0.159 2.013 3.705 0.097 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 5.106 4.992 4.118 0.179 0.193 0.148 0.148 0.148		3.599	Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	j UbiH in 0 COC3277 i COC3277 i i COC3277 i i CoC3277 Salx i SapC i SapC i SapC SapC i i SapC SapC i i SapC SapC i i SapC SapC i i SapC SapF i i SapF SapF SapF i SapF SapF SapF i BacA BacA i i BacA SapF HsdM i ComA i ComA i ComA i ComA i ComA i ComA i SapF SapF SapF i ComA i ComA i ComA i ComA i </td <td>0.331 0.294 0.153 0.386 0.386 0.466 0.408 0.381 0.408 0.381 0.137 0.381 0.228</td> <td>2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226</td> <td>2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998 2.883 2.588 2.588 2.568 0.4110</td> <td>3.612 0.159 2.013 3.705 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.201 5.201 4.992 4.118 0.179 0.193 0.148 5.2425 2.395 0.442 2.395 0.448</td> <td></td> <td>3.599</td> <td>Actin and related protein Septin family protein</td>	0.331 0.294 0.153 0.386 0.386 0.466 0.408 0.381 0.408 0.381 0.137 0.381 0.228	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998 2.883 2.588 2.588 2.568 0.4110	3.612 0.159 2.013 3.705 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.201 5.201 4.992 4.118 0.179 0.193 0.148 5.2425 2.395 0.442 2.395 0.448		3.599	Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH in a COG5277 a COG5277 a COG5277 a Cabcos a CapC b CornA a SapC a SapC a SapC b SapC c CornA c CornA c CornA c CornA c SapD b MdB c SapD c	0.331 0.294 0.153 0.386 0.386 0.466 0.408 0.381 0.408 0.381 0.137 0.381 0.228	2.794 0.347 0.350 0.186 0.355 0.350 0.347 0.268 0.333 2.433 0.348 0.329 0.326 0.441 0.216 0.350 0.148 0.499 0.326 0.226	2.596 2.695 4.400 6.884 0.243 0.243 0.243 0.244 0.214 7.779 7.598 3.468 62.155 2.998 2.883 2.588 0.410 0.410	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.138 0.148 2.425 2.705 2.395 0.442 7.298 0.442 7.298		3.599	Addin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH in a COG5277 a COBS277 a Cobs a Cond a CarnA a SapC a SapC a SapC b BacA b HsdM b SapD b SapD b SapP b SanA b SanA c ConA c SapD b <	0.331 0.294 0.153 0.386 0.386 0.466 0.408 0.381 0.408 0.381 0.137 0.381 0.228	2.794 0.347 0.356 0.055 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.329 0.385 0.441 0.350 0.148 0.326 0.326 0.229 0.262 0.278	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.296 0.214 7.779 7.598 3.468 62.155 2.998 2.883 2.588 2.588 2.568 0.4110	3.612 0.159 2.013 3.705 0.097 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.133 0.148 2.429 2.709 2.395 2.395 2.709 2.395 2.709 2.395		3.599	Addin and related protein Septim family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component ABC-type multiding transport system ATPase component ABC-type multiding transport system ATPase component Component antipole (transport system ATPase component ABC-type multiding transport system ATPase component ABC-type multiding transport system ATPase component Component antipole (transport system ATPase component ABC-type multiding transport system ATPase orgonent ABC-type multiding transport system ATPase orgonents ABC-type multiding transport system A
LBUL_203 Cytoskelet LBUL_012 LBUL_022 L	UbiH in	0.331 0.234 0.153 0.386 0.466 0.466 0.408 0.408 0.381 0.137 0.320 0.222 0.222 0.222	2.794 0.347 0.340 0.055 0.355 0.347 0.268 0.333 2.433 0.448 0.326 0.355 0.448 0.350 0.355 0.4148 0.350 0.355 0.4148 0.350 0.350 0.347 0.326 0.355 0.419 0.326 0.226 0.326 0.226 0.326 0.2278	2.596 2.695 4.400 6.884 0.373 0.296 0.214 7.779 7.598 3.468 2.155 2.998 2.883 2.588 2.768 0.410 0.272 0.303	3.612 0.159 2.013 3.705 0.077 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.138 0.148 2.425 2.705 2.395 0.442 7.298 0.442 7.298		3.599	Actin and related protein Septin family protein
LBUL_203 Cytoskelet LBUL_062 LBUL_071 L	UbiH in	0.331 0.224 0.153 0.386 0.466 0.208 0.406 0.381 0.406 0.381 0.137 0.324 0.222 0.222	2.794 0.347 0.356 0.055 0.055 0.347 0.268 0.333 2.433 0.448 0.329 0.385 0.329 0.385 0.441 0.350 0.148 0.326 0.326 0.229 0.262 0.278	2.596 2.695 4.400 6.884 0.373 0.296 0.214 7.779 7.598 3.468 2.155 2.998 2.883 2.588 2.768 0.410 0.272 0.303	3.612 0.159 2.013 3.705 0.097 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.133 0.148 2.429 2.709 2.395 2.395 2.709 2.395 2.709 2.395		3.599	Acin and related protein Sepin family protein
LBUL_203 Cytoskelet LBUL_012 LBUL_012 LBUL_012 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_017 LBUL_021 LBUL_022 LBUL_022 LBUL_022 LBUL_022 LBUL_022 LBUL_022 LBUL_024 LBUL_024 LBUL_024 LBUL_025 LBUL_05 LBUL_	UbiH in	0.331 0.234 0.153 0.386 0.466 0.466 0.408 0.408 0.381 0.137 0.320 0.222 0.222 0.222	2.794 0.347 0.340 0.055 0.355 0.347 0.268 0.333 2.433 0.448 0.326 0.355 0.448 0.350 0.355 0.4148 0.350 0.355 0.4148 0.350 0.350 0.347 0.326 0.355 0.419 0.326 0.226 0.326 0.226 0.326 0.2278	2.596 2.695 4.400 6.884 0.373 0.095 0.243 0.243 0.296 0.214 7.779 7.599 7.598 2.883 2.588 2.596 2.595 2.5966 2.596 2.596 2.596 2.596 2.596 2.596 2.596 2.596 2.596 2.596	3.612 0.159 2.013 3.705 0.097 0.450 0.085 0.098 0.470 6.937 0.363 5.201 5.106 4.992 4.118 0.179 0.133 0.148 2.429 2.709 2.395 2.709 2.395 2.709 2.395	4.257	3.599	Addin and related protein Septim family protein ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component ABC-type multiding transport system ATPase and permease component ABC-type multiding transport system ATPase and permease component ABC-type antimicrobial peptide transport system ATPase and permease component ABC-type antinterbail peptide transport sy

DNA replication	on, recombinat	on, and rep	air					
LBUL_0002 LBUL_0008	DnaN Ssb	0.464	0.346	2.479 2.714		2.349		DNA polymerase sliding clamp subunit (PCNA homolog) Single-stranded DNA-binding protein
LBUL_0012	DnaB	0.371		2.381		2.545		Replicative DNA helicase
LBUL_0075	XthA		0.382	0.007	0.047			Exonuclease III Ribonuclease HI
LBUL_0152 LBUL_0177	RnhA UvrA	0.331	0.347	0.297 2.596	0.247			Excinuclease ATPase subunit
LBUL_0212	MutT		0.274					NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_0216 LBUL_0238	SbcC UvrA	0.386	0.055		0.159 2.013			ATPase involved in DNA repair Excinuclease ATPase subunit
LBUL_0239	UvrA				3.705			Excinuclease ATPase subunit
LBUL_0247	DinP SPS1			0.125 4.400	0.037			Nucleotidyltransferase/DNA polymerase involved in DNA repair Serine/threonine protein kinase
LBUL_0255 LBUL_0256	SbcC		0.347	6.884				ATPase involved in DNA repair
LBUL_0262 LBUL_0288	UvrA UvrA	0.380	0.268	11.010	0.077			Excinuclease ATPase subunit Excinuclease ATPase subunit
LBUL_0288 LBUL_0290	SPS1			11.010	3.405	5.086		Serine/threonine protein kinase
LBUL_0298	TatD				3.074			Mg-dependent DNase
LBUL_0299 LBUL_0339	COG1658 MGS1	0.434	0.249		4.861 3.118			Small primase-like protein (Toprim domain) ATPase related to the helicase subunit of the Holliday junction resolvase
LBUL_0413	UvrD		0.435					Superfamily I DNA and RNA helicase
LBUL_0414	Lig COG0742	0.359	0.227		9.293 0.480			NAD-dependent DNA ligase (contains BRCT domain type II)
LBUL_0421 LBUL_0433	NPY1	0.339			0.400	2.654		N6-adenine-specific methylase NTP pyrophosphohydrolase containing a Zn-finger probably nucleic-acid-binding
LBUL_0445	UvrA		0.333					Excinuclease ATPase subunit
LBUL_0446 LBUL_0501	COG0675 COG0742		0.195	0.222	0.047			Transposase and inactivated derivatives N6-adenine-specific methylase
LBUL_0510	MGS1			0.381				ATPase related to the helicase subunit of the Holliday junction resolvase
LBUL_0535	RecA UvrB			0.095	0.085		0.359	RecA/RadA recombinase Helicase subunit of the DNA excision repair complex
LBUL_0549 LBUL_0550	UvrA		2.433	0.243	0.085			Excinuclease ATPase subunit
LBUL_0573	Ung				0.333			Uracil DNA glycosylase
LBUL_0578 LBUL_0617	UvrA COG0827		0.448 0.329	0.296				Excinuclease ATPase subunit Adenine-specific DNA methylase
LBUL_0634	COG0742		0.441					N6-adenine-specific methylase
LBUL_0662 LBUL_0683	RadC MutT				5.978 5.121			DNA repair protein NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_0699	COG0742	0.147	0.226		3.769			N6-adenine-specific methylase
LBUL_0704	HolA	4.005		0.264				DNA polymerase III delta subunit
LBUL_0744 LBUL_0777	RecQ HimA	4.095	0.472		3.323			Superfamily II DNA helicase Bacterial nucleoid DNA-binding protein
LBUL_0797	COG1688		0.477					Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily)
LBUL_0870 LBUL_0880	UvrA MutT	4.334			0.363			Excinuclease ATPase subunit NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_0883 LBUL_0900	UvrA		0.350		5.201			Excinuclease ATPase subunit
	GyrB	0.255	0.318		0.325			Type IIA topoisomerase (DNA gyrase/topo II topoisomerase IV) B subunit
LBUL_0901 LBUL_0909	GyrA DinG	0.245	0.242	0.349	0.209			Type IIA topoisomerase (DNA gyrase/topo II topoisomerase IV) A subunit Rad3-related DNA helicase
LBUL_0912	DnaD		2.171	0.324	0.163			Putative primosome component and related protein
LBUL_0913 LBUL_0924	Nth COG0116		2.081	0.229	0.234 4.098			Predicted EndollI-related endonuclease Predicted N6-adenine-specific DNA methylase
LBUL_0982	XerD			0.163	0.210			Site-specific recombinase XerD
LBUL_0989 LBUL_1060	UvrA SbcC	0.408		0.352	4.992			Excinuclease ATPase subunit ATPase involved in DNA repair
LBUL_1069	UvrA			7.779				Excinuclease ATPase subunit
LBUL_1070	UvrA		0.050	7.598				Excinuclease ATPase subunit Predicted DNA modification methylase
LBUL_1089	COG1041 XerD		0.350		0.393			Site-specific recombinase XerD
LBUL_1123 LBUL_1129	MutT	0.258						NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_1142 LBUL_1145	Dcm Vsr			0.373	0.417			Site-specific DNA methylase DNA G:T-mismatch repair endonuclease
LBUL_1160	COG3547	0.403	0.479	0.575				Transposase and inactivated derivatives
LBUL_1165	DnaG		0.333		2.490			DNA primase
LBUL_1168 LBUL_1172	RecO DnaC	0.493	0.323 0.357		2.051			Recombinational DNA repair protein (RecF pathway) DNA replication protein
LBUL_1186	MGS1			0.432				ATPase related to the helicase subunit of the Holliday junction resolvase
LBUL_1188 LBUL_1190	XerD TopA			0.416	2.803			Site-specific recombinase XerD Topoisomerase IA
LBUL_1192	RnhB	0.279	0.313		2.369			Ribonuclease HII
LBUL_1204	UvrA			62.155 2.998				Excinuclease ATPase subunit
LBUL_1213 LBUL_1223	UvrA RecJ		0.325	2.998				Excinuclease ATPase subunit Single-stranded DNA-specific exonuclease
LBUL_1246 LBUL_1255	PolC				4.074			DNA polymerase III alpha subunit (gram-positive type)
LBUL_1255	COG2827 UvrA	0.137			3.622			Predicted endonuclease containing a URI domain Excinuclease ATPase subunit
LBUL_1261 LBUL_1269	SrmB	0.157	0.254		0.116			Superfamily II DNA and RNA helicase
LBUL_1285	COG5406		0.366					Nucleosome binding factor SPN SPT16 subunit
LBUL_1286 LBUL_1292	SbcC UvrA	0.324	0.326	2.588	0.193			ATPase involved in DNA repair Excinuclease ATPase subunit
LBUL_1293	UvrA	0.282	0.278	2.768	0.148			Excinuclease ATPase subunit
LBUL_1296 LBUL_1308	RecG COG1041			0.290 0.462				RecG-like helicase Predicted DNA modification methylase
LBUL_1315	RecN				4.141		0.219	ATPase involved in DNA repair
LBUL_1318 LBUL_1362	XseB COG3547	0.321	0.273		2.170	11.118	2.409	Exonuclease VII small subunit Transposase and inactivated derivatives
LBUL_1402	DnaC	0.021	0.213	0.362	2.109	11.110	2.409	DNA replication protein
LBUL_1403	DnaB				2.056			Replication initiation/membrane attachment protein
LBUL_1407 LBUL_1474	PolA COG5406	2.063		0.416 0.402				DNA polymerase I - 3'-5' exonuclease and polymerase domains Nucleosome binding factor SPN SPT16 subunit
LBUL_1484	COG0816			0.342				Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas
I BUIL 1497	SrmB				2.234			and B. subtilis) Superfamily II DNA and DNA belicase
LBUL_1487 LBUL_1489	DinP				2.234			Superfamily II DNA and RNA helicase Nucleotidyltransferase/DNA polymerase involved in DNA repair
LBUL_1495	MutS			0.355				Mismatch repair ATPase (MutS family)
LBUL_1515 LBUL_1539	DnaX COG0675			0.339	3.376 0.274			DNA polymerase III gamma/tau subunits Transposase and inactivated derivatives
LBUL_1555	MutT				3.346			NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_1601 LBUL_1700	DnaB UvrA			2.872 0.272	0.323			Replicative DNA helicase Excinuclease ATPase subunit
LBUL_1772	UvrA			0.212	2.425			Excinuclease ATPase subunit
LBUL_1842	COG3328 MGS1	0.160	2.121			0.449	0.488	Transposase and inactivated derivatives
LBUL_1944 LBUL_1999	MGS1 SPS1	2.021	2.121		0.359	u.449	0.488	ATPase related to the helicase subunit of the Holliday junction resolvase Serine/threonine protein kinase
LBUL_1999 LBUL_2003	UvrA			2.851				Excinuclease ATPase subunit
LBUL_2020	UvrA					4.257		Excinuclease ATPase subunit
Energy produ	ction and conv	ersion						
LBUL_0010	PPX1 Tas			2.087	2.099		0.199	Inorganic pyrophosphatase/exopolyphosphatase Predicted oxidoreductase (related to anti-alcohol dehudrogenase)
	LdhA		3.717			0.262	0.199	Predicted oxidoreductase (related to aryl-alcohol dehydrogenase) Lactate dehydrogenase and related dehydrogenase
LBUL_0078 LBUL_0084			0.054		2.571			Ribulose kinase
LBUL_0084 LBUL_0099	AraB	0.363	0.354		0.450			No. 1 and the state of the stat
LBUL_0084		0.363	0.354		0.452			Malate/lactate dehydrogenase Uncharacterized flavoprotein
LBUL_0084 LBUL_0099 LBUL_0100	AraB Mdh	0.363	2.794		0.452 0.335			Malate/lactate dehydrogenase Uncharacterized flavoprotein ABC-type Na+ transport system ATPase component

	Our	0.004	0.047	2,596				
LBUL_0177 LBUL_0216	CydD CydC	0.331 0.386	0.347 0.055	2.590	0.159			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis fused ATPase and permease
								components
LBUL_0238 LBUL_0239	NatA NatA				2.013 3.705			ABC-type Na+ transport system ATPase component ABC-type Na+ transport system ATPase component
LBUL_0246	LIdD	0.221	0.285		0.053			L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenase
LBUL_0251 LBUL_0256	LIdD CydD	2.639	0.347	6.884		0.290	0.458	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenase ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0262	CydD	0.380	0.268	0.004	0.077			ABC-type transport system involved in cytochrome of biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0327	NemA		0.461					NADH:flavin oxidoreductase Old Yellow Enzyme family
LBUL_0445 LBUL_0457	CydD PrkB		0.333		6.995			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components Phosphoribulokinase
LBUL_0495	FldA	0.342	0.380		2.657			Flavodoxins
LBUL_0548	Lpd		2.433	0.243	0.425			Pyruvate/2-oxoglutarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3)
LBUL_0550 LBUL_0577	CydD GlcD		0.442	0.243	0.098			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components FAD/FMN-containing dehydrogenase
LBUL_0578	NatA		0.448					ABC-type Na+ transport system ATPase component
LBUL_0618 LBUL_0642	ackA AtpG		0.230 0.493	0.274	4.235			Acetate kinase F0F1-type ATP synthase gamma subunit
LBUL_0644	AtpC		0.495		2.054			F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit)
LBUL_0700	CitC		0.332		2.182			Citrate lyase synthetase
LBUL_0716 LBUL_0726	NfnB SdhA			0.191 0.047	2.746 0.130	4.189	3.051	Nitroreductase Succinate dehydrogenase/fumarate reductase flavoprotein subunit
LBUL_0823	PycA		0.397	0.211	0.345	4.100	2.227	Pyruvate carboxylase
LBUL_0825	PycA		0.295	0.132	0.391			Pyruvate carboxylase
LBUL_0870 LBUL_0882	CydD CydD		0.216		0.363			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0883	CydD		0.350		5.201			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0902	PPX1 LdhA			0.352 0.343			0.498	Inorganic pyrophosphatase/exopolyphosphatase
LBUL_0917 LBUL_0943	NfnB			0.343	2.945		0.490	Lactate dehydrogenase and related dehydrogenase Nitroreductase
LBUL_0989	CydD	0.408			4.992			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1060 LBUL_1067	Ntpl LdhA	0.410		0.352	3.027			H+-ATPase subunit I Lactate dehydrogenase and related dehydrogenase
LBUL_1069	CydC	0.110		7.779	0.021			ABC-type transport system involved in cytochrome bd biosynthesis fused ATPase and permease
								components
LBUL_1070 LBUL_1096	CydD PutA		0.123	7.598 0.177				ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components NAD-dependent aldehyde dehydrogenase
LBUL_1096 LBUL_1138	SdhA			2.770				Succinate dehydrogenase/fumarate reductase flavoprotein subunit
LBUL_1189 LBUL_1204	FixC CydD			0.412 62.155				Dehydrogenase (flavoprotein) ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1204 LBUL_1213	CydD			2.998				ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1228	TtdA	0.302	0.477					Tartrate dehydratase alpha subunit/Fumarate hydratase class I N-terminal domain
LBUL_1261 LBUL_1286	CydD CydD	0.137	0.326					ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1292	NatA	0.324	0.262	2.588	0.193			ABC-type transport system intolved in cyclinicine bu biosynthesis Arr ase and permease components ABC-type Na+ transport system ATPase component
LBUL_1293	CydD	0.282	0.278	2.768	0.148			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1315 LBUL_1339	CydD FumC				4.141 0.165	0.332	0.219	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components Fumarase
LBUL_1340	LdhA				0.105	0.303		Lactate dehydrogenase and related dehydrogenase
LBUL_1356 LBUL_1386	Qor		0.301	0 102	0.051			NADPH:quinone reductase and related Zn-dependent oxidoreductase
LBUL_1386 LBUL_1466	AcyP Lpd		0.500	0.192				Acylphosphatase Pyruvate/2-oxoglutarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3)
LBUL 1481	TrxA			0.179	0.422			Thiol-disulfide isomerase and thioredoxins
LBUL_1488 LBUL_1532	PPX1 UbiB	4.058			3.076			Inorganic pyrophosphatase/exopolyphosphatase 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase
LBUL_1560	Ntpl	0.123	0.022		4.359			H+-ATPase subunit I
LBUL_1562	NatA	0.212					0.162	ABC-type Na+ transport system ATPase component
LBUL_1581 LBUL_1588	PutA NatA			3.670	0.096 0.442			NAD-dependent aldehyde dehydrogenase ABC-type Na+ transport system ATPase component
LBUL_1680	NhaC		0.390		0.442	31.248		Na+/H+ antiporter
LBUL_1690	IscU	0.288			-			NifU homolog involved in Fe-S cluster formation
LBUL_1693 LBUL_1700	CydD CydD			0.272	7.298 0.323			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1772	CydD				2.425			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1787 LBUL_1810	UgpQ			0.224	0.411			Glycerophosphoryl diester phosphodiesterase
LBUL_1810 LBUL_1823	UbiH GpsA	0.404		2.745 0.119	4.943		0.434	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductase Glycerol-3-phosphate dehydrogenase
LBUL_1868	LdhA		3.201	3.363				Lactate dehydrogenase and related dehydrogenase
LBUL_1900 LBUL_1915	COG1149 GlcD		0.321	2.324 3.429				MinD superfamily P-loop ATPase containing an inserted ferredoxin domain FAD/FMN-containing dehydrogenase
LBUL_1930	FumC			3.423	0.016	0.254	3.051	Fumarase
LBUL_1950	PycA						7.197	Pyruvate carboxylase
LBUL_1955 LBUL_2003	NemA NatA			2.592 2.851				NADH:flavin oxidoreductase Old Yellow Enzyme family ABC-type Na+ transport system ATPase component
LBUL_2018	COG1149			2.001	0.181			MinD superfamily P-loop ATPase containing an inserted ferredoxin domain
LBUL_2020	CydD	0.004				4.257	0.500	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_2035	FixC	0.201					3.583	Dehydrogenase (flavoprotein)
Function unk								
LBUL_0034 LBUL_0060	COG4720 COG5617		0.321	2.081	0.259 2.133			Predicted membrane protein Predicted integral membrane protein
LBUL_0081	COG4720		0.471		2.100	0.207	0.200	Predicted membrane protein
LBUL 0082	COG2096 COG4853	0.400			0.444		0.221	Uncharacterized conserved protein
LBUL_0116 LBUL_0119	COG4853 COG1576	0.192			0.444	24.895		Uncharacterized protein Uncharacterized conserved protein
LBUL_0137	LemA					0.388		Uncharacterized conserved protein
LBUL_0140	XkdP COG4086		0.404		8.677 0.237		0.297 0.400	Uncharacterized protein containing LysM domain Predicted secreted protein
LBUL_0153 LBUL_0163	COG5438	0.308	0.094		0.231			Predicted multitransmembrane protein
LBUL_0164	COG5438		0.277		0.400		0.382	Predicted multitransmembrane protein
LBUL_0176 LBUL_0200	COG3181 COG3273				0.438 3.628			Uncharacterized protein Uncharacterized conserved protein
LBUL_0205	COG0344	0.289	0.250		0.020			Predicted membrane protein
LBUL_0207	COG3274		0.235	0 700				Uncharacterized protein
LBUL_0218 LBUL_0254	COG3274 COG1598			8.702	0.301			Uncharacterized protein Uncharacterized conserved protein
LBUL_0266	COG2512	0.318						Uncharacterized membrane-associated protein/domain
LBUL_0286 LBUL_0307	COG1511 COG4506			9.611 0.316	0.457			Predicted membrane protein Uncharacterized protein
LBUL_0319	COG2302	0.268	0.407	0.310				Uncharacterized conserved protein contains S4-like domain
LBUL_0438	COG3759				0.413			Predicted membrane protein
LBUL_0454 LBUL_0465	COG4721 COG4320	0.241			2.078			Predicted membrane protein Uncharacterized protein
LBUL_0494	COG2246	0.291	0.428		3.447			Predicted membrane protein
LBUL_0497	Rbn			0.001	2.261			Predicted membrane protein
LBUL_0510 LBUL_0518	COG3880 COG4116			0.381	0.399			Uncharacterized protein with conserved CXXC pairs Uncharacterized protein
LBUL_0519	COG2357				0.307			Uncharacterized protein
LBUL_0529	HdeD COG4544		0.349	2.661			0.359	Uncharacterized conserved protein
LBUL_0535 LBUL_0551	HdeD			0.165	0.113			Uncharacterized conserved protein Uncharacterized conserved protein
LBUL_0557	COG0391			0.340			0.371	Uncharacterized conserved protein
LBUL_0558	COG1481			0.198				Uncharacterized protein

LBUL_0582	COG1624		0.290					Uncharacterized conserved protein
LBUL_0583 LBUL_0608	COG4856 COG5652		0.439		2.888			Uncharacterized protein Predicted integral membrane protein
LBUL_0609	COG0217			0.439	2.166			Uncharacterized conserved protein
LBUL_0610	SpolIIAA	7.998		18.355				Uncharacterized protein
LBUL_0645	COG4836				0.216			Predicted membrane protein
LBUL_0653 LBUL_0654	COG5506 COG2302	0.360 0.441		0.206				Uncharacterized conserved protein Uncharacterized conserved protein contains S4-like domain
LBUL_0658	COG2302	0.1111	0.358					Uncharacterized conserved protein contains S4-like domain
LBUL_0671	COG2815	0.342	0.297					Uncharacterized protein
LBUL_0678	COG1799		0.100		2.468			Uncharacterized protein
LBUL_0680	COG2302 COG4471	0.323	0.422		3.940 3.627			Uncharacterized conserved protein contains S4-like domain Uncharacterized protein
LBUL_0698 LBUL_0713	HdeD	0.323	0.339	0.443	3.027			Uncharacterized conserved protein
LBUL_0722 LBUL_0756	COG4359			0.147				Uncharacterized conserved protein
LBUL_0756	COG4475			0.124	0.427			Uncharacterized protein
LBUL_0769 LBUL_0807	COG1354 COG2966	0.272			0.131			Uncharacterized conserved protein Uncharacterized conserved protein
LBUL_0815	COG4907			0.322	3.462			Predicted membrane protein
LBUL_0822	COG3199		0.322	0.224	0.222			Uncharacterized conserved protein
LBUL_0828	COG3007		0.288	0.104	0.321		2.147	Uncharacterized paraquat-inducible protein B
LBUL_0871 LBUL_0910	COG3273 COG5353	0.213		0.467				Uncharacterized conserved protein Uncharacterized protein
LBUL_0930	COG2302	2.875		0.467	0.046	0.334		Uncharacterized protein Contains S4-like domain
LBUL_0934	COG2848				0.112	0.394		Uncharacterized conserved protein
LBUL_0936	DegV			0.135				Uncharacterized protein
LBUL_0969	COG2013			0.493			0.347	Uncharacterized conserved protein Uncharacterized phage-associated protein
LBUL_1011 LBUL_1057 LBUL_1060 LBUL_1089	GepA COG4924		0.290	0.493				Uncharacterized protein
LBUL_1060	COG4717			0.352				Uncharacterized conserved protein
LBUL_1089	COG3270		0.350					Uncharacterized conserved protein
LBUL_1127	COG0327	0.180		2.770	3.312			Uncharacterized conserved protein
LBUL_1138 LBUL_1145	COG3976 COG2852			0.373				Uncharacterized protein Uncharacterized protein
LBUL_1148	COG4694	0.413	0.206	0.267				Uncharacterized protein
LBUL_1152	COG1479			0.293				Uncharacterized conserved protein
LBUL_1189	COG3349			0.412		0.040		Uncharacterized conserved protein
LBUL_1194	COG4479 DegV			0.378		2.910		Uncharacterized protein Uncharacterized protein
LBUL_1208 LBUL_1211	COG4269			0.378	0.392			Predicted membrane protein
LBUL_1223 LBUL_1245	COG4199		0.325					Uncharacterized protein
LBUL_1245	COG0779	0.476	0.000					Uncharacterized protein
LBUL_1263 LBUL_1264 LBUL_1283 LBUL_1286	COG3763 COG4224		2.328 3.451	0.329 0.183	0.329 0.238	0.217		Uncharacterized protein Uncharacterized protein
LBUL_1283	COG2739		0.441	0.105	2.088	0.217		Uncharacterized protein
LBUL_1286	COG4372		0.326					Uncharacterized protein with the myosin-like domain
LBUL_1298	COG1302		4 404	0.260	0.355			Uncharacterized protein
LBUL_1304 LBUL_1322	COG4825 COG1302		4.434	5.059 0.382				Uncharacterized membrane-anchored protein Uncharacterized protein
LBUL_1368	COG4018		0.345	0.328				Uncharacterized protein
LBUL_1373	COG4483	0.103	0.098					Uncharacterized protein
LBUL_1378 LBUL_1382	COG4485		0.453		4.450			Predicted membrane protein
LBUL_1302	COG3382 ErfK		0.340		4.159 2.907			Uncharacterized conserved protein Uncharacterized protein
LBUL_1434 LBUL_1442	ErfK		0.007	0.226	2.001			Uncharacterized protein
LBUL_1447 LBUL_1468	COG4372			0.123				Uncharacterized protein with the myosin-like domain
LBUL_1468	COG4478 COG4470			0.297				Predicted membrane protein Uncharacterized protein
LBUL_1470 LBUL_1483 LBUL_1485 LBUL_1514	COG3906			0.383				Uncharacterized protein
LBUL_1485	COG4472			0.436				Uncharacterized protein
LBUL_1514	COG0718				2.115			Uncharacterized protein
LBUL_1559	COG2855	2.155	3.993		2.118			Predicted membrane protein
LBUL_1580 LBUL_1670	COG4720 COG4687			0.189	2.118			Predicted membrane protein Uncharacterized protein
LBUL_1708	COG0392		0.390	0.100				Predicted integral membrane protein
LBUL_1750	COG0398			0.301	0.383			Uncharacterized conserved protein
LBUL_1757	COG1511	0.198		4.153				Predicted membrane protein
LBUL_1777	COG1426 COG2246		0.246	0.282				Uncharacterized protein Predicted membrane protein
LBUL_1797 LBUL_1810	COG3349		0.240	2.745	4.943			Uncharacterized conserved protein
LBUL_1822 LBUL_1854	COG1426		8.143		0.338			Uncharacterized protein
LBUL_1854	COG5017			2.298				Uncharacterized conserved protein
LBUL_18/5	COG3610 COG2966	0.257	0.310	2.281	0.371			Uncharacterized conserved protein Uncharacterized conserved protein
LBUL_1875 LBUL_1876 LBUL_1896 LBUL_1919	COG4858	0.207	0.364		2.491			Uncharacterized membrane-bound protein
LBUL_1919	ErfK			0.305	0.129			Uncharacterized protein
0		and a						
General functi LBUL_0010	COG0618	oniy		2.087				
LBUL_0029	COG0390				2.099			Exopolyphosphatase-related protein
LDOL_0023					2.099 0.388			ABC-type uncharacterized transport system permease component
LBUL_0039	COG2910	3.297	15.670	2.087				ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase
LBUL_0039 LBUL_0042	COG2910 COG1942	3.297 2.092	15.670		0.388			ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxalocrotonate tautomerase homolog
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075	COG2910 COG1942 COG1216 ElsH	3.297 2.092	15.670 0.382					ABC-type uncharacterized transport system permease component Putative NADH-flawin reductase Uncharacterized protein 4-oxolocrotonate tautomerase homolog Predicted glycosyltransferase Metal-dependent hydrolase
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078	COG2910 COG1942 COG1216 EIsH ARA1	3.297 2.092	0.382		0.388		0.199	ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4 oxalocorotonate tautomerase homolog Predicted grocositransferase Metal-dependent hydrotase Metal-dependent hydrotase Metal-dependent hydrotase related to diketogulonate reductase
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084	COG2910 COG1942 COG1216 EIsH ARA1 LdhA	3.297 2.092			0.388 40.987	0.262	0.199	ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxaloccrotonate tautomerase homolog Predicted glycosyltransferase Metal-dependent hydrolase Aldoktor reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084 LBUL_0117	COG2910 COG1942 COG1216 EISH ARA1 LdhA PhnP	3.297 2.092	0.382		0.388	0.262		ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4 oxalocorotonate tautomerase homolog Predicted ghocystimanferase Metal-dependent hydrotase Addoketo reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrotase the beta-lactamase superfamily I
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084 LBUL_0117 LBUL_0118 LBUL_0118	COG2910 COG1942 COG1216 EIsH ARA1 LdhA PhnP COG3975 COG3576	3.297 2.092	0.382 3.717		0.388 40.987	0.262	0.199 0.415	ABC-type uncharacterized trainsport system permease component Putative NADH-flavin reductase Uncharacterized protein 4 oxalocorotonate tautomerase homolog Predicted ghocosyltransferase Metal-dependent hydrolase Aldoketo reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the beta-lactamase superfamily I Predicted protease with the C-terminal PDZ domain Predicted protease with the C-terminal PDZ domain
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084 LBUL_0117 LBUL_0118 LBUL_0118	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3576 COG4586	3.297 2.092	0.382	2.025	0.388 40.987 0.335	0.262		ABC-type uncharacterized trainsport system permease component Putative NADH-flawin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glycosyltransferase Metal-dependent hydrolase Addokato reductase related to diletogulonate reductase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase and related dehydrogenase Head-dependent hydrolase Head-dependent hydrolase Head-dependent hydrolase Addokato reductase related to diletogulonate reductase Lactate dehydrogenase and related dehydrogenase Head-dependent hydrolase Addokato reductase Addokato reductase Addokato reductase Addokato reductase Addokato reductase Addokato reductase Addokato reductase Addokato reductase Addokatorovenase Addokatorov
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0175 LBUL_0117 LBUL_0118 LBUL_0123 LBUL_0129 LBUL_0131	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3576 COG3576 COG3694	3.297 2.092	0.382 3.717	2.025	0.388 40.987 0.335 0.424	0.262		ABC-type uncharacterized transport system permease component Putative NADH-Havin reductase Uncharacterized protein 4 oxalocorotonate tautomerase homolog Predicted ghocosyltransferase Metal-dependent hydrolase Aldoketo reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the beta-lactamase superfamily I Predicted protease with the C-terminal PDZ domain Predicted protease with the C-terminal PDZ domain Predicted protease transcript system permetually related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system permease component
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084 LBUL_0117 LBUL_0118 LBUL_0123 LBUL_0123 LBUL_0136	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3576 COG4586	3.297 2.092	0.382 3.717	2.025	0.388 40.987 0.335	0.262		ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrolase Metal-dependent hydrolase Hadokato reductase related to diletogulonate reductase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase and related dehydrogenase Predicted protesses with the C-terminal PDZ domagni Predicted favin-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system PTPase component ABC-type uncharacterized transport system permease component Putative Z-dependent protease contain TRP repeats
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0075 LBUL_0078 LBUL_0084 LBUL_0117 LBUL_0118 LBUL_0123 LBUL_0129 LBUL_0129 LBUL_0136 LBUL_0140	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3576 COG4586 COG4586 COG4583	2.092	0.382 3.717 2.794	2.025	0.388 40.987 0.335 0.424 2.487		0.415	ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glycocyltransferase Metal-dependent hydrolase Addokato reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the betal-actamase superfamily I Predicted protease with the C-terminal PD2 domain ABC-type uncharacterized transport system ATPase component ABC-type uncharacterized transport system PTPase component ABC-type uncharacterized transport system PTPases Predicted double-stranded RAVRINA-ONA hybrid birding protein
LBUL_0039 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0117 LBUL_0118 LBUL_0129 LBUL_0129 LBUL_0136 LBUL_0136 LBUL_0156	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3576 COG3658 COG3694 COG4586 COG3658 COG3658 COG3658 COG341 COG3654 COG341 COG3654 COG365 COG3	3.297 2.092 2.071	0.382 3.717 2.794	2.025 0.138 0.297 0.441	0.388 40.987 0.335 0.424 2.487 8.677 0.247	0.262	0.415	ABC-type uncharacterized trainsport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted ghocosyltransferase Metal-dependent hydrolase Addoketo reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the beta-la-actamase superfamily I Predicted protease with the C-terminal PDZ domain Predicted protease of transport system permease component ABC-type uncharacterized transport system permease component Putative Zn-dependent protease contains TPR repeats Predicted double-stranded RNA/RNA-DNA hybrid binding protein Predicted double-stranded RNA/RNA-DNA hybrid binding protein
LBUL_0039 LBUL_0042 LBUL_0061 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0118 LBUL_0118 LBUL_0123 LBUL_0131 LBUL_0131 LBUL_0140 LBUL_0152	COG2910 COG1942 COG1216 EIsH ARA1 LdhA PhnP COG3975 COG3576 COG3694 COG4586 COG3694 COG3694 COG3658 COG3658 COG3654 COG3654 COG3654 COG3654 COG3654 COG3654 COG365	2.092	0.382 3.717 2.794 0.404	2.025 0.138 0.297	0.388 40.987 0.335 0.424 2.487 8.677		0.415	ABC-type uncharacterized transport system permease component Putative NADH-flavin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glycocyltransferase Metal-dependent hydrolase Addokato reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the betal-actamase superfamily I Predicted protease with the C-terminal PD2 domain ABC-type uncharacterized transport system ATPase component ABC-type uncharacterized transport system PTPase component ABC-type uncharacterized transport system PTPases Predicted double-stranded RAVRINA-ONA hybrid birding protein
LBUL_0039 LBUL_0042 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0017 LBUL_0112 LBUL_0129 LBUL_0120 LBUL_0136 LBUL_0165 LBUL_0165	COG2910 COG1942 COG1216 EIsH ARA1 LdhA PhnP COG3975 COG3576 COG4586 COG3694 COG3694 COG3694 COG3694 COG3658 COG3658 COG33311 ComFC COG1754 COG10400	2.092	0.382 3.717 2.794	2.025 0.138 0.297 0.441	0.388 40.987 0.335 0.424 2.487 8.677 0.247 0.287		0.415	ABC-type uncharacterized trainsport system permease component Putative NADH-Haivn reductase Uncharacterized protein 4-oxalocrotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrotase Metal-dependent hydrotase relaxot failed dehydrogenase Metal-dependent hydrotase of tablet dehydrogenase Metal-dependent hydrotase of the beta-factamase superfamily I Predicted favin-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system ATPase component Putative dybordse orthansite transferase contains TRP repeats Predicted glocosyl hydrotase Predicted glocosyl hydrotase Metal-dependent protease contains TRP repeats Predicted glocosyl hydrotase MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease contains TRP repeats Predicted glocosyl hydrotase MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease MED-type uncharacterized transport system Permease component Putative Zh-dependent protease MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease MED-type uncharacterized transport system ATPase component Putative Zh-dependent protease MED-type uncharacterized transport system MED-type uncharacterized transport
LBUL_0039 LBUL_0042 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0078 LBUL_0078 LBUL_0173 LBUL_0140 LBUL_0129 LBUL_0129 LBUL_0120 LBUL_0131 LBUL_0140 LBUL_0140 LBUL_0156 LBUL_0156 LBUL_0165 LBUL_0165 LBUL_0165 LBUL_0177	COG2910 COG1942 COG1216 EIsH ARA1 LdhA PhnP COG3975 COG3576 COG3576 COG3576 COG3576 COG3588 COG35894 COG35858 COG3404 COG3541 COG1754 COG0400 Imp COG1123	2.092	0.382 3.717 2.794 0.404	2.025 0.138 0.297 0.441	0.388 40.987 0.335 0.424 2.487 0.247 0.247 0.287 0.438		0.415	ABC-type uncharacterized transport system permease component Putative NADH-flawin reductase Uncharacterized protein 4-oxalocrotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase of the beta-factamase superfamily I Predicted favin-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system permease component ABC-type uncharacterized transport system permease component Predicted glocosyl hydrolase Predicted Glocost-transder RAN-RNA-DNA hybrid binding protein Predicted Combine-transder RAN-RNA-DNA hybrid binding protein TRAP-type uncharacterized transport system periplasmic component TRAP-type uncharacterized transport system periplasmic townia duplicated ATPase
LBUL_0039 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0160 LBUL_0112 LBUL_0123 LBUL_0123 LBUL_0131 LBUL_0131 LBUL_0136 LBUL_0160 LBUL_0160 LBUL_0176 LBUL_0176	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3575 COG3576 COG4586 COG4586 COG3684 COG3684 COG3684 COG36858 COG3640 LCOMT5C COG1754 COG1723 COG4533	2.092	0.382 3.717 2.794 0.404 0.138	2.025 0.138 0.297 0.441 0.285 2.596	0.388 40.987 0.335 0.424 2.487 8.677 0.247 0.287		0.415	ABC-type uncharacterized transport system permease component Putative NAD+Havin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted ghocsystimaniferase Metal-dependent hydrolase Addokato reductase related to diketogulonate reductase Lactate dehydrogenase and related dehydrogenase Metal-dependent hydrolase of the betal-actamase superfamily I Predicted ghocksen and related dehydrogenase Predicted favio-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase ABC-type uncharacterized transport system partnesse component ABC-type uncharacterized transport system partnesse component Putative 2n-dependent proteiness contains TPR repeats Predicted amichophosphoritosyltransferase Uncharacterized -terminal domain of topoisomerase IA Predicted asienes TRA-type uncharacterized transport system permetses component APC-type uncharacterized transport system permetses Predicted amichophosphoritosyltransferase ABC-type uncharacterized transport system permitses in the transport system Predicted asienes TRA-type uncharacterized transport system periplesmic component APC-type uncharacterized transport system periplesmic component
LBUL_0039 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0078 LBUL_0078 LBUL_0078 LBUL_0173 LBUL_0118 LBUL_0129 LBUL_0129 LBUL_0129 LBUL_0120 LBUL_0140 LBUL_0156 LBUL_0165 LBUL_0165 LBUL_0165 LBUL_0177 LBUL_0177	COG2910 COG1942 COG1216 ElsH ARA1 LdhA PhnP COG3975 COG3676 COG4586 COG3694 COG4586 COG3694 COG4583 COG3654 COG3654 COG3754 COG1754 COG1754 COG1754 COG1754 COG400 Imp COG1754 COG4533 COG3919	2.092 2.071 0.331	0.382 3.717 2.794 0.404 0.138	2.025 0.138 0.297 0.441 0.285	0.388 40.987 0.335 0.424 2.487 0.247 0.247 0.287 0.438		0.415	ABC-type uncharacterized transport system permease component Putative NADH-Haivn reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase and related dehydrogenase Predicted glocosyltransferase ABC-type uncharacterized transport system ATPase component Predicted dolocoses with the C-tenemial PD2 domain Predicted favior-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system permease component Predicted double-stranded RNA/RNA-DNA hybrid binding protein Predicted amildophosphronbos/transferase Uncharacterized tansport system periplasmic component Predicted double-stranded RNA/RNA-DNA hybrid binding protein Predicted amildophosphronbos/transferase Incharacterized transport system periplasmic component Predicted double-stranded RA/SD-type tansport system periplasmic component Predicted double-transferad transport system periplasmic component Predicted double-transferad transport system periplasmic component Predicted double-tisted transport system periplasmic component Predicted ADV-type appendent forderses Predicted ADV-type transport Predicted
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LBUL_0039 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0017 LBUL_0112 LBUL_0123 LBUL_0123 LBUL_0123 LBUL_0131 LBUL_0131 LBUL_0155 LBUL_0	COG2910 COG91942 COG1942 EIBH ARA1 LdhA PhnP COG3975 COG3576 COG3576 COG35876 COG35876 COG3580 COG33814 COG3154 COG4533 COG3919 Bax COG2194	2.092 2.071 0.331	0.382 3.717 2.794 0.404 0.138 0.347	2.025 0.138 0.297 0.441 0.285 2.596	0.388 40.987 0.335 0.424 2.487 0.247 0.247 0.287 0.438		0.415	ABC-type uncharacterized transport system permease component Putative NADH-Haivn reductase Uncharacterized protein 4-oxalocrotonate tautomerase homolog Predicted glocosyttransferase Metal-dependent hydrotase Metal-dependent hydrotase Metal-dependent hydrotase of the beta-lactamase superfamily I Predicted glocosyttransferase Metal-dependent hydrotase of the beta-lactamase superfamily I Predicted favion-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system ATPase component Predicted glocosyt hydrotase Metal-dependent protease orthain ETP2 domain Predicted favion-nucleotide-binding protein structurally related to pyridoxine 5-phosphate oxidase ABC-type uncharacterized transport system permease component Putative Zn-dependent protease contains TRP repeats Predicted glocosyt hydrotase Metal-dependent protease Uncharacterized C-terminal domain of topoisomerase IA Predicted C-terminal domain of topoisomerase IA Predicted ADV-type uncharacterized transport system periplasmic component Predicted ADV-type uncharacterized transport system periplasmic component ATRA-type uncharacterized transport system periplasmic component Predicted advised transport system periplasmic component Predicted metal-subtranterises ABC-type uncharacterized transport system ABC-type uncharacterized transport system ABC-type uncharacterized transport system ABC-type uncharacteri
LBUL_0039 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0017 LBUL_0112 LBUL_0123 LBUL_0123 LBUL_0123 LBUL_0131 LBUL_0131 LBUL_0155 LBUL_0	COG2910 COG91942 COG1942 ElsH ARA1 LdhA PhnP COG3976 COG36576 COG36594 COG34594 COG34594 COG34594 COG34594 COG34503 COG36594 COG302154 COG4533 COG453 COG455 CO	2.092 2.071 0.331 4.362 0.181	0.382 3.717 2.794 0.404 0.138 0.347 0.150 0.274	2.025 0.138 0.297 0.441 0.285 2.596 0.350	0.388 40.967 0.335 0.424 2.487 8.677 0.247 0.247 0.287 0.438 0.249 6.229		0.415	ABC-type uncharacterized transport system permease component Putative NAD+Haivn reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glycosyltransferase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase ABC-type uncharacterized transport system permease component ABC-type uncharacterized transport system permease component ABC-type uncharacterized transport system permease component Predicted glycosyl hydrolase Predicted glycosyl hydrolase Predicted aductore-transfer MAVRNA-DNA hydrid birding protein Predicted double-transder RAVRNA-DNA hydrid birding birding protein Predicted metal-selfur transport system periplasmic component Predicted
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LBUL_0039 LBUL_0042 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0175 LBUL_0117 LBUL_0131 LBUL_0131 LBUL_0131 LBUL_0131 LBUL_0131 LBUL_0140 LBUL_0140 LBUL_0150 LBUL_0150 LBUL_0150 LBUL_0150 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0151 LBUL_0255 LBUL_0555 LBUL_0555 LBUL_05555 LBUL_05555 LBUL_055555 LBUL_0555555 LBUL_0555	COG2910 COG91942 COG1216 ElisH ARA1 LdhA PhmP COG3975 COG3576 COG3576 COG3586 COG36894 COG4586 COG36894 COG4512 COG4786 COG4512 COG4786 COG4512 COG4783 COG4513 COG4513 COG512 COG376 COG304 COG312 COG32 COG3	2.092 2.071 0.331 4.362 0.181 0.202 0.386	0.382 3.717 2.794 0.404 0.138 0.347 0.150 0.274 0.155 0.055 2.215	2.025 0.138 0.297 0.441 0.285 2.596 0.350 2.028	0.388 40.987 0.335 0.424 2.487 0.247 0.247 0.247 0.247 0.247 0.249 6.229 0.117 0.159 0.144		0.415 0.297 0.433	ABC-type uncharacterized transport system permease component Putative NAD+Haivn reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent hydrolase Metal-dependent proteins succurally related to pyridoxine 5'-phosphate oxidase Predicted flow-nucleotide-binding protein succurally related to pyridoxine 5'-phosphate oxidase Predicted glocosyl hydrolase Predicted amickophosphoritosyltransferase Uncharacterized transport system permease component Predicted amickophosphoritosyltransferase Predicted amickophosphoritosyltransferase Predicted amickophosphoritosyltransferase Nucharacterized transport system periplasmic component Predicted desterase TRAP-type uncharacterized transport system periplasmic component Predicted amickophosphoritosyltransferase BC-type uncharacterized transport system periplasmic component Predicted desterase TRAP-type uncharacterized transport system periplasmic component Predicted ATP-grasp protein Predicted ATP-grasp protein Predicted ATP-grasp protein Predicted Taular acterized transport system periplasmic component ABC-type uncharacterized transport system periplasmic component Predicted ATP-grasp protein Predicted ATP-grasp protein Predicted Taular ABC-type transport system periplasmic component ABC-type uncharacterized transport system periplasmic component ABC-type uncharacterized transport system periplasmic contain duplicated ATP-ase ABC-type uncharacterized transport system periplasmic contain duplicated ATP-ase Predicted flowin-nucleotid-binding protein ABC-type uncharacterized transport system periplasmic contain duplicated ATP-ase Predicted flowin-nucleotid-binding protein structurally related to pyridoxine 5'-phosphate oxidase Predicted Ho superfamily hydrolase Predicted Ho superfamily hydrolase
LBUL_0039 LBUL_0042 LBUL_0042 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0075 LBUL_0173 LBUL_0131 LBUL_0131 LBUL_0131 LBUL_0131 LBUL_0140 LBUL_0140 LBUL_0140 LBUL_0140 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_0145 LBUL_025 LBUL_0225 LBUL_0223 LBUL_0223 LBUL_0223 LBUL_0223 LBUL_0223	COG2910 COG91942 COG1216 ElsH ARA1 LdmA POG 003375 COG3375 COG3576 COG3576 COG3576 COG3576 COG3576 COG35876 COG35876 COG35876 COG3589 COG3301 PaaD Bax COG31912 Bax COG2194 Mut COG4533 COG4533 COG4533 COG4533 COG4533 COG4533 COG4533	2.092 2.071 0.331 4.362 0.181 0.202 0.386	0.382 3.717 2.794 0.404 0.138 0.347 0.150 0.274 0.155 0.055 2.215	2.025 0.138 0.297 0.441 0.285 2.596 0.350 2.028 0.074	0.388 40.987 0.335 0.424 2.497 0.247 0.247 0.247 0.247 0.247 0.249 6.229 0.117 0.159 0.144 2.491 2.013	0.312	0.415	ABC-type uncharacterized transport system permease component Putative NADH-Haivn reductase Uncharacterized protein 4-oxalocrotonate tautomerase homolog Predicted glocosystmansferase Metal-dependent hydrotase Metal-dependent hydrotase Metal-dependent hydrotase Metal-dependent hydrotase of the beta-lactamase superfamily I Predicted flocoses with the C-terminal PD2 domain Predicted subscriptions PD2 domain Predicted subscriptions PD4 domain of topoisonnerase IA Predicted C-terminal domain of topoisonnerase IA Predicted C-terminal domain of topoisonnerase IA Predicted attracterized transport system periplasmic component Predicted TP3-related protein Predicted TP3-related protein AC-type uncharacterized transport system periplasmic component AP3-so components of valuous ABC-type transport systems contain duplicated ATPase Metal-doperaterized transport system periplasmic component AP3-bype uncharacterized transport systems periplasmic component AP3-bype uncharacterized transport sys
LBUL 0032 LBUL 0042 LBUL 0042 LBUL 0047 LBUL 0078 LBUL 0078 LBUL 0078 LBUL 0078 LBUL 0078 LBUL 0172 LBUL 0172 LBUL 0172 LBUL 0172 LBUL 0173 LBUL 0175 LBUL 0175 LBUL 0175 LBUL 0176 LBUL 0177 LBUL 0	COG2910 COG91942 COG1216 ElsH ARA1 LdhA PhµP COG3975 COG3984 COG3988 COG3984 C	2.092 2.071 0.331 4.362 0.181 0.202 0.386	0.382 3.717 2.794 0.404 0.138 0.347 0.150 0.274 0.155 0.055 2.215	2.025 0.138 0.297 0.441 0.285 2.596 0.350 2.028 0.074	0.388 40.987 0.335 0.424 2.487 8.677 0.247 0.247 0.247 0.249 6.229 0.249 6.229 0.117 0.159 0.144 2.491	0.312	0.415 0.297 0.433	ABC-type uncharacterized transport system permease component Putative NADH-Havin reductase Uncharacterized protein 4-oxalocorotonate tautomerase homolog Predicted glocosyltransferase Metal-dependent hydrolase Addokato reductase related to dietogulonate reductase Lactate dehydrogenase and related dehydrogenase Lactate dehydrogenase and related dehydrogenase Predicted glocosyltransferase Addokato reductase with the C-terminal PD2 domain Predicted favioranceterized transport system Parese component ABC-type uncharacterized transport system permease component Predicted glocosyl hydrolase Predicted glocosyl hydrolase Predicted double-stranded RAV/RNA-DNA hybrid binding protein Predicted double-tranded RAV/RNA-DNA hybrid binding protein RRAP-type uncharacterized transport system periplasmic component Predicted ADV-terminal bBC-type transport system periplasmic component Predicted Metal-sulfur cluster biosynthetic protein NTP pryonbenders for various ABC-type transport systems contain duplicated ATPase ABC-type uncharacterized transport system periplasmic component Predicted metal-activity transport system periplasmic component APTase components of various ABC-type transport systems periplasmic component ABC-type uncharacterized transport system periplasmic component Metal-dependent amidae-minina-protein succurally relaxed to pyricioxin 5-phosphate oxidase Metal-dependent amidae-minina-protexincurally relaxed to pyricioxin 5-phosphate oxidase Metal-

LBUL_0246 LBUL_0251 LBUL_0252			0.005		0.050			
LBUL_0251	COG2070 COG2070	0.221	0.285		0.053	0.000	0.458	Dioxygenase related to 2-nitropropane dioxygenase
	COG2070 COG2071	2.639 2.315				0.290	0.458	Dioxygenase related to 2-nitropropane dioxygenase Predicted glutamine amidotransferase
LBUL_0255	SPS1	2.010		4.400				Serine/threonine protein kinase
LBUL 0256	ArpD		0.347	6.884				ABC-type protease/lipase transport system ATPase and permease components
I BUI 0262	COG1123	0.380	0.268		0.077			ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_0282 LBUL_0290	COG4111		2.411					Uncharacterized conserved protein
	SPS1				3.405	5.086		Serine/threonine protein kinase
LBUL_0295	COG1512				4.915			Beta-propeller domains of methanol dehydrogenase type
LBUL_0296	COG4087		0.168		2.240			Soluble P-type ATPase
LBUL_0297	ARC1 COG1099				2.240			EMAP domain
LBUL_0298			0.392		2.057		0.432	Predicted metal-dependent hydrolase with the TIM-barrel fold
LBUL_0303 LBUL_0306	LpxD COG1078		0.328		2.007		0.432	UDP-3-0-(3-hydroxymyristoyl) HD superfamily phosphohydrolase
LBUL_0326	AbgB		0.520	2.960				Metal-dependent amidase/aminoacylase/carboxypeptidase
LBUL_0339	COG0714			2.000	3.118			MoxR-like ATPase
LBUL_0348	COG1160	0.379	0.465					Predicted GTPase
LBUL_0393	PfoR			5.484				Predicted membrane protein putative toxin regulator
LBUL_0412	Bax				2.460			Uncharacterized FlgJ-related protein
LBUL_0413 LBUL_0414	COG3973		0.435					Superfamily I DNA and RNA helicase
LBUL_0414	COG5275		0.227		9.293			BRCT domain type II
LBUL_0419 LBUL_0421	LCB5				2.183			Sphingosine kinase
LBUL_0421	COG1092	0.359			0.480			Predicted SAM-dependent methyltransferase
LBUL_0422	COG4889	0.466	3.059		0.450			Predicted helicase
LBUL_0427	COG4087 PutP							Soluble P-type ATPase Na+/oroline symporter
LBUL_0431 LBUL_0433	MutT		0.241			2.654		NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_0445			0.333			2.004		ATPase components of ABC transporter with duplicated ATPase domains
LBUL_0445	Uup COG0670		0.333		4.139		0.116	Integral membrane protein interacts with FtsH
LBUL_0454	COG4449	0.241			2.078		0.110	Predicted protease of the Abi (CAAX) family
LBUL_0457	COG4240		0.368		6.995			Predicted kinase
LBUL_0479	TlyC			0.430				Hemolysins and related protein containing CBS domains
LBUL_0480	COG2236				0.202			Predicted phosphoribosyltransferase
LBUL 0486	PfoR			5.679				Predicted membrane protein putative toxin regulator
LBUL_0498 LBUL_0500	COG2068		0.448		5.087			Uncharacterized MobA-related protein
LBUL_0500	COG1073		0.293					Hydrolase of the alpha/beta superfamily
LBUL_0501 LBUL_0505	COG1092		0.195					Predicted SAM-dependent methyltransferase
	TlyC		0.480					Hemolysins and related protein containing CBS domains
LBUL_0506	COG1160				4.576			Predicted GTPase
LBUL_0510	COG0714			0.381				MoxR-like ATPase
LBUL_0516 LBUL_0530	CoiA		0.340	0.384				Competence protein
LBUL_0530	PqqL		0.261		3.543			Predicted Zn-dependent peptidase Predicted Zn-dependent peptidase
LBUL_0532	PqqL FabG		0.451		3.043			Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_0548	GltD		0.401		0.425			NADPH-dependent glutamate synthase beta chain and related oxidoreductase
LBUL_0549	Lhr			0.095	0.085			Lhr-like helicase
LBUL_0550	COG1123		2.433	0.243	0.098			ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_0551	COG2194			0.165	0.113			Predicted membrane-associated metal-dependent hydrolase
LBUL 0556	COG1660				0.334			Predicted P-loop-containing kinase
LBUL_0572	Cof				2.538			Predicted hydrolase of the HAD superfamily
LBUL_0578	COG1123		0.448					ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_0579 LBUL_0580	COG4132 COG4132	0.442	0.396					ABC-type uncharacterized transport system permease component
LBUL_0580			0.268					ABC-type uncharacterized transport system permease component
LBUL_0581	COG4134		0.402					ABC-type uncharacterized transport system periplasmic component Predicted nucleic-acid-binding protein (contains the HHH domain)
LBUL_0582	COG1623 Cof	2.582	0.290	0.484				
LBUL_0585 LBUL_0589	Gph	0.358		0.404				Predicted hydrolase of the HAD superfamily Predicted phosphatase
LBUL_0606	COG4667	0.000		13.802	8.345			Predicted phosphatase Predicted esterase of the alpha-beta hydrolase superfamily
LBUL_0610	COG1855	7.998		18.355	0.545			ATPase (PiIT family)
LBUL_0623	COG3083	1.000		0.258				Predicted hydrolase of alkaline phosphatase superfamily
LBUL_0634	COG4123		0.441					Predicted O-methyltransferase
LBUL_0661	COG0637		0.448	2,433	8.747			Predicted phosphatase/phosphohexomutase
LBUL_0674	COG4671	0.499	0.220					Predicted glycosyl transferase
LBUL_0683	MutT				5.121			NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_0686	COG1103	0.402	0.328		5.142			pyridoxal phosphate-dependent protein
LBUL_0688	COG1365		2.445		8.246			Predicted ATPase (PP-loop superfamily)
LBUL_0696 LBUL_0699	Era	0.448	0.332		2.191			GTPase
	COG1092	0.147	0.226		3.769			Predicted SAM-dependent methyltransferase
LBUL_0701	COG1750				2.301			serine protease
	COG0595				2.687			Predicted hydrolase of the metallo-beta-lactamase superfamily
LBUL_0707			2 5 9 7	2 420				CTRoss
LBUL_0707 LBUL_0709	GTPBP1		3.587	2.430	2.048			GTPase
LBUL_0707 LBUL_0709 LBUL_0712	GTPBP1 COG0218			2.430 0.330	2.048			GTPase Predicted GTPase
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717	GTPBP1 COG0218 COG4533		3.587 0.254	0.330	2.048			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722	GTPBP1 COG0218 COG4533 COG4087			0.330		4.189	3.051	GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726	GTPBP1 COG0218 COG4533 COG4087 COG2081		0.254	0.330	0.130	4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Solubile P-type ATPase Predicated flavorotetin
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0742 LBUL_0744	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159	4.095		0.330		4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicated flavoprotein Predicated mata-dependent hydrolase of the TIM-barrel fold
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0742 LBUL_0744 LBUL_0744	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg	4.095	0.254 0.317 0.472	0.330	0.130	4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicated flavoprotein Predicated flav-dependent hydrolase of the TIM-barrel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicate draft Pase
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0742 LBUL_0744 LBUL_0747 LBUL_0749	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC	4.095	0.254 0.317 0.472 0.339	0.330	0.130 2.395	4.189	3.051	GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted motal-dependent hydrolase of the TIM-barrel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicted GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0742 LBUL_0744 LBUL_0744 LBUL_0749 LBUL_07769	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160		0.254 0.317 0.472 0.339 0.278	0.330	0.130	4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicated flavoprotein Predicated flav-dependent hydrolase of the TIM-barnel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicate drase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicate drase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicated TPase
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0744 LBUL_0747 LBUL_0747 LBUL_0746 LBUL_0776 LBUL_0804	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH	4.095	0.254 0.317 0.472 0.339	0.330 0.147 0.047	0.130 2.395	4.189	3.051	GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavoprotein Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicted GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase 3-coxosol+(ac/v-carriter-protein)
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0744 LBUL_0747 LBUL_0747 LBUL_0746 LBUL_0776 LBUL_0804	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH COG3889		0.254 0.317 0.472 0.339 0.278	0.330 0.147 0.047 0.428	0.130 2.395 3.234	4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicated flavoprotein Predicated flavoprotein Predicated flavoprotein Mith a unique C-terminal domain including a metal-binding cysteine cluster Predicate GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicated GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicated GTPase 3-oxoacyl-(acyl-carrier-protein) Predicated STPase
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0722 LBUL_0724 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0746 LBUL_0814 LBUL_0816	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2081 COG2159 COG1205 Obg ElaC COG160 FabH COG3889 PerM		0.254 0.317 0.472 0.339 0.278 0.145	0.330 0.147 0.047 0.428 0.294	0.130 2.395 3.234 3.126	4.189	3.051	GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicad flavoprotein Predicad flavoprotein tydrolase of the TIM-barrel fold Flavinor that that dependent hydrolase of the TIM-barrel fold Flavinor that that dependent hydrolase of the table-barrel fold Predicted GTPase Netal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase S-xxxxxy1-(excircter-protein) Predicted solute binding protein Predicted permease
LBUL_0707 LBUL_0709 LBUL_0712 LBUL_0717 LBUL_0722 LBUL_0722 LBUL_0742 LBUL_0747 LBUL_0749 LBUL_0749 LBUL_0749 LBUL_0804 LBUL_0804 LBUL_0816	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH COG3889		0.254 0.317 0.472 0.339 0.278	0.330 0.147 0.047 0.428	0.130 2.395 3.234	4.189	3.051	GTPase Predicated GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicated flavoprotein Predicated flavoprotein Mydrolase of the TIM-barnel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicate GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicated STPase 3-oxoacy/-(acy/-carriter-protein) Predicated permease 3-oxoacy/-(acy/-carriter-protein)
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0722 LBUL_0722 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0749 LBUL_0749 LBUL_0814 LBUL_0814 LBUL_0816 LBUL_0821	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH COG3889 PerM FabH		0.254 0.317 0.472 0.339 0.278 0.145 0.371	0.330 0.147 0.047 0.428 0.294 0.262	0.130 2.395 3.234 3.126 0.200	4.189	3.051	GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavcyordein Prediced flavcyordein Hard-dependent hydrolase of the TIM-barnel fold Prediced metal-dependent hydrolase of the TIM-barnel fold Netal-dependent hydrolase of the beta-lactamase superfamily III Prediced GTPase -xxxxxxife.cvcrartier.protein) Predicted solute binding protein Prediced solute binding protein Prediced solute binding protein Detyforgenese -xxxxxife.cvcrartier.protein) Detyforgenese with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0726 LBUL_0726 LBUL_0742 LBUL_0742 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0747 LBUL_0744 LBUL_0814 LBUL_0814 LBUL_0818 LBUL_0821 LBUL_0822	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH COG3889 PerM FabH FabG COG2232 Fabl	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.318	0.330 0.147 0.047 0.428 0.294 0.262 0.258	0.130 2.395 3.234 3.126 0.200 0.196	4.189	2.147	GTPase GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavcyordein Predicted flavcyordein Predicted flavcyordein Predicted GTPase GT
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0749 LBUL_0749 LBUL_0749 LBUL_0814 LBUL_0814 LBUL_0814 LBUL_0818 LBUL_0818 LBUL_0825 LBUL_0825 LBUL_0869	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1205 COG1205 FabH COG3889 PerM FabH FabH FabH COG2232 FabI COG4590		0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.371 0.378 0.295	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.391 0.321	4.189		GTPase GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Columb P-type ATPase Predicted GTPase Predicted GTPase Fredicted GTPase Metal-dependent hydrolase of the bta-lactamase superfamily III Predicted GTPase S-oxoacy1-(acy-carrier-protein) Predicted GTPase S-oxoacy1-(acy-carrier-protein) Predicted Premase S-oxoacy1-(acy-carrier-protein) Predicted Premase S-oxoacy1-(acy-carrier-protein) Predicted Premase ADC-type uncharacterized transport system permases Columb D-type C
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0742 LBUL_0744 LBUL_0747 LBUL_0747 LBUL_0747 LBUL_0747 LBUL_0814 LBUL_0818 LBUL_0818 LBUL_0821 LBUL_0828 LBUL_0828 LBUL_0829 LBUL_0829	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1205 PabH COG3889 PerM FabH FabG COG2232 FabI COG4590 COG1123	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.371 0.371 0.378 0.295 0.288	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.391			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavQprotein Predicted flavQprotein Predicted flavQprotein Predicted flavQprotein Meta-Aspentent hydrolase of the TIM-barnel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteline cluster Predicted adTPase Meta-Aspentent hydrolase of the beta-lactamase superfamily III S-owago(+Goy(-carrifice-protein) Predicted Solute binding protein Predicted ATP-Agependent carboligase related to biolin carboxylase Enoyl-(ac)-carrifice-protein) Predicted ATP-Agependent carboligase related to biolin carboxylase Enoyl-(ac)-carrifice-protein) ABC-type uncharacterized transport system permease component ATPase components of valous ABC-type transport systems contain duplicated ATPase
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0749 LBUL_0749 LBUL_0749 LBUL_0804 LBUL_0804 LBUL_0814 LBUL_0814 LBUL_0818 LBUL_0825 LBUL_0825 LBUL_0829 LBUL_0869	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1205 Obg ElaC COG1205 PabH FabH FabH FabH FabH FabH COG2232 FabI COG4590 COG4590 COG1123 COG3858	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.371 0.378 0.295	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.391 0.321	4.189		GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted Theorement Predicted Theorement Predicted GTPase Metal-dependent hydrolase of the TMI-barrel fold Distinct helices family with a unique C-terminal domain including a metal-binding cysteine cluster Predicted GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase S-oxaacyl-(acyl-carriter-protein) Predicted solute binding protein Predicted solute binding protein Predicted Solute with different specificities (related to short-chain alcohol dehydrogenase) Provide ATP Areinerprotein Dehydrogenase Mit different specificities Predicted Agrees ABC-type uncharacterized transport system permease component ATPase Predicted Agrees Predicted Agrees Predicted Solute NBC-type transport systems contain duplicated ATPase Predicted Prediced Predices Predicted Solute NBC-type transport systems permease Predicted Agrees Predicted Solute NBC-type transport systems Predicted Solute NBC-type transport systems Predicted Solute NBC-type transport system Predicted Solute
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0816 LBUL_0816 LBUL_0816 LBUL_0821 LBUL_0821 LBUL_0828 LBUL_0829 LBUL_0726 LBUL_0744 LBUL_0749 LBUL_0864 LBUL_0	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH COG3889 PerM FabG COG4590 COG4590 COG4590 COG4590 COG4590 COG4590 COG3858 MuT	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.318 0.295 0.288 0.315	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.391 0.321			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavQprotein Predicted flavQprotein Predicted flavGPTase Predicted flavGPTase Metal-dependent hydrolase of the tTM-barrel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicted flavGPTase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase S-oxeoy1-(acyl-carrite-protein) Predicted ATP-dependent carboligase related to biotin carboxylase Enoyl-(acyl-carrite-protein) Dehydrogenase with different specificilies (related to short-chain alcohol dehydrogenase) Predicted ATP-dependent carboligase related to biotin carboxylase Enoyl-(acyl-carrite-protein) ABC-type uncharacterized transport system permease component ATP-ase components of valous ABC-type transport systems contain duplicated ATP-ase Predicted glycosyl hydrolase
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0814 LBUL_0814 LBUL_0814 LBUL_0818 LBUL_0825 LBUL_0825 LBUL_0829 LBUL_0	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2159 COG1205 Obg ElaC COG1160 FabH FabH FabH FabH FabH COG2232 FabI COG2232 FabI COG4590 COG1123 COG3858 MuIT COG1235	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.318 0.288 0.288 0.288 0.315 0.216	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.321 0.363			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavoprotein Bergenet Research Predicted Stransport System periplasmic component Soluble P-type ancharacterized transport system periplasmic component Metal-dependent hydrolase of the TM-barrel fold Netal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase Accuration protein) Predicted GTPase S-oxoacyl-(acyl-carriter-protein) Predicted solute binding protein Predicted ATP-dependent carboligase related to biotin carboxylase Deflydrogenase with different specificities (related to short-chain alcohol dehydrogenase) Predicted ATP-dependent carboligase related to biotin carboxylase Eroyl-(acyl-carriter-protein) Predicted Predicted Predicted Strater-protein) Predicted ATP-dependent carboligase related to biotin carboxylase Eroyl-(acyl-carriter-protein) Predicted Predicted ATP-dependent carboligase related to biotin carboxylase Provident ATP-dependent carboligase related to short-chain alcohol dehydrogenase) Predicted Predicted Predicted Strater-protein AC -bype constrate/exponent ATP-system States ABC-type transport systems contain duplicated ATP-ase NTP prophosphohydrolase including oxidative damage regain protein ATP-ase components of valous ABC-type transport systems contain duplicated ATP-ase
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_0816 LBUL_0816 LBUL_0816 LBUL_0821 LBUL_0821 LBUL_0828 LBUL_0848LBUL_0848 LBUL_0848 LBUL_0848LBUL_0848 LBUL_0848LBUL_0848 LBUL_0848 LBUL_0848LBUL_0848 LBUL_0848 LBUL_0848LBUL_0848 LBUL_0	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2219 COG2205 ElaC COG1205 FabH FabG COG32889 PerM Fabb COG3282 FabH COG2322 Fabl COG32858 MuT COG4590 COG1123 COG1123	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.318 0.295 0.288 0.315	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132	0.130 2.395 3.234 3.126 0.200 0.196 0.391 0.321 0.321 0.363 5.201			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted flavoprotein Predicted flavoprotein Predicted flavoprotein Hydrolase of the TIM-barrel fold Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster Predicted GTPase Metal-dependent hydrolase of the beta-lactamase superfamily III Predicted GTPase 3-oxeoxyl-tacyt-carrite-protein) Predicted ATP-dependent specificilies (related to short-chain alcohol dehydrogenase) Predicted ATP-dependent carboligase related to biotin carboxylase Enoyl-tacyt-carrite-protein) ABC-type uncharacterized transport system permease component ATPase components of various ABC-type transport systems contain duplicated ATPase Predicted glycosyl hydrolase NTP pryotophorshordsaise including oxidative damage repair protein ATPase components of various ABC-type transport systems contain duplicated ATPase Predicted glycosyl hydrolase
LBUL_0707 LBUL_0712 LBUL_0712 LBUL_0712 LBUL_0722 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0724 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0744 LBUL_0804 LBUL_0804 LBUL_0804 LBUL_0804 LBUL_0805 LBUL_0	GTPBP1 COG0218 COG4533 COG4087 COG2081 COG2081 COG2081 COG2159 COG1205 PabH COG3889 PerM FabH FabH FabH FabH COG3889 FabH COG4123 COG4123 COG4123 COG4123 COG4123	0.215	0.254 0.317 0.472 0.339 0.278 0.145 0.371 0.318 0.288 0.288 0.288 0.315 0.216	0.330 0.147 0.047 0.428 0.294 0.262 0.258 0.132 0.104	0.130 2.395 3.234 3.126 0.200 0.196 0.321 0.363			GTPase Predicted GTPase ABC-type uncharacterized transport system periplasmic component Soluble P-type ATPase Predicted Texporeted Predicted GTPase Predicted Structure Structure Structure Predicted Structure Structure Structure Predicted Structure
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LBUL_1129 LBUL_1138	MutT COG3380	0.258		2,770				NTP pyrophosphohydrolase including oxidative damage repair protein Predicted NAD/FAD-dependent oxidoreductase
LBUL_1148	Uup	0.413	0.206	0.267				ATPase components of ABC transporter with duplicated ATPase domains
LBUL_1157 LBUL_1169	COG4087 Era	0.432 0.256	0.499	0.328	2.176	7.961	0.290	Soluble P-type ATPase GTPase
LBUL_1171	COG0319	0.371	0.315	0.400				Predicted metal-dependent hydrolase
LBUL_1186 LBUL_1189	COG1223 GltD			0.432 0.412				Predicted ATPase (AAA+ superfamily) NADPH-dependent glutamate synthase beta chain and related oxidoreductase
LBUL_1193 LBUL_1204	COG1161 ArpD	0.188	0.137	62.155	4.149			Predicted GTPase ABC-type protease/lipase transport system ATPase and permease components
LBUL_1204 LBUL_1213 LBUL_1214	COG1123			2.998				ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_1214	COG0603 COG0618		0.325		4.248			Predicted PP-loop superfamily ATPase Exonolyphosobatase-related protein
LBUL_1223 LBUL_1225	COG0618 COG1160	0.341	0.325					Predicted GTPase
LBUL_1235 LBUL_1241	COG1350 COG1160	9.381	3.000	23.087 3.477	2.835			Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB) Predicted GTPase
LBUL_1241	COG0613			3.477	4.074			Predicted of Pase Predicted metal-dependent phosphoesterase (PHP family)
LBUL_1249	COG4589 COG4123		0.454		3.622			Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase
LBUL_1255 LBUL_1260	PheB	0.366			3.022			Predicted O-methyltransferase ACT domain-containing protein
LBUL_1261 LBUL_1269	ArpD Lhr	0.137	0.254		0.116			ABC-type protease/lipase transport system ATPase and permease components Lhr-like helicase
LBUL_1285	MDN1		0.366		0.110			AAA ATPase containing von Willebrand factor type A (vWA) domain
LBUL_1286 LBUL_1291	COG1106 COG4174	0.330	0.326 0.229	2.883	0.179			Predicted ATPase ABC-type uncharacterized transport system permease component
LBUL 1292	COG1123	0.324	0.262	2.588	0.193			ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_1293	COG1123 COG1205	0.282	0.278	2.768 0.290	0.148			ATPase components of various ABC-type transport systems contain duplicated ATPase Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster
LBUL_1296 LBUL_1297	COG1461			0.290	0.412			Predicted kinase related to dihydroxyacetone kinase
LBUL_1305 LBUL_1308	COG1162 COG4122	0.315		0.462				Predicted GTPase Predicted O-methyltransferase
LBUL_1315	COG4637			0.402	4.141		0.219	Predicted ATPase
LBUL_1330 LBUL_1333	COG1759 COG2144		0.339 0.334		0.063 0.045		2.116	ATP-utilizing protein of ATP-grasp superfamily (probably carboligase) Selenophosphate synthetase-related protein
LBUL_1334	COG0121		0.371		0.052		2.314	Predicted glutamine amidotransferase
LBUL_1335 LBUL_1336	COG2144 ThiJ		0.453 0.442		0.073 0.039		2.397	Selenophosphate synthetase-related protein Putative intracellular protease/amidase
LBUL_1340	LdhA		0.112		0.105	0.303		Lactate dehydrogenase and related dehydrogenase
LBUL_1341 LBUL_1351	COG1691 COG2936		0.500		0.136 5.195	0.286		NCAIR mutase (PurE)-related protein Predicted acyl esterase
LBUL_1354 LBUL_1356	COG1350		0.157	0.356	0.034			Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)
LBUL_1356	COG4976 SsnA		0.301	2.801	0.051			Predicted methyltransferase (contains TPR repeat) Cvtosine deaminase and related metal-dependent hydrolase
LBUL_1358 LBUL_1368	COG3968		0.345	0.328				Uncharacterized protein related to glutamine synthetase
LBUL_1374 LBUL_1382	GlpG ARC1	0.299	0.340		4.159			Uncharacterized membrane protein (homolog of Drosophila rhomboid) EMAP domain
LBUL_1390	COG1399	0.353	0.477					Predicted metal-binding possibly nucleic acid-binding protein
LBUL_1414 LBUL_1419	ARC1 Hit			0.415 0.375				EMAP domain Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolase
LBUL_1423	ComFC						2.350	Predicted amidophosphoribosyltransferase
LBUL_1450 LBUL_1466	RfbX HcaD		0.500		2.425			Membrane protein involved in the export of O-antigen and teichoic acid Uncharacterized NAD(FAD)-dependent dehydrogenase
LBUL_1477 LBUL_1486	COG4768			0.278	0.507			Uncharacterized protein containing a divergent version of the methyl-accepting chemotaxis-like domain
LBUL 1487	COG2872 Lhr				2.597 2.234			Predicted metal-dependent hydrolase related to alanyl-tRNA synthetase HxxxH domain Lhr-like helicase
LBUL_1488 LBUL_1502	COG0618			0.000	3.076			Exopolyphosphatase-related protein
LBUL_1506 LBUL_1507	Riml FcbC			0.363				Acetyltransferase Predicted thioesterase
LBUL_1507	COG0313 COG1216		0.070	0.482				Predicted methyltransferase
LBUL_1542 LBUL_1555	COG1216 MutT		0.376		3.346			Predicted glycosyltransferase NTP pyrophosphohydrolase including oxidative damage repair protein
LBUL_1562	COG1123	0.212			0.440		0.162	ATPase components of various ABC-type transport systems contain duplicated ATPase
LBUL_1588 LBUL_1606	COG4152 COG4639				0.442 2.903			ABC-type uncharacterized transport system ATPase component Predicted kinase
LBUL_1635	Riml	0.045	0.000		0.347	0.058		Acetyltransferase
LBUL_1658 LBUL_1664	COG2270 COG1090	2.845 0.485	2.903		0.017			Permease of the major facilitator superfamily Predicted nucleoside-diphosphate sugar epimerase
LBUL_1680 LBUL_1691	COG2056 COG1103		0.390 0.365		2.204	31.248		Predicted permease pyridoxal phosphate-dependent protein
LBUL 1693	YhbG		0.305		7.298			ABC-type (unclassified) transport system ATPase component
LBUL_1700 LBUL_1707	COG1123 COG2194			0.272	0.323 4.510			ATPase components of various ABC-type transport systems contain duplicated ATPase Predicted membrane-associated metal-dependent hydrolase
LBUL_1749 LBUL_1751	Riml			0.355	0.253			Acetyltransferase
LBUL_1751	COG1647 COG1645			0.156	4.797			Esterase/lipase Uncharacterized Zn-finger containing protein
LBUL_1756 LBUL_1757	COG2409	0.198		4.153	4.101			Predicted drug exporter of the RND superfamily
LBUL_1762 LBUL_1763	MhpC Riml	0.308		5.544	4.319			Predicted hydrolase or acyltransferase (alpha/beta hydrolase superfamily) Acetyltransferase
LBUL_1772	ArpD	0.000			2.425			ABC-type protease/lipase transport system ATPase and permease components
LBUL_1775 LBUL_1785	MhpC COG1913			0.408 0.173	2.682 0.396			Predicted hydrolase or acyltransferase (alpha/beta hydrolase superfamily) Predicted Zn-dependent protease
LBUL_1800	COG1019	0.210	0.119					Predicted nucleotidyltransferase
LBUL_1802 LBUL_1808	RfbX COG1216	0.074 0.472	0.109	3.024	2.394	4.640		Membrane protein involved in the export of O-antigen and teichoic acid Predicted glycosyltransferase
I BUI 1810	HcaD			2.745	4.943			Uncharacterized NAD(FAD)-dependent dehydrogenase
LBUL_1823 LBUL_1835	COG2085 FabG	0.404		0.119 6.551			0.434	Predicted dinucleotide-binding protein Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_1841 LBUL_1843	RfbX COG1216	0.273	0.426					Membrane protein involved in the export of O-antigen and teichoic acid
LBUL_1848	COG1216 COG1216	0.288	0.304					Predicted glycosyltransferase Predicted glycosyltransferase
LBUL_1848 LBUL_1861	HfIX LdhA		3.201	0.267	0.170			GTPase
LBUL_1868 LBUL_1885	Cof		3.201	3.363				Lactate dehydrogenase and related dehydrogenase Predicted hydrolase of the HAD superfamily
LBUL_1897	Obg COG0431	0.244	0.284 0.171					Predicted GTPase Predicted flavoprotein
LBUL_1906 LBUL_1907	COG0431	0.394	0.253					Predicted flavoprotein
LBUL_1936 LBUL_1942	COG2110 COG3442			0.230	0.193 3.898			Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 Predicted glutamine amidotransferase
LBUL_1944	COG0714	2.021	2.121		3.090	0.449	0.488	MoxR-like ATPase
LBUL_1950 LBUL_1954	COG2232 ComFC	0.368	0.393	2.979	5.512		7.197	Predicted ATP-dependent carboligase related to biotin carboxylase Predicted amidophosphoribosyltransferase
LBUL_1955	COG1646	0.000		2.979				Predicted phosphate-binding protein with TIM-barrel fold
LBUL_1959 LBUL_1961	RarD Cof		0.206		0.417 0.424			Predicted permease Predicted hydrolase of the HAD superfamily
LBUL_1961 LBUL_1962 LBUL_1996	COG4814	0.328	0.310					Uncharacterized protein with an alpha/beta hydrolase fold
LBUL_1996 LBUL_1999	Med SPS1	0.328			0.420 0.359			Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein Serine/threonine protein kinase
LBUL_2001	Med	0.484				0.0		Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein
LBUL_2002 LBUL_2003	Med COG3845			2.851	0.308	0.330		Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein ABC-type uncharacterized transport systems ATPase components
LBUL_2004	COG4603		0.416	3.269				ABC-type uncharacterized transport system permease component
LBUL_2005 LBUL_2017	COG1079 COG0802	0.300	0.241	3.352	0.132	0.169		Uncharacterized ABC-type transport system permease component Predicted ATPase or kinase
LBUL_2020	COG1123					4.257		ATPase components of various ABC-type transport systems contain duplicated ATPase

Incognic ion transport and metabolism ABC-type cobalit transport system permeases component CD LBUL 0123 NatA 0.5 0.32 LBUL 0124 NatA 0.5 0.47 6.179 NatA NatC-type cobalit transport system permeases component CD LBUL 0126 NatA 0.22 0.257 6.179 NatC-type phosphate/hosphonate transport system permeases LBUL 0176 PhrD 0.438 ABC-type phosphate/hosphonate transport system permease LBUL 0177 COSG388 0.247 0.369 0.438 LBUL 0178 COSG388 0.247 0.369 0.488 LBUL 0178 COSG388 0.245 0.349 0.489 LBUL 0178 COSG388 0.245 0.349 0.489 LBUL 0216 AbC-D 0.348 0.448 0.448 LBUL 0217 Tauk 0.141 0.348 0.448 LBUL 0226 AbC-D 0.327 0.288 0.215 LBUL 0226 JAUL 0226 JAUL 0226 JAUL 0226 JAUL 0226 JAUL 0226 JAUL 0226	smic component s component as component as component ariplasmic components Pase component asse component smic component
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LBUL_0884 Cb/Q 2.167 0.322 ABC-type colabil transport system permease component Cb LBUL_0885 Mg/E 0.355 Mg/E (contain CSA) (component Cb LBUL_0889 AbcC 0.408 4.992 ABC-type colabil transport system ATPase component LBUL_1070 Cb/O 7.779 ABC-type colabil transport system ATPase component LBUL_1107 Cb/O 7.598 ABC-type colabil transport system ATPase component LBUL_1187 TrAA 0.432 7.761 0.290 Cation transport system ATPase component LBUL_1187 ZinA 0.432 2.770 0.290 Cation transport system protein B LBUL_1187 FeeB 0.256 0.499 2.176 Fe2-t transport system protein B LBUL_1187 FeeB 0.188 0.137 4.149 Fe2-t transport system protein B LBUL_1181 FeeB 0.188 0.137 4.248 ABC-type notail in transport system Protein B LBUL_1212 TauC 4.248 ABC-type notail in transport system Protein B Fe2-transport system Protein B LBUL_1212 Cystantor	
LBUL_0989 AbcC 0.408 4.92 ABC-type relation transport system ATPase component LBUL_1070 CbiO 7.779 ABC-type robalt transport system ATPase component LBUL_1070 CbiO 7.579 ABC-type robalt transport system ATPase component LBUL_1187 TrA 0.432 7.961 0.200 Cation transport system ATPase component LBUL_1187 ZnA 0.432 0.228 7.961 0.200 Cation transport system protein B LBUL_1187 Fee8 0.256 0.499 2.176 Fe24- transport system protein B LBUL_1183 Fee8 0.186 0.137 4.149 Fe24- transport system protein B LBUL_1213 AbcC 2.998 ABC-type colatininin (PAs-indicing Intrasport system protein B LBUL_1214 TauC 2.998 ABC-type colatinining Protein Signer protein Signer protein B LBUL_1214 TauC 4.248 ABC-type colatinining Protein Signer protein Sign	iQ and related transporter
LBUL_11070 CbiO 7.598 ABC-type collabilitransport system ATPase component LBUL_1137 TriA 0.432 0.270 0.990 Cation transport system protein B LBUL_1157 ZinA 0.432 0.228 7.961 0.90 Cation transport system protein B LBUL_1157 FeeB 0.256 0.499 2.176 Fee2 + transport system protein B LBUL_1138 Fee3 0.188 0.137 2.146 Fee2+ transport system protein B LBUL_1131 Fee3 0.188 0.137 2.149 Fee2+ transport system protein B LBUL_1213 AbcC 2.998 ABC-type notation transport system Protein B Fee3- transport system Protein B LBUL_1214 TauC 4.248 ABC-type notation transport system protein B Educt system protein B LBUL_122C CyceD 0.424 0.472 0.331 CyceTransport system protein System protein System protein Submark 11 LBUL_122C CyceD 0.341 CyceTransport system Protein	
LBUL_1138 TrkA 2.770 Predicted flavorate in involved in K+ transport LBUL_1157 ZnA 0.432 0.328 7.961 0.290 Calion transport ATPase LBUL_1159 FeoB 0.256 0.499 2.176 Feo2 + transport system protein B LBUL_1124 FeoB 0.188 0.137 4.149 Feo2 + transport system protein B LBUL_124 FeoC 62.155 ABC-type collamin/Fe3+siderophores transport systems reasons transport system Fease component LBUL_1214 TauC 2.998 ABC-type collamin/Fe3+siderophores transport system system prevalue LBUL_1214 TauC 4.248 ABC-type collamin/Fe3+siderophorate transport system prevalue LBUL_1225 CycD 0.341 Collar transport system API and transport system prevalue LBUL_1225 COS4100 6.367 2.770 13.996 4.313 Cystathiorine beta-tyste anily protein involved in almity notein involved in almity transport moved in alminy transport moved in almity transport moved in almity transport	
LBUL_1157 ZnA 0.432 0.228 7.961 0.290 Cation transport ATPase LBUL_1169 FeoB 0.256 0.499 2.176 Feo2+ transport system protein B LBUL_1193 FeoB 0.256 0.499 2.176 Feo2+ transport system protein B LBUL_1193 Feo2 62.155 ABC-type cotaliamin Feo3+-siderophores transport systems of the system ATPase component LBUL_1217 AbcC 2.999 4.248 ABC-type redialing transport system ATPase component LBUL_1220 CzcD 0.424 0.472 0.331 Co2/C04 efflux system component LBUL_1225 CycN 0.341 Co2/C04 efflux system component Co2/C04 efflux system component LBUL_1226 Co2H00 6.367 2.770 13.396 4.313 Cystem-toine bate-tysee annity protein involved in aluminutor	
LBUL_1193 FeeB 0.188 0.137 4.149 Fe2+ transport system protein B LBUL_1214 ApcC 62.155 ABC-type ontains/iFe3+-aiderophores transport systems or transport systems or transport system ATP ase component LBUL_1213 AbcC 2.998 ABC-type nutates/utransport system ATP ase component LBUL_1210 AbcC 2.424 A272 0.331 LBUL_1225 CysN 0.341 ADC-type nutates/utransport system protein B LBUL_1225 COCH10 6.367 2.770 13.936 4.313	
LBUL_1213 AbcC 2.99 ABC-type mitratios/lifenation transport system ATPase component LBUL_1214 TauC 4.248 ABC-type mitratios/lifenate/bicarbonate transport system per LBUL_1220 CzcD 0.424 0.472 0.331 LBUL_1225 CysN 0.341 CorZn/Cd efflux system component LBUL_1226 COG410 6.367 2.770 13.996 4.313	
LBUL_1214 TauC 4.248 ABC-type intradisultonate/bicarbonate transport system per LBUL_1220 LBUL_1225 CyzD 0.424 0.472 0.331 Co/2nC/Id efflux system component Co/2nC/Id efflux system component LBUL_1225 CysD 0.341 GTPase - Subtraite transport system per LBUL_1236 COG410 6.367 2.770 13.996 4.313 Cystathiorine beta-types a mily protein involved in alumitority	ATPase components
LBUL_1225 CysN 0.341 GTPase - Sulfate adenylate transferase subunit 1 LBUL_1236 COG4100 6.367 2.770 13.936 4.313 Cystathionine beta-lyase family protein involved in aluminum	mease component
LBUL_1236 COG4100 6.367 2.770 13.936 4.313 Cystathionine beta-lyase family protein involved in aluminun LBUL_1241 CvsN 3.477 GTDate - Sulfata advandate transforme average and the second statement of	
COLLET. OVER OUTLABE OUTLABE ADDITION OF THE OUTLABE A	1 resistance
LBUL_1241 CysN 3.477 GTPase - Sulfate adenylate transferase subunit 1 LBUL_1261 CbiO 0.137 ABC-type cobalt transport system ATPase component LBUL_1255 CysC 0.366 Adenylysulfate kinase and related kinase	
LBUL_1286 CbiO 0.326 ABC-type cobalt transport system ATPase component	
LBUL_1291 DppB 0.330 0.229 2.883 0.179 ABC-type dipeptide/oligopeptide/nickel transport systems per LBUL_1292 DppD 0.324 0.262 2.588 0.193 ABC-type dipeptide/oligopeptide/nickel transport system AT	Pase component
LBUL 1293 DppD 0.282 0.278 2.768 0.148 ABC-type dipeptide/oligopeptide/nickel transport system AT LBUL_1327 ArsC 2.498 0.293 0.494 Arsenate reductase and related protein glutaredoxin family	Pase component
LBUL_1372 PspE 0.337 0.425 2.875 Rhodanese-related sulfurtransferase	
LBUL_1466 TrkA 0.500 Predicted flavoprotein involved in K+ transport LBUL_1562 ZnuC 0.212 0.162 ABC-type Mr/Zn transport systems ATPase component	
LBUL_1588 NatA 0.442 ABC-type Na+ transport system ATPase component LBUL_1652 CynX 2.471 Cyanate permease	
LBUL_1658 NarK 2.845 2.903 0.017 0.058 Nitrate/nitrite transporter	
LBUL_1693 DppF 7.298 ABC-type dipeptide/oligopeptide/nickel transport system ATI LBUL_1700 COG3638 0.272 0.323 ABC-type phosphate/phosphonate transport system ATPasr	
LBUL_1707 AsIA 4.510 Arylsulfatase A	
LBUL_1810 TrkA 2.745 4.943 K+ transport systems NAD-binding component	
LBUL_1861 FeoB 0.267 0.170 Fe2+ transport system protein B LBUL_1870 COG3709 0.429 Uncharacterized component of phosphonate metabolism	
LBUL_1897 FeoB 0.284 Fe2+ transport system protein B	
LBUL_1929 CitT 0.030 0.274 Di- and tricarboxylate transporter	
LBUL_2003 COG3638 2.851 ABC-type phosphate/phosphonate transport system ATPase LBUL_2020 AbcC 4.257 ABC-type metal ion transport system ATPase component	Pase component
LBUL_2021 SUL1 0.077 Sultate permease and related transporter (MFS superfamily, LBUL_2036 FeoB 0.267 6.275 Fe2+ transport system protein B	Pase component
	Pase component
Intracellular trafficking and secretion 0.404 8.677 0.297 Tip pilus assembly protein FimV LBUL_017 FinJ 6.229 Muramidase (flagellum-specific)	Pase component
LBUL_0197 FlgJ 6.229 Muramidase (flagellum-specific) LBUL_0370 SecY 0.337 0.313 2.524 2.739 2.994 Preprotein translocase subunit SecY	Pase component
LBUL 0412 FlgJ 2.460 Muramidase (flagellum-specific)	Pase component
LBUL_0559 ClpP 0.411 0.444 Protease subunit of ATP-dependent Clp protease	Pase component
LBUL_0610 PulE 7.998 18.355 Type II secretory pathway ATPase PulE/Tfp pilus assembly	Pase component e component)

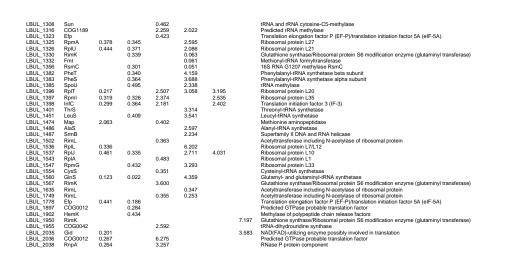
LBUL_0612	ComGC PilM		0.445		0.459			Competence protein ComGC
LBUL_0646 LBUL_0663	PilM		0.383		3.612			Tfp pilus assembly protein ATPase PilM Tfp pilus assembly protein ATPase PilM
LBUL_0676	PilM		0.434					Tfp pilus assembly protein ATPase PilM
LBUL_0929	LspA	3.422		0.481	0.021	0.269		Lipoprotein signal peptidase
LBUL_1069 LBUL_1070	YidC VirB11			7.779 7.598				Preprotein translocase subunit YidC Type IV secretory pathway VirB11 protein involved in flagella biosynthesis
LBUL_1124	LepB			0.337				Signal peptidase I
LBUL 1204	TadG			62.155				FIp pilus assembly protein TadG
LBUL_1226 LBUL_1282	SEC63		2.857		2.867			Preprotein translocase subunit Sec63
LBUL_1282 LBUL_1285	Ffh FtsY		0.358 0.366		4.280			Signal recognition particle GTPase Signal recognition particle GTPase
LBUL 1286	COG5391		0.326					Phox homology (PX) domain protein
LBUL_1296 LBUL_1417	SecA			0.290				Phox homology (PX) domain protein Preprotein translocase subunit SecA (ATPase RNA helicase)
LBUL_1417	EcsB		0.458					Predicted ABC-type exoprotein transport system permease component
LBUL_1491	YajC SecE		0.464		3.319 2.743			Preprotein translocase subunit YajC Preprotein translocase subunit SecE
LBUL_1546 LBUL_1601	FlaH		0.404	2.872	2.743			Predicted ATPase involved in biogenesis of flagella
LBUL_1756	FlhB				4.797			Flagellar biosynthesis pathway component FlhB
LBUL_1757	SecD	0.198		4.153				Preprotein translocase subunit SecD
LBUL_1900	CpaE		0.321	2.324				Flp pilus assembly protein ATPase CpaE
LBUL_2037	YidC			3.726				Preprotein translocase subunit YidC
Lipid metabolis	sm							
LBUL_0099	COG1924	0.363	0.354		2.571			Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)
LBUL_0106	PIsC			3.130	0.000			1-acyl-sn-glycerol-3-phosphate acyltransferase
LBUL_0150 LBUL_0161	Cls AccC		0.475		2.993			Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthase Biotin carboxylase
BUL 0165	Acco		0.138					Esterase/linase
LBUL_0165 LBUL_0303	IspD		0.392		2.057		0.432	4-diphosphocytidyl-2-methyl-D-erithritol synthase
LBUL_0419	LCB5				2.183			Sphingosine kinase
LBUL_0433	ldi IonD		0.448		5.087	2.654		Isopentenyldiphosphate isomerase
LBUL_0498 LBUL_0500	IspD PldB		0.448		5.087			4-diphosphocytidyl-2-methyl-D-erithritol synthase Lysophospholipase
LBUL_0534	PgsA		0.386					Phosphatidylglycerophosphate synthase
LBUL_0700	TagD		0.332		2.182			Cytidylyltransferase
LBUL_0748	COG1835		0.496					Predicted acyltransferase
LBUL_0804 LBUL_0805	PaaJ HMG1	0.215	0.145 0.386					Acetyl-CoA acetyltransferase Hydroxymethylglutaryl-CoA reductase
LBUL_0805 LBUL_0818	PksG		0.386	0.262	0.200			Hydroxymethylglutaryl-CoA reductase 3-hydroxy-3-methylglutaryl CoA synthase
LBUL_0819	AcpP			0.322	0.405			Acyl carrier protein
LBUL_0820	FabD		0.259	0.188	0.275			(acyl-carrier-protein) S-malonyltransferase
LBUL_0822	FabB		0.322	0.224 0.211	0.222		2.227	3-oxoacyl-(acyl-carrier-protein) synthase
LBUL_0823 LBUL_0824	AccB FabA		0.397	0.211	0.345		2.227	Biotin carboxyl carrier protein 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratase
LBUL_0825	COG4770		0.295	0.132	0.391			Acetyl/propionyl-CoA carboxylase alpha subunit
LBUL_0826	AccD		0.280	0.243	0.281		2.010	Acetyl-CoA carboxylase beta subunit
LBUL_0827	AccA		0.261		0.367			Acetyl-CoA carboxylase alpha subunit
LBUL_0880	ldi	4.334	0.470	0.450				Isopentenyldiphosphate isomerase
LBUL_0904 LBUL_0905	ERG12 MVD1	0.232	0.179 0.157	0.456				Mevalonate kinase Mevalonate pyrophosphate decarboxylase
LBUL_0906	ERG12	0.156	0.171		3.061			Mevalonate brophosphate decarboxylase
LBUL_0918	Aes				4.671			Esterase/lipase
LBUL_0932	AccC	2.215			0.059	0.369		Biotin carboxylase
LBUL_1067 LBUL_1189	MmsB FodB	0.410		0.412	3.027			3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenase
LBUL_1189	FadB CdsA		0.454	0.412				3-hydroxyacyl-CoA dehydrogenase CDP-diglyceride synthetase
LBUL 1256	PIsC		0.237		14.967			1-acyl-sn-glycerol-3-phosphate acyltransferase
LBUL_1294 LBUL_1295	AcpP			0.288				Acyl carrier protein
LBUL_1295	PlsX			0.416				Fatty acid/phospholipid biosynthesis enzyme
LBUL_1330	AccC		0.339		0.063	0.303		Biotin carboxylase
LBUL_1340 LBUL_1506	AccC FatA			0.298	0.105	0.303		Biotin carboxylase Acyl-ACP thioesterase
LBUL_1549	PldB	2.842		0.200				Lysophospholipase
LBUL_1567	AccC			3.600				Biotin carboxylase
LBUL_1607	FabA		0.438		4.364		2.378	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratase
LBUL_1630 LBUL_1751	ERG12 Aes			0.381 0.156	0.121			Mevalonate kinase Esterase/lipase
LBUL_1762	PldB			5.544				Lysophospholipase
LBUL_1775 LBUL_1800	PldB			0.408	2.682			Lysophospholipase
LBUL_1800	TagD	0.210	0.119					Cytidylyltransferase
LBUL_1950	AccC						7.197	Biotin carboxylase
Nucleotide trar	sport and me	tabolism						
LBUL_0079	NrdA					0.271	0.172	Ribonucleotide reductase alpha subunit
LBUL_0156	PrsA	2.071	0.475	0.441		0.312	0.433	Phosphoribosylpyrophosphate synthetase
LBUL_0161 LBUL_0172	CarB COG3613		0.475 0.262					Carbamoylphosphate synthase large subunit (split gene in MJ) Nucleoside 2-deoxyribosyltransferase
LBUL_0172	CarB		0.202	0.350				Carbamoylphosphate synthase large subunit (split gene in MJ)
LBUL_0185	NrdD				0.356		0.272	Oxygen-sensitive ribonucleoside-triphosphate reductase
LBUL_0212	COG1051 GuaB	0.004	0.274		0.050			ADP-ribose pyrophosphatase
LBUL_0246			0.285		0.053	0.045		IMP dehydrogenase/GMP reductase Xanthine/uracil permease
BUI 0249		0.221						
LBUL_0249 LBUL_0250	UraA Apt	0.221		2.210	0.308	0.215 0.211		
LBUL_0249 LBUL_0250 LBUL_0251	UraA Apt GuaB	2.639		2.210	0.308	0.215 0.211 0.290	0.458	Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252	UraA Apt GuaB GuaA	2.639 2.315		2.210	0.308	0.211	0.458	Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein IMP dehydrogenae/GMP reductase GMP synthasen PP-ATPase domain/subunit
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264	UraA Apt GuaB GuaA Udp	2.639	0.186	2.210	0.308	0.211	0.458	Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282	UraA Apt GuaB GuaA	2.639 2.315		2.210	5.175	0.211	0.458	Adenine'guanine phosphonibosyltransferase and related PRPP-binding protein IMP dehydrogenase'GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase ADP-ribose pyrophosphatase Deoxycridivited deaminase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0294 LBUL_0302	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt	2.639 2.315	0.186 2.411 0.331	2.210		0.211	0.458	Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein IMP dehydrogenaes/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphory/ase DP-ribose pynohosphatase Deoxycjtd/ytat deaminase Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0284 LBUL_0294 LBUL_0302 LBUL_0306	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt	2.639 2.315	0.186 2.411 0.331 0.328	2.210		0.211	0.458	Adenine/guanine phosphoribosyltransforses and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase ADP-ribose pyrophosphatase Deoxycytidytate deaminase Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein dGTP triphosphorylardise
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0294 LBUL_0302 LBUL_0306 LBUL_0327	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461		5.175	0.211	0.458	Adenine/guanine phosphonibosyltransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphortyase Adenine/guanise Adenine/guanie phosphortbosyltransferase and related PRPP-binding protein dGTP inphosphortydrolase Dirydrocratte dehydrogenase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0302 LBUL_0306 LBUL_0327 LBUL_0371	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD Adk	2.639 2.315	0.186 2.411 0.331 0.328	2.210 2.217		0.211	0.458	Adenine/guanine phosphoribosyltransforase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorydase ADP-ribose pyrophosphatase Deoxycytidytate deaminase Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein dGTP triphosphorydrolase Dihydroorotate dehydrogenase Adernitet kinase and related kinase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0284 LBUL_0294 LBUL_0302 LBUL_0306 LBUL_0327 LBUL_0371 LBUL_0433 LBUL_0457	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461		5.175 4.203 6.995	0.211 0.290	0.458	Adenine/guanine phosphonibosyltransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphortyase Adenine/guanise Adenine/guanie phosphortbosyltransferase and related PRPP-binding protein dGTP inphosphortydrolase Dirydrocratte dehydrogenase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0282 LBUL_0300 LBUL_0300 LBUL_0327 LBUL_03371 LBUL_0433 LBUL_0457 LBUL_0463	UraA Apt GuaB GuaA Udp COG1051 COMEB Apt Dgt PyrD Adk COG1051 Udk GppA	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461 0.329		5.175	0.211 0.290 2.654	0.458	Adenine/guanine phosphonibosyttransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Undine phosphonylase ADP-ribose pyrophosphatase Deoxycytdylate deaminase Adenine/guanine phosphonibosyttransferase and related PRPP-binding protein Adenine/guanine phosphonibosyttransferase Adenine/guanine phosphonibosyttransferase Adenine/guanine phosphonibosyttransferase Adenine/guanine phosphonibosyttransferase Adenine/guanine phosphonibosyttransferase Adenine/guanine phosphonibosyttransferase Adenine/guani
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0251 LBUL_0254 LBUL_0264 LBUL_0282 LBUL_0284 LBUL_0302 LBUL_0302 LBUL_03071 LBUL_0453 LBUL_0453 LBUL_0463 LBUL_0473	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD Adk COG1051 Udk GppA URH1	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461 0.329		5.175 4.203 6.995 3.773	0.211 0.290	0.458	Adenine/guanine phosphoribosyltransforses and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase ADP-ribose pyrophosphatase Deoxycytidytate deaminase Adenine/guanine phosphoribosyltransferase and related PRPP-binding protein dGTP triphosphorylabidiase Dihydroorotate dehydrogenase Adenytate kinase and related kinase ADP-ribose pyrophosphatase Uridine kinase Exopolyphosphatase Exopolyphosphatase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0282 LBUL_0282 LBUL_0282 LBUL_0327 LBUL_0327 LBUL_0327 LBUL_0327 LBUL_0323 LBUL_0433 LBUL_0463 LBUL_0463	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD Adk COG1051 Udk GppA URH1 Hpt	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461 0.329 0.368		5.175 4.203 6.995 3.773 0.202	0.211 0.290 2.654	0.458	Adenine/guanine phosphoriboxytransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase ADP-ribose pyrophosphatase Dexxysrtightaide deaminase Adenine/guanine phosphoriboxytransferase and related PRPP-binding protein dGTP inphosphoriphosphatase Dihydroproteite dehydrogenae Dihydroproteite dehydrogenae Data DP-ribose pyrophosphatase Uridine kinase Exxpolythosphatase Inosine-uridine nucleoside N-ribohydrolase Hipoxanthine-guanine phosphoriboxytransferase
LBUL_0249 LBUL_0250 LBUL_0251 LBUL_0252 LBUL_0264 LBUL_0284 LBUL_0284 LBUL_0284 LBUL_0302 LBUL_0302 LBUL_0313 LBUL_0433 LBUL_0463 LBUL_0463 LBUL_0483 LBUL_0483 LBUL_0632 LBUL_0646	UraA Apt GuaB GuaA Udp COG1051 ComEB Apt Dgt PyrD Adk COG1051 Udk GppA URH1 Hpt Tdk GppA	2.639 2.315 0.252	0.186 2.411 0.331 0.328 0.461 0.329		5.175 4.203 6.995 3.773 0.202 4.287 0.459	0.211 0.290 2.654	0.458	Adenine'guanine' phosphoribosyttransferase and related PRPP-binding protein IMP dehydrogenase/GMP reductase GMP synthase PP-ATPase domain/subunit Uridine phosphorylase ADP-ribose pyrophosphatase Deoxyorigtiyate deaminase Adenine'guanine phosphoribosyttransferase and related PRPP-binding protein dGTP inphosphoryladolase Dihydroorotate dehydrogenase Adening'ate Xinase and related Kinase Dihydroorotate dehydrogenase Adening kinase Exopolyhosphatase Inosine-uridine nucleoside N-ribohydrolase Inosine-uridine nucleoside N-ribohydrolase Tyymidine kinase Exopolyhosphatase
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Lab. 2:10 Apr. 2:10 <t< td=""><td>LBUL_1129</td><td>COG1051 Cdd</td><td>0.258</td><td>0.461</td><td></td><td></td><td></td><td></td><td>ADP-ribose pyrophosphatase Cytidine deaminase</td></t<>	LBUL_1129	COG1051 Cdd	0.258	0.461					ADP-ribose pyrophosphatase Cytidine deaminase
Link 1:20 Link 1:20 Lin	LBUL_1213	Gmk		0.401	2.998				Guanylate kinase
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Lal. 13 Part 0.42 0.03 2.10 ACAI static manage and the right price and price a	LBUL_1272			0.339			0.418		5-nucleotidase/2' 3-cyclic phosphodiesterase and related esterase Phosphoribosylamine-divcine lidase
Link 1. 193 Public Project ProjectProject Project Project Proj	LBUL_1331	PurH				0.047		2.100	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)
Lab. 1.30 Put 0.47	LBUL_1332			0.224				2 1 1 6	Folate-dependent phosphoribosylglycinamide formyltransferase PurN
Lab. 130 Publ. 130 <td< td=""><td>LBUL_1334</td><td></td><td></td><td>0.334</td><td></td><td>0.045</td><td></td><td>2.110</td><td>Glutamine phosphoribosylpyrophosphate amidotransferase</td></td<>	LBUL_1334			0.334		0.045		2.110	Glutamine phosphoribosylpyrophosphate amidotransferase
Lul. 130 Part Products of	LBUL_1335	PurL		0.453		0.073		2.397	Phosphoribosylformylglycinamidine (FGAM) synthase synthetase domain
LBL 138 Pure Productional production of production of the ADM synthesis (PLAM synthesis) LBL 138 Pure Production of production of production of the ADM synthesis (PLAM synthesis) LBL 139 Pure Production of production of the ADM synthesis (PLAM synthesis) LBL 139 Pure Production of production of the ADM synthesis (PLAM synthesis) LBL 140 LBL 140 LBL 141 LBL 140 LBL 140 LBL 140 LBL 1400 LBL 1	LBUL_1336			0.442				2 216	Phosphoribosylformylglycinamidine (FGAM) synthase glutamine amidotransferase domain Phosphoribosylformylglycinamidine (FGAM) synthase PurS component
Lab. 1.50 Prof. 0.30 Prophology information calcular (all by CAR) synthesis) Lab. 1.50 Apr. 0.30 Apr. Description of the synthesis of the PT Imply synthesis Lab. 1.50 Apr. 0.30 Apr. Description of the synthesis of the PT Imply synthesis Lab. 1.50 Apr. 0.30 Apr. Description of the synthesis of the PT Imply synthesis Lab. 1.50 Apr. 0.30 Description of the synthesis of the PT Imply synthesis Lab. 1.50 Apr. 0.30 Apr. Description of the PT Imply synthesis Lab. 1.50 Apr. 0.30 Apr. Description of the PT Imply synthesis Lab. 1.50 Col 1.50 0.30 Apr. Description of the PT Imply synthesis Lab. 1.50 Col 1.50 1.50 Apr. Description of the PT Imply synthesis Lab. 1.50 Col 1.50 1.50 Apr. Description of the PT Imply synthesis Lab. 1.50 Col 1.50 1.50 Apr. Description of the PT Imply synthesis Lab. 1.50 Col 1.50 1.50 Apr. Description of the PT Imply sy	LBUL_1338	PurC				0.034		2.177	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
Lan L. 19 Part Production Sympositic Symposit Sympositic Sympositic Sy	LBUL_1339	PurB				0.165	0.332		Adenylosuccinate lyase
Link 19 Add Sec 1 Add Sec 1 Add Sec 1 Add Sec 1 Link 19 Add Sec 1 Se	LBUL_1340					0.105	0.303		Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase) Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase
Link 1, 40 Part of the interval of the	LBUL_1358				2.801	0.150	0.200		Adenosine deaminase
Link Link <thlink< th=""> Link Link <thl< td=""><td>LBUL_1405</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></thl<></thlink<>	LBUL_1405								
Lub, 1-10 Lub, 1-10 <thlub, 1-10<="" th=""> <thlub, 1-10<="" th=""> <thl< td=""><td>LBUL_1419</td><td></td><td></td><td></td><td>0.375</td><td></td><td></td><td>2 350</td><td>Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolase</td></thl<></thlub,></thlub,>	LBUL_1419				0.375			2 350	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolase
Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Address and status and related status Link L, Pier Loop Construction Construction Construction Link L, Pier Loop Constru	LBUL_1423	PyrE							Orotate phosphoribosyltransferase
Lub, 1-90 COG177 COG177 0.349 0.449 Analysis projections (photophase projections (PAC) photophase (PAC	LBUL_1426	Adk		0.364					
Laku, Leis Code of SA J.36 All Actions pryphosphates All Actions pryphosphates Laku, Teo Code of SA J.36 S.36 All Actions pryphosphates All Actions pryphosphates Laku, Teo Code of SA J.36 S.36 S.36 All Actions pryphosphates All Actions pryphosphates Laku, Teo Prestard Productions produc	LBUL_1471	COG0127			0.212			0.314	5 -nucleotidase/2' 3 -cyclic phosphodiesterase and related esterase Xanthosine triphosphate pyrophosphatase
Link 1, 190 COC 0008 US 2.003 Predict multiplication inclusion inclusin inclusin inclusion inclusion inclusin inclusion inclusion inclu	LBUL_1555	COG1051				3.346			ADP-ribose pyrophosphatase
Link L., Tr. OCSU13 0.18 3.98 Hadra (16.5) 2-600 (Hospitalized) Link L., Tr. OCSU13 0.18 0.28 0.27 0.26 Link L., Too Pork 0.28 0.27 0.27 0.26 0.27 0.28 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 <td< td=""><td>LBUL_1567</td><td></td><td></td><td></td><td>3.600</td><td></td><td></td><td></td><td>Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)</td></td<>	LBUL_1567				3.600				Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)
Laur, Hang, Laur, Hang, Park, P	LBUL_1606	COG4088		0 158					Predicted nucleotide kinase Nucleoside 2-deoxyribosyltransferase
LBLU, 190 Prof. USA 1.56 Add synthetic control of synthetic synth	LBUL_1870	Gmk		0.429					Guanylate kinase
LBul, 199 PyD 2.928 Dip DipAdvocation delyndrymmes LBU, 2016 COG 14/3 0.100 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 2017 COG 14/3 0.100 Dipadvocation delyndrymmes Typen idee anting probate sytically participantic cortain C-terminal PDZ domain LBU, 1018 DyD 2.744 2.477 Typen idee anting probate sytically participantic cortain C-terminal PDZ domain LBU, 1018 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 1018 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 1017 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 2017 CydD 0.750 0.700 Dipadvocation delyndrymmes Dipadvocation	LBUL_1930					0.016	0.254		Adenylosuccinate lyase
LBul, 199 PyD 2.928 Dip DipAdvocation delyndrymmes LBU, 2016 COG 14/3 0.100 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 2017 COG 14/3 0.100 Dipadvocation delyndrymmes Typen idee anting probate sytically participantic cortain C-terminal PDZ domain LBU, 1018 DyD 2.744 2.477 Typen idee anting probate sytically participantic cortain C-terminal PDZ domain LBU, 1018 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 1018 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 1017 DyD 0.750 0.750 Dipadvocation delyndrymmes Dipadvocation delyndrymmes LBU, 2017 CydD 0.750 0.700 Dipadvocation delyndrymmes Dipadvocation	LBUL_1950		0.368	0 393	2 979	5 512		7.197	Carbamoylphosphate synthase large subunit (split gene in MJ) Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase
LBUL_2000 COCI-1420 0.132 0.199 Decknowledge learning of space methods in some in the set of space methods in some in space from involved	LBUL_1955		0.000	0.555		0.012			
LBUL 2010 UBA U	LBUL_2017						0.169		Deoxynucleoside kinase
Partner Partner Partner Partner Partner LBUL_0101 Cyclo 2.794 2.497 Cyclo 2.497 LBUL_0101 Cyclo 2.331 0.347 2.596 Cyclo 2.497 LBUL_0101 Cyclo 0.331 0.347 2.596 Cyclo 2.399 AC-types transport system involved in cyclorbrone to biosynthesis ATPase and permases compore LBUL_0202 Cyclo 0.357 C.201 AC-types transport system involved in cyclorbrone to biosynthesis ATPase and permases compore LBUL_0202 Cyclo 0.347 6.844 0.77 Cyclo 2.309 AC-type transport system involved in cyclorbrone bo biosynthesis ATPase and permases compore LBUL_0202 Cyclo 0.347 6.844 0.77 Cyclo 0.347 6.844 0.77 Cyclo System involved in cyclorbrone bo biosynthesis ATPase and permases compore LBUL_0202 Cyclo 0.357 0.257 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 0.258 <td< td=""><td>LBUL_2018 LBUL_2021</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>Deoxynucieoside kinase Xanthine/uracil permease</td></td<>	LBUL_2018 LBUL_2021								Deoxynucieoside kinase Xanthine/uracil permease
LBUL, 019 MpX 2.784 -0.475 Type-in-like setting profession (***) capacity professio			n nrot-l- ·	1000101	0.070.005				
LBUL, 055 CydD 2.784 ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinors bot biosynthesis ATPase and permase componer ALC-type transport system involved in cydCrinore bot biosynthesis ATPas	LBUL_0118	DegQ	n, protein tu	umover, cha	perones			0.415	Trypsin-like serine protease typically periplasmic contain C-terminal PDZ domain
LBLL_045 Cytu 1.57.9 ABC-type alfast transport system permasse component LBUL_0770 Cytu 0.338 0.55 0.199 ABC-type alfast transport system monode in cytochrome bd biosynthesis AFPase and permasse component LBUL_0250 CytuC 0.388 0.055 0.199 ABC-type transport system involved in cytochrome bd biosynthesis AFPase and permasse component LBUL_0250 CytuC 0.390 0.376 0.388 0.075 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.388 0.076 0.378 0.388 0.076 0.378 0.388 0.368 0.471 0.486 0.471 0.486 0.471 0.486 0.471 0.486 0.471 0.486 0.471 0.486 0.471 0.486 0.471 0.486 0.471 <td< td=""><td>LBUL_0129</td><td>CydD</td><td></td><td>2.794</td><td></td><td>0.407</td><td></td><td></td><td>ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components</td></td<>	LBUL_0129	CydD		2.794		0.407			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBLL_0177 Cyc0 0.31 0.37 2.595 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0203 Cyc0 2.013 1.59 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0204 Cyc0 3.705 3.705 3.705 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0204 Cyc0 0.337 0.268 0.077 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0204 Cyc0 0.337 0.288 0.087 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0204 Cyc0 0.337 0.288 0.087 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0204 Cyc0 0.330 0.371 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0205 Cyc0 0.330 0.371 ABC-ype transport system invoked in cyclotione do biosynthesia ATPase and permease component LBL_0205 Cyc0 0.331 0.471 ABC-ype transport system invoked	LBUL_0136	ritpX CvsU			5.749	2.487			Zn-dependent protease with chaperone function ABC-type sulfate transport system permease component
LBLU_0716 Qu-U 0.183	LBUL_0177	CydD	0.331	0.347					ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_023 CydC Components Components LBUL_0241 COS4870	LBUL_0179	CysU	0.153	0.186				3.599	ABC-type sulfate transport system permease component
LBUL 2033 Cycl 2.013 ABC-type transport system involved in cyclachrome bd biosynthesis ATPase and permease component LBUL 2044 ABC-type transport system involved in cyclachrome bd biosynthesis ATPase and permease component LBUL 2044 ABC-type transport system involved in cyclachrome bd biosynthesis ATPase and permease component ABC-type transport system involved in cyclachrome bd biosynthesis ATPase and permease component ABC-type transport system involved in cyclachrome bd biosynthesis ATPase and permease component ABC-type transport system involved in cyclachrome bd biosynthesis A	LBUL_0216	CydC	0.386	0.055		0.159			
LBUL_D280 CvdD	LBUL_0238	CydC				2.013			
LBUL, 204 ION Constraints 0.380 0.47 Cynetic probase LBUL, 204 INP 0.380 0.37 6.84 0.17 Machine Lange Constraints Machine L	_								components
LBUL_0284 IbA 0.210 0.447 0.448 0.447 0.448 0.447 0.448 0.447 0.448 0.447 0.448 0.447 0.448 0.441 0.441 0.441 0.441 0.441 0.441 0.441 0.441 0.444 0.441 0.444 <		CydD COG4870				3.705	0.308	0 479	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0282 CydD 0.37 6.884 ABC-type transport system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0323 CydD 0.33 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0330 CydD 0.33 ATPase with chaperona activity ATP-braining suburi ATPase with chaperona activity ATP-braining suburi LBUL_0351 CydD 0.33 ATPase with chaperona activity ATP-braining suburi ATPase with chaperona activity ATP-braining suburi LBUL_0351 CydD 0.33 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0550 CydD 0.333 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0550 CydD 0.423 0.424 0.455 Pactical ATP-dependent in protease LBUL_0550 CydD 0.442 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0550 CydD 0.442 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer LBUL_0550 CydD 0.442 Carter of the system involved in cytochrome bd borymhesis ATPase and permases componer ABC-type tr	LBUL_0243				0.210	0.443	0.550		Molecular chaperone (small heat shock protein)
LBUL_0283 C/sU 0.357 0.268 0.065 ABC-type sultate transport system promase component LBUL_0283 C/sD 0.331 3.118 ATPase with chaperona activity ATP-brinding suburit LBUL_0510 C/sD 0.331 ATPase with chaperona activity ATP-brinding suburit LBUL_0516 GR 0.331 ATPase with chaperona activity ATP-brinding suburit LBUL_0516 MCA 0.451 0.471 Negative regulator of genetic component LBUL_0516 MCA 0.451 0.471 Negative regulator of genetic component LBUL_0526 C/pD 2.433 0.43 0.55 MCA LBUL_0526 C/pD 2.433 0.43 0.455 MCA LBUL_0526 C/pD 0.411 0.444 MCA Protesse suburit of ATP-dependent Cip protesse LBUL_0526 C/pD 0.411 0.438 0.459 MCA MCA LBUL_0526 C/pD 0.411 0.438 0.459 MCA MCA LBUL_0526 C/pD 0.433 0.450 MCA	LBUL_0256	CydD			6.884				ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0383 CPA 3.118 ATBase with chaperone activity ATP-binding subunit LBUL_0444 CydD 0.337 ATBase with chaperone activity ATP-binding subunit LBUL_0451 Gwd 0.337 ATBase with chaperone activity ATP-binding subunit LBUL_0515 MecA 0.451 0.471 ATBase with chaperone activity ATP-binding subunit LBUL_0515 MecA 0.451 0.471 ATBase with chaperone activity ATP-binding subunit LBUL_0515 Grad ATBase with chaperone activity ATP-binding subunit Chaperone activity ATP-binding subunit LBUL_0515 Grad ATBase with chaperone activity ATP-binding subunit Chaperone activity ATP-binding subunit LBUL_0525 GrAP 4.318 0.433 0.438 Chaperone activity ATP-binding subunit LBUL_0525 GrAP 4.444 - ABC-type transport system involved in cytochrome bi biosynthesis ATPase and permease component LBUL_0526 GrAP 0.443 0.438 2.524 Papotian methonine suboxie motione activication component LBUL_0526 GrAP 0.433 3.012 MacC-type austant transport system involved in cytochrome bi biosynthesis ATPa	LBUL_0262	CydD	0.380	0.268		0.077			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL, 044 CydD 0.33 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 051 GrA 0.37 APTase with hospore activity ATP-induced in adm coslipy LBUL, 051 GrA 0.27 0.471 Secretory Perplayments Zn-dependent perplayments in adm coslipy LBUL, 053 Frak 0.251 0.441 Secretory Perplayments Zn-dependent perplayments in adm coslipy LBUL, 0560 CydD 0.441 0.426 Thoreadom in admicizate Bact Cype transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0570 CydD 0.442 0.368 Perdicate transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0570 CydD 0.448 BC-type suitale transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0560 CydD 0.448 BC-type suitale transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0560 CydD 0.489 0.477 0.591 Perplay and transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0560 CydD 0.363 ABC-type suitale transport	LBUL_0339	ClpA	0.337	0.200		3.118			ATPase with chaperone activity ATP-binding subunit
LBUL_0715 GrAC 0.372 Glutancokin and related protein LBUL_0715 Meck 0.261 3.54 0.471 LBUL_0715 Meck 0.261 3.54 0.267 LBUL_0715 Meck 0.261 3.54 0.267 LBUL_0715 Frag 0.262 0.359 Productare LBUL_0715 Cropp 0.411 0.442 Meck 0.262 LBUL_0715 Cropp 0.442 0.368 Meck Note Schering Proteins Meck LBUL_0715 Cropp 0.442 0.368 Meck Meck <t< td=""><td>LBUL_0445</td><td>CydD</td><td></td><td>0.333</td><td></td><td></td><td></td><td></td><td>ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components</td></t<>	LBUL_0445	CydD		0.333					ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0515 MecA O_451 O_471 Negative regulator of genetic competence sportation and molitily LBUL_0533 Fm	LBUL_0510	ClpA			0.381				
LBUL_033 Pr 0.261 3.543 Secretedperiptamic 7-redependent spring protase insulinase-like LBUL_064 Trad 0.43 0.44 Tradication reductase LBUL_064 Trad 0.44 Tradication reductase Tradication reductase LBUL_0730 Cyclp 0.44 Secretedperiptamic 7-reductase Tradication reductase LBUL_0730 Cyclp 0.44 Secretedperiptamic 7-reductase RBC-type submic value for cyclc/transe biosynthesis ATPase and permease component LBUL_0730 Cyclp 0.442 0.383 3.612 Medication reductase LBUL_0701 Nark 0.240 2.231 ATP-dependent Lon protease Molecular chaperone LBUL_0701 Lon 2.301 ATP-dependent Lon protease Molecular chaperone LBUL_0701 Lon 0.303 2.563 2.01 ABC-type submiced at transport system permease component LBUL_0702 Cyclb 0.333 3.612 Molecular chaperone LBUL_0701 Lon 2.331 ATP-dependent Lon protease ATP-dependent Lon protease LBUL_0701	LBUL 0515	MecA			0.451	0.471			Negative regulator of genetic competence sporulation and motility
LBUL_0648 TxB 0.425 Thirdeoin reductase LBU_0650 CyD 2.433 0.98 ABC-type transpot system involved in cytochrome to biosynthesis ATPase and permease componer LBU_0550 CyD 0.442 0.444 ABC-type transpot system permease component LBU_0550 CyD 0.442 0.444 ABC-type transpot system permease component LBU_0550 CyD 0.425 ABC-type transpot system permease component LBU_0550 KrA 2.231 ABC-type transpot system permease component LBU_0701 LBU_0701 LBU_0701 LBU_0701 LBU_0701 Company LBU_0701 <	LBUL_0531	Ptr		0.261		3.543			Secreted/periplasmic Zn-dependent peptidase insulinase-like
LBU_0550 CydD 2.433 0.243 0.048 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0578 CydD 0.444 0.358 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0678 CydD 0.442 0.358 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0678 KpF 0.240 2.234 Peptide methionine system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0665 Machae 0.433 3.612 Machae chaperone LBU_0665 Machae 0.333 3.612 Machae chaperone LBU_0767 Traft 0.443 0.493 4.189 3.01 LBU_0767 Traft 0.433 3.612 Machae chaperone LBU_0767 Traft 0.433 4.189 3.01 Traft Machae chaperone LBU_0767 CydD 0.216 - - ABC-type transport system permease component LBU_0707 Traft 0.333 - - - </td <td>LBUL_0535</td> <td></td> <td></td> <td></td> <td></td> <td>0.405</td> <td></td> <td>0.359</td> <td></td>	LBUL_0535					0.405		0.359	
LBUL_073 CydD 0.448 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0636 CysU 0.288 ABC-type sulfae transport system permease component LBU_0646 MarA 0.459 Mature transport system permease component LBU_0646 MarA 0.459 Mature transport system permease component LBU_0646 MarA 0.459 Mature transport system permease component LBU_0767 Nark 0.333 3.612 Mature transport system permease component LBU_0767 Trg 0.413 0.439 2.531 ABC-type sulfae transport system permease component LBU_0767 Trg 0.413 0.543 2.521 ABC-type sulfae transport system permease component LBU_0768 CydU 0.216 0.333 4.992 ABC-type transport system involved in cytochrome to biosynthesis ATPase and permease component LBU_0768 CydU 0.430 0.530 5.201 ABC-type transport system involved in cytochrome to biosynthesis ATPase and permease component LBU_0768 CydU 0.430 0.530 5.201 ABC-type transport	LBUL_0548			2,433	0.243				
LBUL_0579 CysU 0.442 0.396 ABC-type sulfate transport system permease component LBU_0605 MsA 2.234 Peptide methicinics sulfaxide reductase LBU_0605 MsA 0.383 3.612 Milecular chagenrine LBU_0705 MpF 0.240 ABC-type sulfate transport system permease component LBU_0705 Transport system permease component ABC-type sulfate transport system permease component LBU_0705 Transport system permease component ABC-type sulfate transport system permease component LBU_0705 Transport system permease component ABC-type sulfate transport system permease component LBU_0705 Transport system involved in cyclotrome bd biosynthesis ATPase and permease component LBU_0805 CycD 0.216 ABC-type transport system involved in cyclotrome bd biosynthesis ATPase and permease component LBU_0805 CycD 0.333 5.201 ABC-type transport system involved in cyclotrome bd biosynthesis ATPase and permease component LBU_0805 CycD 0.350 2.216 ABC-type transport system involved in cyclotrome bd biosynthesis ATPase and permease component LBU_1105 APF 0.350 2.363	LBUL_0559	CipP	0.411						Protease subunit of ATP-dependent Clp protease
LBUL_0580 CysU 0.288 ABC-type sulfate reductase ABC-type sulfate reductase LBUL_0581 HypF 0.240 Hydrogenase matarport system permease component LBUL_0581 HypF 0.240 Hydrogenase matarport system permease (trigger factor) LBUL_0781 Dna 2.301 ATP-stependent Lon protease LBUL_0785 TrAB 0.047 1.130 4.189 3.051 LBUL_0780 TrAB 0.047 1.130 4.189 3.051 Thioredoxin reductase LBUL_0809 CysU 0.363 4.189 3.051 Thioredoxin reductase ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_0809 CydD 0.236 5.01 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_0104 PpB 0.333 4.992 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1050 CydD 0.236 7.779 CydD CydD CydD ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component L	LBUL_0578	CydD	0.440						ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0605 MsA 2.234 Peptide methicinus esiloxide reductase LBUL_0646 Dnak 0.459 Molecular chaperone LBUL_0705 Dnak 0.383 3.612 Molecular chaperone LBUL_0705 Trag 0.413 0.493 2.2433 PERPENDENDENDENDENDENDENDENDENDENDENDENDENDE	LBUL 0580	CvsU	0.442						ABC-type sulfate transport system permease component
LBUL_0646 Dnak 0.459 Molecular chaperone LBU_0663 Dnak 0.433 0.612 ATF-dependent Lon protease LBU_0701 Lon 2.301 ATF-dependent Lon protease LBU_0707 Lon 2.301 ATF-dependent transport system permease component LBU_0869 CydD 0.047 1.18 3.051 LBU_0870 CydD 0.363 ABC-type statements involved in cytochrome bd biosynthesis ATPase and permease component LBU_0880 CydD 0.216 ABC-type stateminov/sed in cytochrome bd biosynthesis ATPase and permease componer LBU_0880 CydD 0.306 5.201 ABC-type stansport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_0808 CydD 0.408 4.992 ABC-type stansport system involved in cytochrome bd biosynthesis ATPase and permease componers LBU_1009 CydD 0.408 7.779 CydD ABC-type statemaport system involved in cytochrome bd biosynthesis ATPase and permease componers LBU_11018 HB 0.330 S.500 Trans CydD CydD CydD CydD CydD CydD	LBUL_0605	MsrA				2.234			Peptide methionine sulfoxide reductase
LBUL_0663 Dnak 0.383 3.612 Molecular chaperone LBU_0701 Lon 2.381 FKB-type pagenone FKB-type pagenone LBU_0705 Tra 0.443 0.493 2.583 FKB-type pagenone LBU_0706 Tra 0.300 FKB-type pagenone system particles or transport system particles or transport system particles or transport system involved in cytochrome to biosynthesis ATPase and permases componen LBU_0885 CydD 0.350 5.201 ABC-type transport system involved in cytochrome to biosynthesis ATPase and permases componen LBU_0896 CydD 0.350 5.201 ABC-type transport system involved in cytochrome to biosynthesis ATPase and permases component LBU_0996 CydD 0.333 5.201 ABC-type transport system involved in cytochrome bo biosynthesis ATPase and permases component LBU_1004 PpB 0.408 4.992 ABC-type transport system involved in cytochrome bo biosynthesis ATPase and permases component LBU_10168 Pen 0.330 2.350 2.351 ABC-type transport system involved in cytochrome bo biosynthesis ATPase and permases component LBU_1105 APC 0.451 0.392 2.363	LBUL_0635			0.240		0.450			Hydrogenase maturation factor
LBUL_0701 Lon 2.301 ATP-dependent Lon protease LBU_0705 Trg 0.413 0.493 2.583 FKBP-type pepiddy-froyth is trans increase (trigger factor) LBU_0726 Trg 0.300 ATP-dependent Lon protease ATP-dependent Lon protease LBU_0726 Trg 0.300 ATP-dependent Lon protease ATP-dependent Lon protease LBU_0826 Ox10 0.303 5.201 ATP-dependent Lon protease ATP-dependent Lon protease LBU_0828 Overton 0.303 5.201 ATP-dependent lon proteone biologynthesis ATPase and permases componer LBU_0049 Protein Comparities 7.779 ATP-dependent lonvoltant involved in cytochrome biologynthesis ATPase and permases components LBU_1006 CydD 0.330 5.201 ABC-type transport system involved in cytochrome biologynthesis ATPase and permases components LBU_1006 CydD 0.333 7.79 ABC-type transport system involved in cytochrome biologynthesis ATPase and permases components LBU_1107 Marce Protease Transport system involved in cytochrome biologynthesis ATPase and permases component LBU_1108 Proteinase Componentis ABC-type	LBUL 0663			0.383		3.612			Molecular chaperone
LBUL_0726 Trike 0.047 0.130 4.189 3.051 Thoredoxin reductase LBU_0890 CysU 0.363 ABC-type sulfate transport system permease component LBU_0882 CydD 0.216 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0882 CydD 0.300 5.201 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_0882 CydD 0.408 0.333 Permetsion transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_1090 CydD 0.408 0.333 Permetsion transport system involved in cytochrome bd biosynthesis ATPase and permease components LBU_1070 ATM1 7.598 Protein-Lisoaparatie carboyinethytinanteriza Protein-Lisoaparatie carboyinethytinanteriza LBU_11070 ATM1 7.598 2.76 dependent protease Protein-Lisoaparatie carboyinethytinateriza LBU_11124 TaF 0.337 2.76 dependent protease Thoredoxin reductase LBU_1124 TaF 2.770 Thoredoxin reductase Thoredoxin reductase LBU_1125 Apd	LBUL_0701	Lon				2.301			ATP-dependent Lon protease
LBUL_0809 CysU 0.300 ABC-type strangort system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_0807 CydD 0.216 ABC-type strangort system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_0808 CydD 0.408 4.992 ABC-type trangort system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_0808 CydD 0.408 4.992 ABC-type trangort system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1007 MPBI 0.333 Peglo/typic/typic/ticstrans tomoved in cytochrome bd biosynthesis ATPase and permease component LBUL_1007 ATM 7.79 Peglo/typic/typic/ticstrans tomoved in cytochrome bd biosynthesis ATPase and permease component LBUL_1008 CydD - 7.598 ABC-type trangort system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1108 Perdio-Liscosylate perfudase (N+Emmin laytem) transpert system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1108 APF 0.437 2.966 Sublishin-like serine protease with chaptore function LBUL_1101 Hitx - 2.687 Zn-dependent protease with chaptore function LBUL_1124 CydD 2.428 A	LBUL_0710	fig TryB	0.413	0.493	0.047		4 190	3.051	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
LBUL, 0870 CydD 0.363 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0883 CydD 0.350 5.201 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL, 0893 CydD 0.408	LBUL_0869	CysU	0.300		0.047	0.130	4.109	3.001	ABC-type sulfate transport system permease component
LBUL_0882 CydD 0.216 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBU_0883 CydD 0.303 4.992 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBU_1004 PpB 0.333 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBU_1004 PpB 0.333 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBU_1004 PATM 7.79 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases components LBU_1007 ATM1 7.598 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases components LBU_1019 Ppm 0.330 0.500 Pyrotein-i-i-sosagrate perdusas (N-ternant) pyroglutany perdusas) LBU_11101 Htpx 2.963 Zri-dependent protease with chaptore function LBU_1124 Traff 0.357 Zri-dependent protease with chaptore function LBU_1124 Traff 0.367 2.976 Subtilismi-like serine protease in cytochrome bd biosynthesis ATPase and permases component LBU_1124 Traff Cardo 2.775 There decare LBU_1227 Orad 2.867 Drafe ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component<	LBUL 0870	CydD				0.363			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_0999 CydD 0.408 4.992 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_1004 PBB .033 .2033 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease LBU_1004 PPB .333 .2030 .2030 .2030 LBU_1008 PC .330 .2500 .2030 .2000 .2010 LBU_10103 Pep .333 .500 .2063 .2010<	LBUL_0882	CydD CydD				5 201			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1004 PpiB 0.33 Pertid/s-prof/tors/instance (rotamase) - cyclophilin family LBU_1007 ATM 7.779 ABC-type transport system involved in cytochrome bd biosynthesis tard ATPase and permease components LBU_1008 Pom 0.350 ABC-type transport system involved in cytochrome bd biosynthesis tard ATPase and permease LBU_1018 Pom 0.433 0.300 Profein-L-isosapartie carboxyline hyturns/lerase LBU_1108 Pom 0.431 0.300 Profein-L-isosapartie carboxyline hyturns/lerase LBU_1104 APC 0.451 0.392 8.84 0.419 2.796 LBU_11141 ThF 0.451 0.392 8.84 0.419 2.796 LBU_11143 ThF 0.451 0.392 8.84 0.419 2.796 LBU_1124 Visition-line carboxyline hytochrease Throredoxin reductase Throredoxin reductase LBU_1124 Visition-line carboxyline hytochrease Throredoxin reductase Throredoxin reductase LBU_1212 Oral 2.857 2.867 Dral-class molecular transport system involved in cytochrome bd biosynthesis ATPase and permease componer	LBUL_0989	CydD	0.408	0.000					ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBU_1099 CydC 7.79 ABC-kpt transport system involved in cylcchrome bd biosynthesis tued ATPase and permease LBU_1098 CydC 7.59 ABC-kpt transport system involved in cylcchrome bd biosynthesis tued ATPase and permease LBU_1019 Perp 0.350 7.598 ABC-kpt transport system involved in cylcchrome bd biosynthesis tued ATPase components LBU_1019 Perp 0.37 2.363 2.500 LBU_11111 HbX 2.363 2.74 dependent involved in cylcchrome bd biosynthesis tued ATPase and permease LBU_11124 TaF 0.337 7 Type IV secretorese LBU_11124 TaF 0.337 Type IV secretorese Type IV secretorese LBU_1124 TaF 0.357 2.766 ABC-kpt transport system involved in cylcchrome bd biosynthesis ATPase and permease component LBU_1124 TaF 2.428 ABC-kpt stransport system involved in cylcchrome bd biosynthesis ATPase and permease component LBU_1225 Dnal 2.857 2.867 Dnal-class molecular chaperone with chaperone bd biosynthesis ATPase and permease component <	LBUL_1004	PpiB							Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
LBUL_1070 ATM T.598 ABC-kype transport system involved in Fe-S cluster assembly permease and ATPase components BLU_1070 ATM ABC-kype transport system involved in Fe-S cluster assembly permease and ATPase components Pyroniloon-catoxylate peptidase (N-terminal pyroqlutamy) peptidase) LBU_1070 Htp 2.363 2.764 pep-nden tortexase Pyroniloon-catoxylate peptidase (N-terminal pyroqlutamy) peptidase) LBU_1114 Htp 2.363 2.764 pep-nden tortexase Trafe LBU_1118 TraF 0.337 3.376 Subtilism-like series protexase LBU_1124 HsU 0.432 ATP-dependent protexase visits protexase trafe LBU_1124 HsU 0.432 ATP-dependent protexase hsVU (Cjp/Q) ATPase subunit LBU_12124 Orad 2.575 ABC-kype transport system involved in cytochrome bd biosynthesis ATPase and permease component LBU_12124 Orad 2.575 2.867 Dna_4 class molecular chaperone GrpE (net shock protein) LBU_1224 Orad 2.576 2.867 Dna_4 class molecular chaperone other classe component LBU_1225 DnaK 0.326 0.477 Melecular chaperone timolycein involved in cytochrome bd biosynthesis ATPase and permease componer	LBUL_1069	Cyac			1.119				Abo-type transport system involved in cytochrome od biosynthesis fused ATPase and permease components
LBUL_1089 Perm 0.350 Protein-L-isosgnative carboxylane phylicans/terase LBUL_1010 HtpX 2.863 C.500 Protein-L-isosgnative carboxylane phylicans (N-terminal pyroglutamy) peptidase) LBUL_11101 HtpX 2.863 C.500 Zh-dependent protease with chaperone function LBUL_11101 HtpX 0.451 0.392 Zh-dependent protease with chaperone function LBUL_11101 HtpX 0.451 0.392 Type IV secretores LBUL_11102 Tar B 0.451 0.392 Type IV secretores LBUL_1120 O.452 0.432 Type IV secretores Type IV secretores LBUL_1120 O.402 62.155 ABC-type transport system involved in cytochrome b biosynthesis ATPase and permease component LBUL_1222 Dnal 2.867 Dnal-class molecular chaperone with cheroren biosynthesis ATPase and permease component LBUL_1222 Dnal 0.367 0.479 Zh-640 per transport system involved in cytochrome b biosynthesis ATPase and permease component LBUL_1221 OrdD 0.326 2.878 0.148 ABC-type transport system involved in cytochrome b biosynthesis ATPase and permease c	LBUL_1070				7.598				ABC-type transport system involved in Fe-S cluster assembly permease and ATPase components
LBUL_1101 HpX 2.363 Zn-dependent protease with chaptore function LBUL_1104 ApF 0.451 0.392 Cardependent protease with chaptore function LBUL_1124 Tar F 0.451 0.392 Type IV secretores LBUL_1124 Tar F 0.337 Type IV secretores Type IV secretores LBUL_1124 Tar F 0.337 Type IV secretores Type IV secretores LBUL_1212 Tar F 0.357 Cardependent Proteose Type IV secretores LBUL_1213 Tar F 2.775 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1212 OrdD 2.987 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1225 OrdD 0.367 0.479 Molecular chaperone LBU_1226 GreB 0.367 0.479 Molecular chaperone LBU_1226 GreB 0.326 E ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1235 GreB 0.326 L348 ABC-type transport system inv	LBUL_1089	Pcm	0.400						Protein-L-isoaspartate carboxylmethyltransferase
LBUL_1126 AprE 0.451 0.392 8.88 0.419 2.796 Subilisin-like series protease LBUL_1124 TraF 0.337 Type IV secretory pathway protease TraF LBUL_1124 TraB 2.770 Thioredoin reductase LBU_1126 NHU 0.432 ATP-dependent protease Is/IVU (Cip/Q) ATPase subunit LBU_1224 CydD 2.988 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1225 OrbaI 2.577 2.887 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1226 OrbaI 2.577 2.867 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1226 OrbaI 2.577 2.768 1.484 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1226 CydD 0.326 2.578 0.148 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBU_1232 CydD 0.324 0.626 2.588 0.148 ABC-type transport system involved in cytochrome bd biosynthesis ATPase	LBUL_1093	Pcp HtpX	0.433	0.500		2,363			Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase) Zn-dependent protease with chaperone function
LBUL_1138 Tn/B 2.770 Thioredoxin reducinase LBUL_1138 HsU 0.432 ATP-dependent protease HsI/U (ClpYQ) ATPase subunit LBUL_124 CydD 62.155 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1217 CydD 2.998 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1217 CydD 2.857 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1227 OnaK 0.37 2.867 Molecular chaperone LBUL_1227 OnaK 0.37 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1226 CydD 0.326 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1232 CydD 0.326 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1232 CydD 0.328 0.148 ABC-type transport system involved in cyclochrome bd biosynthesis ATPase and permease componer LBUL_1335 HypE 0.334 0.045 2.116 LBU	LBUL_1105	AprE	0.451	0.392	8.884		2.796		Subtilisin-like serine protease
LBUL_1212 CydD 62.155 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1212 CydD 2.987 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1212 Dnal 2.857 2.867 Dnal-class molecular chaperno with Charme bd biosynthesis ATPase and permases component LBUL_1226 Dnal 0.307 0.377 Molecular chaperno with Charme bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1235 CydD 0.282 2.588 0.193 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1235 CydD 0.282 0.282 2.588 0.148 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1335 HypE 0.334	LBUL_1124	TraF			0.337				Type IV secretory pathway protease TraF
LBUL_1212 CydD 62.155 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1212 CydD 2.987 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1212 Dnal 2.857 2.867 Dnal-class molecular chaperno with Charme bd biosynthesis ATPase and permases component LBUL_1226 Dnal 0.307 0.377 Molecular chaperno with Charme bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1226 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1235 CydD 0.282 2.588 0.193 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1235 CydD 0.282 0.282 2.588 0.148 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permases component LBUL_1335 HypE 0.334	LBUL_1138				2.770				i nioredoxin reductase ATP-dependent protease HsIVU (CloYO) ATPase subunit
LBUL_1212 CysU 4.248 ABC-type sulfate transport system permease component LBUL_1226 Dnal 2.857 2.867 Dnal-class molecular chaperone with C-terminal Zn finger domain LBUL_1227 Dnak 0.367 0.479 Molecular chaperone with C-terminal Zn finger domain LBUL_1228 GrpE 0.367 0.479 Molecular chaperone Molecular chaperone LBUL_1228 CydD 0.377 ABC-type suffate permone with C-terminal Zn finger domain Molecular chaperone Molecular chaperone LBUL_1228 CydD 0.376 ABC-type suffate permose component Molecular chaperone Molecu	LBUL_1204	CydD			62.155				ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1227 Dnak 0.367 0.479 Molecular chaperone LBUL_1228 GrpE 0.302 0.479 Molecular chaperone LBUL_1226 GrpE 0.302 0.479 Molecular chaperone LBUL_1226 GvpE 0.302 0.479 Molecular chaperone LBUL_1286 GvdD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1386 GvdD 0.326 1.48 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1333 HypE 0.334 0.045 2.16 Hydrogenase maturation factor LBUL_1338 HypE 0.433 0.045 2.16 Hydrogenase maturation factor LBUL_1326 HypF 0.192 Partwidtem involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1336 HypE 0.334 0.045 2.16 Hydrogenase maturation factor LBUL_1426 Tras 0.409 0.507 2.377 Partwidtase Partwidtase LBUL_1426 Tras 0.507	LBUL_1213				2.998	4 0 4 0			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1227 Dnak 0.367 0.479 Molecular chaperone LBUL_1228 GrpE 0.302 0.479 Molecular chaperone LBUL_1226 GrpE 0.302 0.479 Molecular chaperone LBUL_1226 GvpE 0.302 0.479 Molecular chaperone LBUL_1286 GvdD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1386 GvdD 0.326 1.48 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1333 HypE 0.334 0.045 2.16 Hydrogenase maturation factor LBUL_1338 HypE 0.433 0.045 2.16 Hydrogenase maturation factor LBUL_1326 HypF 0.192 Partwidtem involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1336 HypE 0.334 0.045 2.16 Hydrogenase maturation factor LBUL_1426 Tras 0.409 0.507 2.377 Partwidtase Partwidtase LBUL_1426 Tras 0.507	LBUL_1214 LBUL_1226			2.857					
LBUL_1228 GrpE 0.302 0.477 Molecular chapenon GrpE (heat shock protein) LBUL_1218 CydD 0.37 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1228 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1280 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1283 CydD 0.324 0.262 2.588 0.183 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1315 CydD 0.34 0.045 2.118 Hydrogenase maturation factor LBUL_1424 SurA 0.481 2.137 Hydrogenase maturation factor LBUL_1424 SurA 0.481 2.137 Paroulin-like periodity-profi Isomerase LBUL_1424 SurA 0.479 0.422 Thioredoxin roductians LBUL_1434 CGS118 0.179 0.422 Thioredoxin and operionase otholisoynthesis ATPase and permease componer LBU_1441 CGS118 0.179 0.422	LBUL_1227	DnaK	0.367						Molecular chaperone
LBUL_1286 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1282 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1315 CydD 0.326 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1315 CydD 0.334 0.045 2.116 LBUL_1315 CydD 0.334 0.045 2.116 LBU_1315 HypE 0.334 0.045 2.116 LBU_1325 HypE 0.430 0.0192 HypE LBU_1435 HypE 0.450 0.192 Hydrogenase maturation factor LBU_1436 Transport system involved in cytochrome bd biosynthesis ATPase and permease componer EBU Hydrogenase maturation factor LBU_1436 Graft Trab 0.192 Hydrogenase maturation factor Hydrogenase maturation factor LBU_1436 Trabe and permease componer EBU Hydrogenase maturation factor Hydrogenase maturation factor LBU_1437 Graft 0.192 Hydrogenase maturation factor	LBUL_1228		0.302	0.477					Molecular chaperone GrpE (heat shock protein)
LBUL_1282 CydD 0.324 0.262 2.588 0.193 ABC-type transport system involved in cytochrome bb biosynthesis ATPase and permease component LBUL_133 CydD 0.282 0.278 2.768 0.148 ABC-type transport system involved in cytochrome bb biosynthesis ATPase and permease component LBU_1335 KypE 0.453 0.045 2.116 Hydrogenase maturation factor LBU_1342 SiAA 0.451 0.073 2.397 Hydrogenase maturation factor LBU_1424 SiAA 0.481 0.073 2.397 Hydrogenase maturation factor LBU_1424 SiAA 0.481 0.073 2.397 Hydrogenase maturation factor LBU_1448 COG3118 0.192 2.492 Thioredoxin roductase Thioredoxin roductase LBU_1449 COG3118 0.491 0.422 Thioredoxin roductase Co-chapteronin GreS (18P10) LBU_1505 COC124 0.437 0.422 Co-chapteronin GreS (18P10) Inactive hornolog of metal-dependent protease putative molecular chaperone LBU_1556 CydD 0.212 0.422 ABC-type	LBUL_1201	CydD	0.137	0.326					ABC-type transport system involved in cytochrome of biosynthesis ATPase and permease components ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1233 CydD 0.282 0.278 2.78 0.148 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1315 CydD 4.141 0.219 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1335 HypE 0.334 0.045 2.116 Hydrogenase maturation factor LBUL_1336 HypF 0.192 0.192 Provide participation factor LBUL_1386 HypF 0.192 Provide participation factor Provide participation factor LBUL_1481 COG3118 0.491 0.422 Provide participation factor LBUL_1481 COG3124 0.437 Co-chaperonin Groß F1(R910) Co-chaperonin Groß F1(R910) LBU_1576 COC6 3.376 CoC-cheated protein involved in cytochrome bd biosynthesis ATPase and permease component LBU_1578 CydD 0.212 Thiored/mini formalin-containing protein LBU_1578 CoC4 0.437 Co-chaperonin Groß F1(R910) LBU_1578 CoC4 0.424 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component	LBUL_1292	CydD	0.324	0.262	2.588	0.193			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1333 HypE 0.334 0.045 2.116 Hydrogenase maturation factor LBUL_1335 HypE 0.434 0.073 2.377 Hydrogenase maturation factor LBUL_1346 HypF 0.192 Parvuln-like pedit/dy-royli isomerase Hydrogenase maturation factor LBUL_1424 SurA 0.481 0.473 Parvuln-like pedit/dy-royli isomerase LBUL_1447 Totas 0.490 0.422 Thioredown reductase LBUL_1447 GroS 0.495 Co-chaperonin GroS f(HSP10) Co-chaperonin GroS f(HSP10) LBUL_1547 COC12 0.376 Cdc-related portein Axo sperfamily PTPase LBUL_1547 CydC 0.422 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease component LBUL_1542 CydC 0.424 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease	LBUL_1293	CydD	0.282	0.278	2.768	0.148		0.210	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1336 HypF 0.453 0.073 2.37 Hydrogenase maturation factor LBUL_1424 SWA 0.481 Hydrogenase maturation factor LBUL_1424 SWA 0.481 Parvulin-kite petidy-provid isomerase LBUL_1448 COG3118 0.192 Thioredoxin reductase LBUL_1441 COG3118 0.19 0.422 LBUL_1450 COC124 0.437 Cochaperonin GreS (1RSP10) LBUL_1503 COC3124 0.437 Cochaperonin GreS (1RSP10) LBUL_1515 COC6 3.376 Cochaperonin involved in cytochrome bd biosynthesis ATPase and permease LBUL_1552 CydC 0.422 0.442 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease	LBUL_1315			0.334				0.219	
LBUL_1326 HypF 0.192 Hydrogenase mutuation factor LBUL_1326 Hydrogenase mutuation factor Parvulnike petity6/-provise Parvulnike petity6/-provise LBUL_1426 TraB 0.500 Parvulnike petity6/-provise Parvulnike petity6/-provise LBUL_1446 COG311 0.500 Thioredoxin domain-containing protein LBUL_1503 COG3124 0.497 Thioredoxin domain-containing protein LBUL_1515 COG1214 0.437 Inactive hornolog of metal-dependent protease putative molecular chaperone LBUL_1515 COC6 3.376 Cd6-related protein AAS superfamily ATPase Cdp-rotype transport system involved in cytochrome bd biosynthesis LTPase and permease componer LBUL_1552 Cyd2 0.442 ABC-type transport system involved in cytochrome bd biosynthesis LTPase and permease	LBUL_1335	HypE						2.397	Hydrogenase maturation factor
LBUL_1466 TmB 0.500 Thioredoxin reductase LBUL_1476 COGS118 0.179 0.422 Thioredoxin redoxin domain-containing protein LBUL_1497 GroS 0.489 0.456 Co-chaperonin GroES (HSP10) LBUL_1515 CDC6 3.376 Co-chapteronin dometal-containing proteins	LBUL_1386	HypF			0.192				Hydrogenase maturation factor
LBUL_1497 GroS 0.489 0.456 Co-chaperonin GnES (HSP10) LBUL_1503 COGR124 0.437 Inactive homolog of metal-dependent protease putative molecular chaperone LBUL_1515 CDC6 3.376 Cdc6-related protein AAA superfamily ATPase LBUL_15162 CydD 0.212 0.162 ABC-type transport system involved in cytochrome bd biosynthesis TuPase and permease componer LBUL_1586 CydC 0.442 ABC-type transport system involved in cytochrome bd biosynthesis tused ATPase and permease	LBUL_1424								Farvummike peptidyi-pronyi isomerase Thioredoxin reductase
LBUL_1497 GroS 0.489 0.456 Co-chaperonin GnES (HSP10) LBUL_1503 COGR124 0.437 Inactive homolog of metal-dependent protease putative molecular chaperone LBUL_1515 CDC6 3.376 Cdc6-related protein AAA superfamily ATPase LBUL_15162 CydD 0.212 0.162 ABC-type transport system involved in cytochrome bd biosynthesis TuPase and permease componer LBUL_1586 CydC 0.442 ABC-type transport system involved in cytochrome bd biosynthesis tused ATPase and permease	LBUL_1481	COG3118		0.000		0.422			Thioredoxin domain-containing protein
LBUL_1515 CDC6 3.376 Cdc6-related protein AAA superfamily ATPase LBUL_1552 CydD 0.212 0.162 ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease componer LBUL_1558 CydC 0.442 ABC-type transport system involved in cytochrome bd biosynthesis fused ATPase and permease	LBUL_1497	GroS	0.489		0.456				
LBUL_1562 CydD 0.212 0.162 ABC-type transport system involved in cytochrome bd biosynthesis IATPase and permease componer LBUL_1588 CydC 0.442 ABC-type transport system involved in cytochrome bd biosynthesis ItseAI ATPase and permease					0.437	3,376			Cdc6-related protein AAA superfamily ATPase
LBUL_1588 CydC 0.442 ABC-type transport system involved in cytochrome bd biosynthesis fused ATPase and permease	LBUL_1562	CydD	0.212					0.162	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
components	LBUL_1588	CydC				0.442			
·									componenta

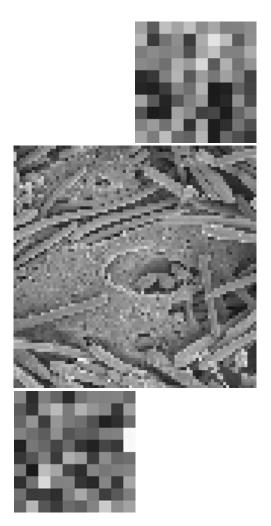
I DI II 1601	Sms			2.872				Dradiated ATD dependent earling protocol
LBUL_1601 LBUL_1689	SufB			2.072	2.957			Predicted ATP-dependent serine protease ABC-type transport system involved in Fe-S cluster assembly permease component
LBUL_1692 LBUL_1693	SufB SufC				3.794 7.298			ABC-type transport system involved in Fe-S cluster assembly permease component ABC-type transport system involved in Fe-S cluster assembly ATPase component
LBUL_1700	CydD			0.272	0.323			ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1710 LBUL_1772	Spy CydD				5.122 2.425			Predicted O-linked N-acetylglucosamine transferase SPINDLY family ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_1785	COG5549			0.173	0.396			Predicted Zn-dependent protease
LBUL_1833 LBUL_1944	COG0229 ClpA	2.021	0.201 2.121	0.161		0.449	0.488	Conserved domain frequently associated with peptide methionine sulfoxide reductase ATPase with chaperone activity ATP-binding subunit
LBUL_2003 LBUL_2020	CydD			2.851				ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components
LBUL_2020 LBUL_2035	CydD TrxB	0.201				4.257	3.583	ABC-type transport system involved in cytochrome bd biosynthesis ATPase and permease components Thioredoxin reductase
	etabolites biosy	intheeie tr	aneport and	cataboliem				
LBUL_0129	Ttg2A		2.794					ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0177 LBUL_0216	Ttg2A Ttg2A	0.331 0.386	0.347 0.055	2.596	0.159			ABC-type transport system involved in resistance to organic solvents ATPase component ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0238	Ttg2A	0.500	0.055		2.013			ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0239 LBUL_0249	Ttg2A BenE				3.705 0.308	0.215		ABC-type transport system involved in resistance to organic solvents ATPase component Uncharacterized protein involved in benzoate metabolism
LBUL_0256	Ttg2A		0.347	6.884		0.215		ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0262	Ttg2A PncA	0.380	0.268		0.077 2.013			ABC-type transport system involved in resistance to organic solvents ATPase component Amidase related to nicotinamidase
LBUL_0279 LBUL_0339	AcoR				3.118			Transcriptional activator of acetoin/glycerol metabolism
LBUL_0445 LBUL_0500	Ttg2A COG0412		0.333 0.293					ABC-type transport system involved in resistance to organic solvents ATPase component Dienelactone hydrolase
LBUL_0532	FabG		0.451		0.405			Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_0548 LBUL_0550	COG1233 Ttg2A		2.433	0.243	0.425 0.098			Phytoene dehydrogenase and related protein ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0553 LBUL_0578	DmpA Ttg2A		2.448 0.448	0.284	0.181			L-aminopeptidase/D-esterase ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0726	COG1233			0.047	0.130	4.189	3.051	Phytoene dehydrogenase and related protein
LBUL_0818 LBUL_0819	BcsA AcpP		0.371	0.262 0.322	0.200 0.405			Predicted naringenin-chalcone synthase Acyl carrier protein
LBUL_0820	COG3321		0.259	0.188	0.275			Polyketide synthase modules and related protein
LBUL_0821 LBUL_0822	FabG FabB		0.318 0.322	0.258 0.224	0.196 0.222			Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase) 3-oxoacyl-(acyl-carrier-protein) synthase
LBUL_0828	FabG		0.288	0.104	0.321		2.147	Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_0870 LBUL_0882	Ttg2A Ttg2A		0.216		0.363			ABC-type transport system involved in resistance to organic solvents ATPase component ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0883	Ttg2A COG3458		0.350		5.201			ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_0918 LBUL_0989	COG3458 COG4181	0.408			4.671 4.992			Acetyl esterase (deacetylase) Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis ATPase component
LBUL_0990 LBUL_1069	COG3127 Ttg2A	0.381	0.148	7.779	4.118			Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis permease component ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1070	Ttg2A			7.598				ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1138 LBUL_1189	CÕG1233 COG1233			2.770 0.412				Phytoene dehydrogenase and related protein Phytoene dehydrogenase and related protein
LBUL_1204	Ttg2A			62.155				ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1213 LBUL_1261	Ttg2A Ttg2A	0.137		2.998				ABC-type transport system involved in resistance to organic solvents ATPase component ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1292	Ttg2A	0.324	0.262	2.588	0.193			ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1293 LBUL_1294	Ttg2A AcpP	0.282	0.278	2.768 0.288	0.148			ABC-type transport system involved in resistance to organic solvents ATPase component Acyl carrier protein
LBUL_1335 LBUL_1358	DIT1		0.453	2.801	0.073		2.397	Pyoverdine/dityrosine biosynthesis protein Imidazolonepropionase and related amidohydrolase
LBUL_1358 LBUL_1466	Hutl COG1233		0.500	2.801				Phytoene dehydrogenase and related protein
LBUL_1562	Ttg2A	0.212			0.442		0.162	ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_1588 LBUL_1664	Ttg2A FabG	0.485						ABC-type transport system involved in resistance to organic solvents ATPase component Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_1693 LBUL_1700	Ttg2A COG4181			0.272	7.298 0.323			ABC-type transport system involved in resistance to organic solvents ATPase component Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis ATPase component
LBUL_1751	COG0412			0.156				Dienelactone hydrolase
LBUL_1772 LBUL_1810	Ttg2A COG1233			2.745	2.425 4.943			ABC-type transport system involved in resistance to organic solvents ATPase component Phytoene dehydrogenase and related protein
LBUL_1835	FabG			6.551				Dehydrogenase with different specificities (related to short-chain alcohol dehydrogenase)
LBUL_1944 LBUL_2003 LBUL_2020	AcoR Ttg2A	2.021	2.121	2.851		0.449	0.488	Transcriptional activator of acetoin/glycerol metabolism ABC-type transport system involved in resistance to organic solvents ATPase component
LBUL_2020 LBUL_2035	Ttg2A COG1233	0.201				4.257	3.583	ABC-type transport system involved in resistance to organic solvents ATPase component Phytoene dehydrogenase and related protein
LBUL_2035	0061233	0.201					3.583	Phytoene denydrogenase and related protein
Signal transdu LBUL_0010	uction mechani COG3887	sms		2.087	2.099			Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
LBUL_0012	RAD55	0.371		2.381				RecA-superfamily ATPase implicated in signal transduction
LBUL_0064 LBUL_0088	Rtn LuxS		0.327	12.958	0.466			FOG: EAL domain LuxS protein involved in autoinducer Al2 synthesis
LBUL_0111	OmpR	0.373						Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
LBUL_0112 LBUL_0118	VicK SdrC				0.476		0.415	Signal transduction histidine kinase Predicted secreted protein containing a PDZ domain
LBUL_0145	HisJ			5.749 0.255				ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0159 LBUL_0173	Crp PtsN			0.255	0.441			cAMP-binding protein - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinase Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
LBUL_0176	HisJ HisJ	0.412	0.171		0.438			ABC-type amino acid transport/signal transduction systems periplasmic component/domain ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0255	SPS1			4.400				Serine/threonine protein kinase
LBUL_0261 LBUL_0290	HisJ SPS1	0.421	0.335	2.825	0.088 3.405	5.086		ABC-type amino acid transport/signal transduction systems periplasmic component/domain Serine/threonine protein kinase
LBUL_0339	AtoC	0.370	0.495		3.118			Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains
LBUL_0348 LBUL_0434	TypA COG5001	0.379	0.465	11.955				Predicted membrane GTPase involved in stress response Predicted signal transduction protein containing a membrane domain an EAL and a GGDEF domain
LBUL_0479 LBUL_0506	COG3448			0.430	4.576			CBS-domain-containing membrane protein Predicted membrane GTPase involved in stress response
LBUL_0510	TypA PspF			0.381				Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain
LBUL_0515 LBUL_0519	MecA SpoT			0.451	0.471 0.307			Negative regulator of genetic competence sporulation and motility Guanosine polyphosphate pyrophosphohydrolase/synthetase
LBUL_0535	RAD55		0.000				0.359	RecA-superfamily ATPase implicated in signal transduction
LBUL_0594 LBUL_0621	COG2199 OmpR		0.386	0.403				FOG: GGDEF domain Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
LBUL_0650	UspA	0.400	0.000	0.166				Universal stress protein UspA and related nucleotide-binding protein
LBUL_0674 LBUL_0696	COG1819 TypA	0.499 0.448	0.220 0.332		2.191			Glycosyl transferase related to UDP-glucuronosyltransferase Predicted membrane GTPase involved in stress response
LBUL_0701	SdrC		3.587	2,430	2.301			Predicted secreted protein containing a PDZ domain
LBUL_0709 LBUL_0776	ТурА ТурА		3.587	2.430	2.048 3.234			Predicted membrane GTPase involved in stress response Predicted membrane GTPase involved in stress response
LBUL_0872 LBUL_0885	OmpR LytS	0.378	0.355		2.434			Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Putative regulator of cell autolysis
LBUL_0902	COG3887		0.000	0.352				Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
LBUL_0919 LBUL_0933	ROM1 COG3830				4.804 0.117	0.322		RhoGEF Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPase ACT domain-containing protein
LBUL_1172	PhoH	0.493	0.357					Phosphate starvation-inducible protein PhoH predicted ATPase
LBUL_1201 LBUL_1214	COG2199 HisJ	0.172			2.038 4.248			FOG: GGDEF domain ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_1225	ТурА	0.341						Predicted membrane GTPase involved in stress response

LBUL_1233 LBUL_1265 LBUL_1265 LBUL_1267 LBUL_1401 LBUL_1488 LBUL_1515 LBUL_1577 LBUL_1617 LBUL_1617 LBUL_1757 LBUL_1757 LBUL_1935 LBUL_1940 LBUL_1940 LBUL_1949 LBUL_1949 LBUL_2018	LuxS TypA LexA HisJ SpoT COG3887 RAD55 COG2199 RAD55 Tar LytT COG1819 COG2365 COG2365 COG2365 AtoC SPS1 PrkA	0.201 0.198 2.021	0.345 2.433 0.468 2.121	3.477 0.390 3.867 2.872 4.153 0.258 2.298 0.181	3.277 0.378 3.314 3.076 3.376 0.415 0.324 0.361 0.359 0.181	0.449	0.375	LuxS protein involved in autoinducer AI2 synthesis Predicted membrane GTPase involved in stress response SGS-response transcriptional repressors (ReA-mediated autopeptidase) ABC-type amino acid transport/signal transduction systems perplasmic component/domain Guanosine polytophather pryprologohybridicales/inheitase Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain Predicted signaling protein consisting of a modified GGDEF domain and a DHH RecA-superfamily ATPase implicated in signal transduction Methyl-accepting chemicatas protein Response regulator of the LyfK/AIgR family Glycosyl transferase related to UDP glucuronosyltransferase Protein tyrosine/serine phosphatase Protein tyrosine/serine phosphatase Protein tyrosine/serine phosphatase Protein tyrosine/serine phosphatase Segment Devisite containing CheV-like receiver AAA-type ATPase and DNA-binding domains Segment Protein kinase
Transcription LBUL_0038 LBUL_0057 LBUL_0095 LBUL_0099 LBUL_0104 LBUL_0111 LBUL_0111	COG1959 FliA LysR NagC LysR OmpR RocR	0.363 0.373	0.332 0.354	0.271 6.107	2.571 0.269 0.476	6.050		Predicted transcriptional regulator protein DNA-directed RNA polymerase specialized sigma subunit Transcriptional regulator Transcriptional regulatorsugar kinase Transcriptional regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Transcriptional regulators consisting PAS AAA-type ATPase and DNA-binding domains
LBUL_0140 LBUL_0157 LBUL_0204 LBUL_0244 LBUL_0255 LBUL_0266	NOT5 AcrR LytR GreA SPS1 COG2865	0.268	0.404 2.127 0.423	0.405 0.327 4.400	8.677		0.297 0.347	CCR4-NOT transcriptional regulation complex NOT5 subunit Transcriptional regulator Transcriptional regulator Transcription elongation factor Serinethreconine protein kinase Predicted transcriptional regulator protein
LBUL_0290 LBUL_0339 LBUL_0343 LBUL_0376 LBUL_0399	SPS1 AcoR RpoC RpoA PhnF	0.316	0.291	2.246 0.487	3.405 3.118	5.086		Freductor transcriptional regulatory protein Serine/Threoring protein kinase Transcriptional activator of acetoir/glycarol metabolism DNA-directed RNA polymerase alpha subunit/160 kD subunit DNA-directed RNA polymerase alpha subunit/40 kD subunit Transcriptional regulators
LBUL_0479 LBUL_0488 LBUL_0510 LBUL_0519	COG4109 ARO8 PspF SpoT			0.430 0.224 0.381	0.307			Predicted transcriptional regulator protein containing CBS domains Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs Transcriptional regulators containing an AA-type ATPase domain and a DNA-binding domain Guanosine polytopschate prypotopschotydrolase/synthetase
LBUL_0549 LBUL_0566 LBUL_0587 LBUL_0621 LBUL_0682	Mfd DeoR COG3682 OmpR CspC		4.440	0.095	0.085 0.459 4.766	0.430		Transcription-repair coupling factor (superfamily II helicase) Transcriptional regulator contains signa factor-related N-terminal domain Predicted transcriptional regulator protein Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Cold shock protein
LBUL_0737 LBUL_0738 LBUL_0740 LBUL_0744 LBUL_0770	ARO8 LysR ArgR SrmB COG1386	0.385 0.494 4.095	4.440	3.248	0.065	0.125		Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their evaluaryotic orthologis Transcriptional regulator Agrinine regressor Superfamily II DNA and RNA helicase Predicted transcriptional regulator protein containing the HTH domain
LBUL_0783 LBUL_0872 LBUL_0897 LBUL_0909 LBUL_0979	LysR OmpR MarR DinG SoxR	0.378 8.757	4.324	3.438 0.349	0.189 2.434 3.260			Transcriptional regulatory Transcriptional regulatory Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain Transcriptional regulators Rad3-related DNA helicase Predicted transcriptional regulator protein
LBUL_0981 LBUL_0997 LBUL_1010 LBUL_1068 LBUL_1103	COG2865 COG3620 COG3620 MarR ARO8	0.301		6.701 0.348 0.369 0.340				Predicted transcriptional regulator protein Predicted transcriptional regulator protein Predicted transcriptional regulators Transcriptional regulators Transcriptional regulators Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR
LBUL_1124 LBUL_1163 LBUL_1164 LBUL_1180	COG2932 RpoD RpoD ARO8		0.319	0.337	2.537	0.224		family) and their eukaryotic orthologs Predicide transcriptional regulator protein DNA-directed RNA polymerase sigma subunit (sigma70/sigma32) DNA-directed RNA polymerase sigma subunit (sigma70/sigma32) Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukarvotic orthologs
LBUL_1205 LBUL_1221 LBUL_1229 LBUL_1236	LysR COG1777 HrcA ARO8	0.306 6.367	0.487 2.770	6.447 13.936	6.441 4.313			Transcriptional regulator Predicted transcriptional regulator protein Transcriptional regulator of heat shock gene Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR
LBUL_1265 LBUL_1269 LBUL_1285 LBUL_1286 LBUL_1286	LexA SrmB COG5137 COG1293	0.121	0.254 0.366 0.326	0.390	0.378		0.375	family) and their eukaryotic orthologs SOS-response transcriptional repressors (RecA-mediated autopeptidase) Superfamily II DNA and RNA helicase Histone chargenen involved in gene silencing Prediced RNA-binding protein homologous to eukaryotic snRNP
LBUL_1287 LBUL_1296 LBUL_1308 LBUL_1311 LBUL_1321 LBUL_1381	Rnc RecG NusB RpoZ NusB GreA	0.121	0.044	3.323 0.290 0.462 0.463	4.226 2.105 2.990			dsRNA-specific riboruclease RecG-like helicase Transcription termination factor DNA-driected RNA polymerase subunit K/omega Transcription benoration factor Transcription benoration factor
LBUL_1381 LBUL_1384 LBUL_1401 LBUL_1404 LBUL_1474 LBUL_1487	COG1733 SpoT COG1327 COG5406 SrmB	2.617 2.063	0.437	0.255 0.402	2.990 3.314 2.234			Transcription elongiation tractor Predicted transcriptional regulator protein Guanosine polyphosphate pyrophosphotyrclase/synthetase Predicted transcriptional regulator protein consists of a Zn-ribbon and ATP-cone domains Nucleosome binding factor SPN SPT16 subunit Superfamily IDNA and RNA helicase
LBUL_1515 LBUL_1535 LBUL_1545 LBUL_1551 LBUL_1563	TIP49 TenA NusG RpoE COG1725	0.355	0.366 0.376 0.459	0.321	3.376			DNA helicase TIP49 TB-P-interacting protein Putative transcription activator Transcription antiterminator DNA-directed RNA polymerase specialized sigma subunit sigma24 homolog Predicted transcriptional regulator protein
LBUL_1618 LBUL_1639 LBUL_1665 LBUL_1691	RpiR PurR HipB ARO8	0.070	0.365	0.320 31.959 0.389	2.204			Transcriptional regulators Transcriptional regulators Predicted transcriptional regulator protein Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR tamih) and their uckaryotic orthologs
LBUL_1758 LBUL_1781 LBUL_1815 LBUL_1822 LBUL_1860 LBUL_1925	AcrR LytT LytR COG1476 LytR DeoR	0.270	8.143	0.258	0.200 2.808 0.338		0.223	Transcriptional regulator Response regulator of the LyfAAlgR family Transcriptional regulator Predicted transcriptional regulator Predicted transcriptional regulator Transcriptional regulator Transcriptional regulator
LBUL_1944 LBUL_1957 LBUL_1996 LBUL_1999	PspF CspC PurR SPS1	2.021 0.328	2.121	2.744	3.871 0.420 0.359	0.449	0.488	Transcriptional regulators containis super la duck redaitor venerininal contain Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain Cold shock protein Transcriptional regulators Serine/threeonine protein kinase
Translation, ri LBUL_0007 LBUL_0009	bosomal struct RpsF RpsR	ture and bio 0.354 0.193	genesis 0.326 0.246	2.347	3.275	5.922		Ribosomal protein S6 Ribosomal protein S18

LBUL_0011	Rpll			2.147				Ribosomal protein L9
LBUL_0117 LBUL_0161	YSH1 RimK		0.475		0.335			Predicted exonuclease of the beta-lactamase fold involved in RNA processing Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
LBUL_0219	TyrS	0.000	0.470		3.698	0.290	0.458	Tyrosyl-tRNA synthetase
LBUL_0251 LBUL_0252	COG0042 TrmU	2.639 2.315				0.290	0.458	tRNA-dihydrouridine synthase Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase contains the PP-loop ATPase
LBUL_0273	AnsB			0.186				domain L-asparaginase/ Glu-tRNAGIn amidotransferase subunit D
LBUL_0293 LBUL_0294	TrpS CumB				4.823 5.175			Tryptophanyl-IRNA synthetase Cytosine/adenosine deaminase
LBUL_0297	MetG				2.240			Methionyl-tRNA synthetase
LBUL_0300 LBUL_0303	KsgA GCD1		0.464 0.392		3.318 2.057		0.432	Dimethyladenosine transferase (rRNA methylation) Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation
LBUL_0311	RpmE			2.715	2.847			initiation factor 2B gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon) Ribosomal protein L31
LBUL_0319	COG1188	0.268	0.407	2.715	2.047			Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)
LBUL_0327 LBUL_0328	COG0042 LysU		0.461 0.484					tRNA-dihydrouridine synthase Lysyl-tRNA synthetase (class II)
LBUL_0346	RpsL	0.389						Ribosomal protein S12
LBUL_0347 LBUL_0348	RpsG FusA	0.372 0.379	0.465					Ribosomal protein S7 Translation elongation factors (GTPase)
LBUL_0349 LBUL_0350	RpsJ RpIC	0.429 0.454	0.353 0.364	2.733 2.467	3.095 2.792			Ribosomal protein S10 Ribosomal protein L3
LBUL 0351	RpID	0.400	0.326	2.371	2.825			Ribosomal protein L4
LBUL_0352 LBUL_0353	RpIW RpIB	0.378 0.393	0.302 0.316	2.116 2.018	2.767 2.457			Ribosomal protein L23 Ribosomal protein L2
LBUL_0354 LBUL_0355	RpsS RpIV	0.406	0.335 0.373	2.647 2.036	2.826			Ribosomal protein S19 Ribosomal protein L22
LBUL_0356	RpsC	0.423	0.370	2.201	2.528			Ribosomal protein S3
LBUL_0357 LBUL_0358	RpIP RpmC	0.498		2.632 2.213	2.560 2.669			Ribosomal protein L16/L10E Ribosomal protein L29
LBUL_0359 LBUL_0360	RpsQ RpIN	0.434	0.400	2.665 2.263	2.903 2.442	2.666		Ribosomal protein S17 Ribosomal protein L14
LBUL_0361	RpIX	0.464	0.460	2.485	2.853	2.000		Ribosomal protein L24
LBUL_0362 LBUL_0363	RpIE RpsN	0.414	0.461 0.427	2.609 2.180	2.987 2.835			Ribosomal protein L5 Ribosomal protein S14
LBUL_0364 LBUL_0365	RpsH RpIF	0.453 0.484	0.441 0.457	2.424 2.295	2.695 3.608			Ribosomal protein S8 Ribosomal protein L6P/L9E
LBUL_0366	RpIR		0.483	3.090	2.697			Ribosomal protein L18
LBUL_0367 LBUL_0368	RpsE RpmD	0.376	0.351 0.328	2.188 2.400	2.640 3.397	2.808		Ribosomal protein S5 Ribosomal protein L30/L7E
LBUL_0369 LBUL_0372	RpIO InfA	0.407	0.362	3.318	2.708			Ribosomal protein L15 Translation initiation factor 1 (IF-1)
LBUL_0373	RpmJ	0.419		2.305				Ribosomal protein L36
LBUL_0374 LBUL_0375	RpsM RpsK	0.462		2.288				Ribosomal protein S13 Ribosomal protein S11
LBUL_0377 LBUL_0382	RpIQ RpIM	0.430 0.325	0.442	2.139				Ribosomal protein L17 Ribosomal protein L13
LBUL_0383	RpsI	0.415	0.442					Ribosomal protein S9
LBUL_0421 LBUL_0496	TrmA Map	0.359	0.492		0.480 2.524			SAM-dependent methyltransferase related to tRNA (uracil-5-)-methyltransferase Methionine aminopeotidase
LBUL_0498	GCD1		0.448		5.087			Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)
LBUL_0501	TrmA		0.195					SAM-dependent methyltransferase related to tRNA (uracil-5-)-methyltransferase
LBUL_0506 LBUL_0521	PrfC RluA	0.292		0.447	4.576			Peptide chain release factor RF-3 Pseudouridylate synthase 23S RNA-specific
LBUL_0541	COG1544 SrmB			0.424	0.085			Ribosome-associated protein Y (PSrp-1)
LBUL_0549 LBUL_0633	PrfA			0.095	3.038			Superfamily II DNA and RNA helicase Protein chain release factor A
LBUL_0634 LBUL_0635	HemK SUA5		0.441 0.240					Methylase of polypeptide chain release factors Putative translation factor (SUA5)
LBUL_0654	RpsD	0.441						Ribosomal protein S4 and related protein
LBUL_0658 LBUL_0659	RsuA ValS		0.358 0.457		6.459			16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthase Valyl-IRNA synthetase
LBUL_0680 LBUL_0681	RluA IleS		0.422		3.940 4.516			Pseudouridylate synthase 23S RNA-specific Isoleucyl-IRNA synthetase
LBUL_0688	TrmU		2.445		8.246			Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase contains the PP-loop ATPase domain
LBUL_0695	Def		0.392		2.313			N-formylmethionyl-tRNA deformylase
LBUL_0696 LBUL_0699	FusA TRM1	0.448 0.147	0.332 0.226		2.191 3.769			Translation elongation factors (GTPase) N2 N2-dimethylguanosine tRNA methyltransferase
LBUL_0706	RpsO YSH1	0.235	0.377		2.775	3.616		Ribosomal protein S15P/S13E Brodicted exemusions of the bate locatemore feld invelved in RNA processing
LBUL_0707 LBUL_0709	TufB		3.587	2.430	2.087			Predicted exonuclease of the beta-lactamase fold involved in RNA processing GTPase - translation elongation factors
LBUL_0712 LBUL_0744	InfB SrmB	4.095		0.330				"Translation initiation factor 2 (IF-2; GTPase)" Superfamily II DNA and RNA helicase
LBUL_0747 LBUL_0749	COG0012 YSH1		0.472 0.339					Predicted GTPase probable translation factor Predicted exonuclease of the beta-lactamase fold involved in RNA processing
LBUL_0771	RsuA	0.499						16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthase
LBUL_0776 LBUL_0812	InfB HisS		0.278 0.288		3.234 6.877			"Translation initiation factor 2 (IF-2; GTPase)" Histidyl-tRNA synthetase
LBUL_0813 LBUL_0825	AspS RimK		0.295	0.132	7.026 0.391			Aspartyl-tRNA synthetase Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)
LBUL_0842 LBUL_0870	SpoU		2.513		2.164			rRNA methylase
LBUL_0911	BMS1 AsnS		0.496		0.363 6.099			GTP-binding protein required for 40S ribosome biogenesis Aspartyl/asparaginyl-tRNA synthetase
LBUL_0919 LBUL_0924	COG5099 HemK				4.804 4.098			RNA-binding protein of the Puf family translational repressor Methylase of polypeptide chain release factors
LBUL_0930	RluA RimL	2.875 0.228		0.448	0.046	0.334		Pseudouridylate synthase 23S RNA-specific
LBUL_1000 LBUL_1083	RimL	0.220		0.120				Acetyltransferase including N-acetylase of ribosomal protein Acetyltransferase including N-acetylase of ribosomal protein
LBUL_1089 LBUL_1110	Sun AsnS		0.350		10.118			tRNA and rRNA cytosine-C5-methylase Aspartyl/asparaginyl-tRNA synthetase
LBUL_1111 LBUL_1166	AsnS GlyS	0.378	0.460 0.288		2.030 4.216			Aspartyl/asparaginyl-tRNA synthetase
LBUL_1167	GlyQ	0.576	0.288		3.204			Glycyl-tRNA synthetase beta subunit Glycyl-tRNA synthetase alpha subunit
LBUL_1169 LBUL_1173	SelB RpsU	0.256	0.499		2.176 4.343			Selenocysteine-specific translation elongation factor Ribosomal protein S21
LBUL_1189 LBUL_1197	Gid PcnB			0.412	2.657			NAD(FAD)-utilizing enzyme possibly involved in translation
LBUL_1197 LBUL_1225 LBUL_1226	FusA	0.341						tRNA nucleotidyltransferase/poly(A) polymerase Translation elongation factors (GTPase)
LBUL_1226 LBUL_1239	ZUO1 TruB		2.857	4.501	2.867			Ribosome-associated chaperone zuotin Pseudouridine synthase
LBUL_1241	InfB Tsf	0.408		3.477				"Translation initiation factor 2 (IF-2; GTPase)"
LBUL_1253 LBUL_1254	RpsB	0.408	0.276	3.002	5.257			Translation elongation factor Ts Ribosomal protein S2
LBUL_1255 LBUL_1269	HemK SrmB		0.254		3.622 0.116			Methylase of polypeptide chain release factors Superfamily II DNA and RNA helicase
LBUL_1273 LBUL_1279	RpIS TrmD	0.206 0.191	0.458		0.335			Ribosoma protein L19 tRNA-(guanine-N1)-methyltransferase
LBUL_1280	RimM	0.242	0.448		0.335			RimM protein required for 16S rRNA processing
LBUL_1281 LBUL_1296	RpsP SrmB	0.415	0.391	0.290				Ribosomal protein S16 Superfamily II DNA and RNA helicase
LBUL_1299	RpmB						2.098	Ribosomal protein L28



Experimental evolution of yoghurt cultures improves co-culture growth and interactions



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ABSTRACT

Most microbial ecosystems consist of many different species that influence each other. The evolutionary driving forces that shape the concomitant microbial interaction networks are poorly understood and little experimental information exists on the co-evolution of microbes. Yoghurt is milk fermented by the lactic acid bacteria Streptococcus thermophilus and Lactobacillus bulgaricus. It is one of the best studied mixed cultures and represents a simple and attractive model system for ecological and evolutionary studies. L. bulgaricus and S. thermophilus have coevolved towards optimal growth in milk, where they stimulate each other's growth through multiple nutritional interactions. However, how, with what speed and to what extent these nutritional interactions evolve is not known yet. To address this evolution process, we selected genomically characterized strains of S. thermophilus and L. bulgaricus that had not been grown together before and therefore are expected not to have optimized their metabolism to co-cultivation. These strains were cultivated in co-culture in milk for more than 1000 generations in sequential batch cultures under a constant growth regime. The evolved mixed culture showed improved acidification rate, survival and exopolysaccharide production, which are all important industrial traits. Moreover, combinatorial cocultivation of the parental and evolved strains showed that co-evolution of these strains resulted in increased mutual stimulatory effects. Sequencing of the genomes and transcriptome profiling of the parental and the evolved strains revealed mutations that affected the acquisition of sulfur amino acid and branchedchain amino acids, folic acid and long-chain fatty acids. These results indicate that the canonical nutritional dependencies of S. thermophilus and L. bulgaricus in amino acid, purine and fatty acid metabolism were strengthened in this short adaptation period. As the resulting adapted co-culture has useful industrial properties, this approach not only shows that experimental evolution can be used to study microbial interaction networks but can also be a powerful tool to improve industrial traits paving the way for creating new starter cultures with improved characteristics

INTRODUCTION

Most microbial ecosystems, including industrial fermentations, consist of many different species that have complex interactions contributing to the ecological structure of the community (7, 16). Mutual effects on fitness between interacting

microbes are an effective means of classifying these interactions (reviewed in Sieuwerts et al. (27)). A further unraveling of these interactions is the key in understanding and rationally improving industrial fermentations. Important questions are how stable communities of interacting microorganisms evolve and how the interactions influence the consortium members. Recent advances in the fields of microbial evolution (2, 34) and functional genomics (14) shed light on the mechanisms driving the evolution of interactions. Low complexity microbial ecosystems are attractive models to further study the evolution of interacting organisms. Food fermentations offer this opportunity as they are typically carried out by a small number of dominant strains. Yoghurt can be regarded as the paradigm. It is (bovine) milk fermented by the lactic acid bacteria Streptococcus thermophilus and Lactobacillus delbrueckii subsp. bulgaricus and has great industrial relevance; the worldwide turnover of yoghurt was 34 billion US \$ in 2007 (20). The two lactic acid bacteria stimulate each other's growth and acid production when grown together in milk, in a process referred to as proto-cooperation. Their interactions are mainly related to purine and amino acid (AA) metabolism. L. bulgaricus provides S. thermophilus with amino acids and peptides through the action of its exoprotease PrtB (4, 25, 35). In turn, S. thermophilus provides formic acid, folic acid (6) and carbon dioxide (9), all involved in purine and arginine metabolism. Exopolysaccharides (EPS) are also suggested to play a role in the interactions, but their exact function remains to be established (29).

In this work, we applied experimental evolution to adapt a novel strain combination of genomically characterized S. thermophilus (3) and L. bulgaricus (17) under a strict growth regime. In addition, we addressed the molecular mechanisms and phenotypical traits that form the basis of their stable protocooperation. For this purpose, we used a combination of genomics approaches, i.e. genome re-sequencing and transcriptome profiling. and physiological characterization, i.e. testing of acidification, growth and survival, end metabolite production and EPS production. We observed that the experimental evolution improved important functionalities, such as acid resistance and viscosity, that resemble those of a commercial starter. We linked these improvements to mutations in genes in pathways that were previously shown to be involved in the proto-cooperation between the two bacteria (29). As the resulting adapted coculture has useful industrial properties, this approach not only shows that experimental evolution can be used to study microbial interaction networks but can also be a powerful tool to improve industrial traits paving the way for creating new starter cultures with improved characteristics.

MATERIALS AND METHODS

Strains and culture conditions.

Streptococcus thermophilus CNRZ1066 (3) and Sts (from the commercial starter I-St) were maintained in M17 broth (Oxoid) containing 22% glycerol (Scharlau) at -80°C, Lactobacillus delbrueckii subsp bulgaricus ATCC BAA-365 (17) and lb (from I-St) in MRS broth (Merck) with 22% glycerol at -80°C. Pre-cultures of both species were made as mono cultures in UHT-treated 10% (w/v) reconstituted skim milk (Nilac, NIZO food research), referred to as milk in the rest of the paper, for 24 h at 37°C. Mixed cultures for the experimental evolution studies were obtained by inoculating 10 mL of milk with pre-cultures to a density of approximately 10⁶ cells per mL per strain. The experiments were carried out in duplicate. The cultures were propagated by transferring 1.5% (v/v) daily until a theoretical number of 1000 generations was reached (167 transfers). Acidification and final cell counts were monitored with regular intervals of approximately 3 weeks (i.e. 127 generations). After 49, 97, 133, 219, 304, 365, 456, 517, 602, 699, 809, 930 generations freezer stocks were prepared for later experimentation by mixing of 1 volume 60% glycerol with 2 volumes yoghurt. From one final culture, single colony isolates were obtained that were designated S. thermophilus NIZO3938 and L. bulgaricus NIZO3939. Single colony isolate freezer stocks were obtained by selective plating (M17 agar (Oxoid) supplemented with 1% glucose at 45°C for S. thermophilus and MRS agar (Merck) at 45°C anaerobic for L. bulgaricus). Colonies of these plates were streaked onto new plates. Single colonies from the second plates were grown in liquid media and visually inspected with a microscope for infections.

Pre-cultures in follow-up experiments were made as described above. After 24 h, the optical density at 600 nm was measured in duplicate using 1 volume of milk culture mixed with 9 volumes of a 0.2% NaEDTA (w/v) / 0.2% NaOH (w/v) solution. Final cultures were inoculated to a start OD_{600} of 0,005 per strain (corresponding to approximately 10^6 cells per mL).

For monitoring of acidification activity during the evolution process, 10 mL milk was inoculated with 1% of a 24 h old mixed culture and pH was followed at 37°C for 24 h using the Cinac system (Ysebaert, France). *S. thermophilus* and *L. bulgaricus* were enumerated by spotting serial dilutions onto agar plates as described before (28). *S. thermophilus* was plated onto TY agar supplemented with 1% (w/v) glucose and *L. bulgaricus* was plated onto MRS agar. Both were

incubated at 37°C for 6 h before being transferred to 45°C for another 20 h, *L. bulgaricus* anaerobically.

The acidification rate (Δ lactic acid/ Δ t in mM/h) was calculated as follows. A calibration curve of lactic acid concentration (known y values) in milk versus pH (known x values) was prepared. Using the GROWTH function in Microsoft Excel, the measured pH values in the culture (new x values) were calculated into lactic acid concentration.

Significant differences in acidification rate and CFU counts between samples were calculated with a two-tailed Students t-test (p=0.05).

Viscosity measurements.

For viscosity measurements 120 mL cultures were grown in milk at 37°C for 48 h. Viscosity was measured using a viscosimeter M5 (Haake Fisons) with a rotation speed of 0 increasing to 400 rotations per s at 37°C. Each strain combination was measured in duplicate. Significant differences were determined using a Students t-test (p=0.05) on the average measurements between 50 and 55 rotations per sec.

EPS isolation.

EPS were isolated from 275 mL cultures grown for 24 h at 37°C as described before (29). All isolations were performed in duplicate.

Metabolite analysis with HPLC and GC-MS.

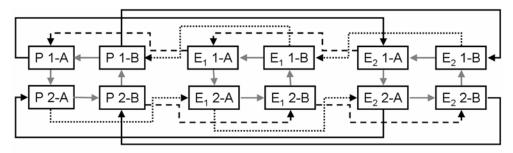
Duplicate samples for HPLC analysis were taken from cultures and frozen at -20°C in 2 mL eppendorf tubes until analysis. For acid analysis, proteins and fat were precipitated with perchloric acid. After filtration using a Spartan 30/B (Schleicher & Schuell) filter, the liquid was used for high pressure liquid chromatography. In a HPX-87H column (BioRad 300 x 7.8 mm) column at 60°C with a flow of 0.6 mL/min 0.005 M sulfuric acid 25 μ L of the solution was injected. For sugar analysis, 1 g of culture was mixed with 10 mL of a solution composed of 4.55 g/L Zn(CH₃COOH)₂.2H₂O (BDH Analar), 2.73 g/L H₃[P(W₃O₁₀)]₄.xH₂O (BDH Analar) and 2.9 mL/L 99.8% acetic acid (BDH Analar). After filtering this solution with a Spartan 30/B filter, was used for chromatography. In a HPX-87H column with a flow of 0.4 mL/min 0.01 (w/v) NaCl, 25 μ L of the solution was injected. Components were detected using a RID-10A (Shimadzu, Japan) and ERC-7510 (Erma optical works Ltd, Japan) refraction index meter at 40°C for organic acids and sugars, respectively. Data were analyzed using Chromeleon (Dionex) and compared to standard series of desired components.

GC-MS analyses were performed as described before (29).

Resequencing and sequence analysis.

The parental strains S. thermophilus CNRZ1066 and L. bulgaricus ATCC BAA-365 and their evolved variants NIZO3938 and NIZO3939 were sequenced using Illumina Solexa sequencing (GATC Biotech AG, Konstanz, Germany). The sequences of the reads were 36 base pairs and covered the genomes 80-120 times (see Supplementary Table 1). Single nucleotide polymorphisms (SNPs) and insertions/deletions (INDELs) were detected by comparing the acquired sequences with the published genome sequences (3, 17) using in-house developed software (van Hijum et al., unpublished). The reads (trimmed at 5' and/or 3' side to various sizes and untrimmed) were aligned to the reference (repetitive sequences of 20 bp were masked by N nucleotides). The alignments of the reads to the repeat-masked reference were filtered based on various cutoffs (e.g. minimal ratio 1/10 minor / major nucleotides; in other words, in order for a SNP / insertion to be selected the major nucleotide in the reads should at least be 10x more frequent than the alternative nucleotides). Only mutations that were present in at least 10 reads and a ratio of major / minor nucleotide of 10 were used for further analysis. The mutations were confirmed by PCR amplification of a 500 bp fragment carrying the mutation site and subsequent sequence analysis. (BaseClear, Leiden, the Netherlands). These fragments were also amplified and sequenced in the duplicate final evolved culture to identify possible mutations in the same regions.

The potential impact of the mutations was determined by assessing the deduced amino acid changes using protein alignment tools and by inspection of 3D structures (http://www.ncbi.nlm.nih.gov/Structure/) of orthologous proteins where relevant and available (18). Intergenic regions were checked for promoter sequences with PPP (http://bamics2.cmbi.ru.nl/websoftware/).



Cy3 → Cy5

Figure 1. Experimental design of the hybridizations for transcriptome profiling. 1 and 2 indicate the first en second exponential phase; A and B indicate two biological duplicates; P, E_1 and E_2 indicate the parental mixed culture, the first evolved mixed culture and the second evolved mixed culture, respectively.

Transcriptome profiling.

The effect of the experimental evolution on gene expression was tested for both evolved cultures. Therefore, parental and evolved mixed cultures were prepared and sampled in the first and second exponential phase (i.e. 4.5 h and 7.5 h for the parental culture and 4 h and 6.25 h for the evolved cultures). mRNA isolation, cDNA synthesis and DNA micro arrays were performed and data were analyzed as described before (29). Figure 1 depicts the experimental design of the hybridizations. Significant differential expression of genes was defined as a fold change of 2 or more and a FDR value of 0.05 or lower. However, also more general effects were taken into account, e.g. a fold change below 2 with a low FDR value.

RESULTS

Experimental evolution.

We selected the strains S. thermophilus CNRZ1066 and L. bulgaricus ATCC BAA-365 as they had been characterized at the genomic level and to the best of our knowledge had no history of co-cultivation. The selected strains both originate from French yoghurt starter cultures. Experimental evolution was applied to study the evolution of their interactions. For this purpose, the selected strains were cultured together in skim milk for more than 1000 generations by serial batch cultivation at 37°C to ensure an approximate ratio of 1 between both yoghurt strains and the possible application of mesophilic probiotics, such as Lactobacillus plantarum (discussed in Chapter 7). The evolution of the population composition and its activity were monitored by determining the colony-forming unit (CFU) counts and acidification kinetics at three week intervals. We observed an incremental increase of the acidification rate (see Figure 2A). This is also illustrated by comparison of the maximal acidification rate (Δ lactic acid/ Δ t) and the time the adapted culture needed to reach this maximal rate (see Figure 2B). In addition, the acidification profile throughout the experiment and the final evolved cultures did not show the transition phase between the two exponential growth phases that is characterized by a temporary reduced acidification rate (29). Moreover, the final colony counts increased in the course of evolution. These step-wise increases suggest the involvement of multiple mutational events. All these observations were confirmed in an independent duplicate experiment (data not shown).

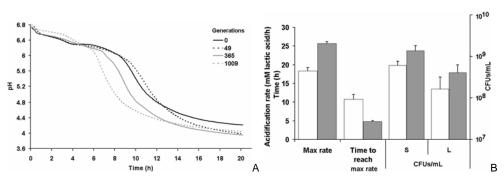


Figure 2. Experimental evolution of a mixed culture of *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365. The strain combination was allowed to adapt to milk for 1009 generations. A, the acidification profiles of the culture through evolutionary time after 0, 49, 365 and 1009 generations. B, maximal acidification rates, times within fermentations to reach these rates, and final CFU counts after 0 (white bars) and 1009 (grey bars) generations of the mixed culture. Error bars indicate standard deviations of sextuplicate experiments. S, *S. thermophilus*; L, *L. bulgaricus*.

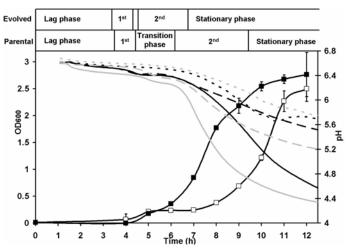


Figure 3. Acidification and growth of parental and evolved cultures. Error bars indicate standard deviations of duplicate measurements. The line with \Box represents OD_{600} of the parental mixed culture; **•** represents OD_{600} of the reconstituted evolved mixed culture. Other lines indicate acidification curves: *S. thermophilus* parental strain CNRZ1066 and evolved strain NIZO3938 (striped black and striped grey, respectively), *L. bulgaricus* parental ATCC BAA-365 and evolved strain NIZO3939 (dashed black and dashed grey, respectively), and the parental and evolved mixed culture (solid black and solid grey, respectively). 1st and 2nd refer to the first and second exponential phase.

Phenotypic comparison of parental and evolved variants.

For further experimentation, 14 representative *S. thermophilus* and *L. bulgaricus* single colony isolates (see below) of the evolved cultures were selected. Of these, two were designated *S. thermophilus* NIZO3938 and *L. bulgaricus* NIZO3939,

hereafter referred to as evolved *S. thermophilus* and *L. bulgaricus*. These two strains combined will be referred to as the reconstituted evolved mixed culture that was subsequently cultivated in milk (see Figure 3). The acidification rate and growth showed global phenotypic changes that were in agreement with the observations described above for the final evolved culture (see Figure 2).

The mono and mixed parental and evolved cultures were analyzed for the levels of lactose, glucose, galactose, lactic acid, acetic acid and volatile flavor compounds. Additionally, the average and maximal growth rate (g of biomass/h), rate of product or substrate production (mmol/h) and the yield of produced biomass/product per consumed lactose (g/mmol or mmol/mmol) were calculated (see Table 2). Lactose uptake and lactic acid production rates were in accordance with the acidification curves in Figure 3. Interestingly, the biomass yield per mol of consumed lactose was higher in the evolved *S. thermophilus* and mixed cultures compared to their parental equivalents.

Of the four major flavor components in yoghurt, the production of acetaldehyde increased in the evolved mixed culture compared to the parental mixed culture, notably due to the faster growth of evolved *S. thermophilus* (see Table 1). The levels of 2-propanone remained equal while the levels of diacetyl and 2,3-pentadione decreased remarkably in the evolved culture.

Table 1. Analysis of volatile compounds in triplicate mono and mixed cultures. The used (combinations of) strains are *S. thermophilus* CNRZ1066, NIZO3938 and Sts, *L. bulgaricus* ATCC BAA-365, NIZO3939 and Ib, and the mixed cultures CNRZ1066/ATCC BAA-365, NIZO3938/NIZO3939 and Sts/lb (I-St). P, parental strain(s); E, evolved strain(s). Significant differences were determined with a Students t-test (p=0,05) per component per type of culture (*S. thermophilus*, *L. bulgaricus* or mixed). The values within a row (i.e. for each component) that have the same letter ($a^{, b, c}_{, c}$) are significantly different.

	Concentration in culture (µM)												
Component	S	. thermophi	lus		L. bulgaricu	IS	Mixed culture						
	Р	E	Sts	Р	E	lb	Р	E	I-St				
Acetaldehyde	108.36 ^a	168.25	156.17 ^a	410.21 ^a	258.04	251.69 ^a	252.16 ^{ab}	367.05 ^a	350.15 ^b				
Methanethiol	2.07	6.90	4.93	9.87 ^a	14.00 ^b	27.00 ^{ab}	21.67	28.33	21.67				
2-Propanone	316.67 ^a	493.33 ^b	813.33 ^{ab}	1020.00 ^a	713.33 ^b	3666.67 ^{ab}	1290.00	1146. ⁶⁷	1366.67				
Dimetylsulfide (DMS)	6.17 ^a	6.67 ^b	11.67 ^{ab}	2.27 ^a	3.23	6.67 ^a	9.37	8.90	9.03				
2-methyl-propanal	2.00 ^a	2.35 ^b	12.13 ^{ab}	4.50 ^a	6.75	3.67 ^a	7.63	7.00	14.47				
Diacetyl	730.00 ^{ab}	360.00 ^{ac}	2466.67 ^{bc}	74.00	28.00	15.00	2333.33 ^a	296.67 ^{ab}	1600.00 ^b				
2-Butanone	38.00 ^a	36.33 ^b	130.00 ^{ab}	41.67	35.00	39.33	68.00 ^a	53.67 ^b	130.00 ^{ab}				
Ethylacetate	11.67 ^a	12.00 ^b	23.33 ^{ab}	13.67 ^a	12.33 ^a	13.67	25.67	17.67 ^a	28.00 ^a				
3-methyl-butanal	0.30	0.35	0.43	1.63 ^a	33.50 ^{ab}	2.30 ^b	1.40 ^{ab}	4.90 ^{ac}	15.67 ^{bc}				
2-methyl-butanal	0.20 ^a	3.50 ^b	1.07 ^{ab}	0.87	5.87	0.70	0.60 ^a	1.60	3.30 ^a				
2-Pentanone	1.33 ^a	6.03 ^b	4.00 ^{ab}	14.00 ^a	11.23 ^b	47.67 ^{ab}	8.57	6.73	12.33				
2,3-pentanedione	41.67 ^{ab}	54.40 ^{ac}	143.33 ^{bc}	3.63	1.63	1.50	423.33 ^{ab}	78.33 ^a	83.67 ^b				
Dimethyldisulfide (DMDS)	0.13	0.47 ^a	0.20 ^a	0.90 ^a	0.90 ^b	1.43 ^{ab}	1.03 ^a	1.87	1.53 ^a				
2-Heptanone	1.77 ^a	8.67 ^b	5.10 ^{ab}	18.00 ^a	16.00 ^b	62.33 ^{ab}	9.40 ^a	9.10 ^b	38.00 ^{ab}				
Dimethyltrisulfide (DMTS)	0.23 ^a	0.53 ^a	0.20	0.73	0.77	1.10	1.60 ^a	2.87 ^a	1.93				

Table 2. Primary carbohydrate metabolism of parental and evolves cultures. For each culture, the amount of produced biomass, the rate of sugar consumption and acid production and the yield of biomass per amount of substrate consumed are depicted for the major growth phase (i.e. second exponential in the *S. thermophilus* and mixed cultures). Standard deviations are in parentheses. Abbreviations: P, parental; E, evolved; Sts, strain Sts; Ib, strain Ib; I-St, mixed culture of Sts and Ib; N.A., not applicable because lower than detection limit. See also Supplementary Figure 1.

	Biomass		Produced su	ubstrate / proc	luct (mM/h))		Yield (/mmol lactose consumed per h)				
	production (g/h)	Lactose	Glucose	Galactose	Lactic acid	Acetic acid	Biomass (g)	Glucose (mmol)	Galactose (mmol)	Lactic Acid (mmol)	Acetic Acid (mmol)	
S. th	ermophilus											
P. 0. 01	0.019	-2.572	N.A.	1.213	2.98	0.019	0.007	0	0.472	1.158	0.007	
	(0.007)	(0.423)		(0.323)	(0.991)	(0.005)	(0.003)	Ū	(0.137)	(0.42)	(0.002)	
Е	0.030	-2.034	N.A.	2.471	6.158	0.035	0.014	0	1.215	3.027	0.017	
	(0.005)	(1.061)		(0.449)	(1.261)	(0.012)	(0.005)		(0.476)	(1.338)	(0.012)	
Sts	0.046	-1.192	N.A.	1.572	3.358	0.079	0.039	0	1.318	2.816	0.066	
	(0.011)	(0.977)		(0.228)	(0.582)	(0.018)	(0.011)		(0.223)	(0.569)	(0.018)	
L. bu	Igaricus											
P	0.024	-2.676	0.768	1.874	2.604	0.094	0.009	0.287	0.700	0.973	0.035	
	(0.001)	(0.476)	(1.798)	(1.262)	(0.357)	(0.012)	(0.001)	(0.856)	(0.601)	(0.17)	(0.006)	
Е	0.020	-2.259	2.686	2.654	2.233	0.107	0.009	1.189	1.175	0.988	0.047	
	(0.004)	(0.464)	(1.164)	(0.085)	(0.459)	(0.029)	(0.002)	(0.541)	(0.039)	(0.213)	(0.013)	
lb	0.021	-1.433	0.188	1.174	2.109	0.151	0.014	0.131	0.820	1.472	0.105	
	(0.001)	(1.424)	(0.163)	(0.096)	(0.045)	(0.004)	(0.001)	(0.232)	(0.136)	(0.064)	(0.005)	
Mixe	d culture											
P	0.094	-4.076	-0.426	4.577	9.709	0.055	0.023	-0.105	1.123	2.382	0.013	
	(0.013)	(0.253)	(0.2)	(0.316)	(0.806)	(0.004)	(0.003)	(0.051)	(0.080)	(0.204)	(0.001)	
Е	Ò.197 ´	-5.849	-1.598	`9.021 [′]	19.958	0.171	`0.034 [´]	-0.273	`1.542 [´]	`3.412 [´]	0.029	
	(0.062)	(1.059)	(0.923)	(2.257)	(4.138)	(0.042)	(0.066)	(0.977)	(2.390)	(4.381)	(0.045)	
I-St	0.107	-4.175	N.A.	3.678	6.859	0.107	0.026	0	0.881	1.643	0.026	
	(0.007)	(0.088)		(0.243)	(0.531)	(0.031)	(0.001)		(0.021)	(0.046)	(0.003)	

Phenotypic and genetic heterogeneity.

Long-term propagation experiments with single-strain cultures may lead to a mixed culture of closely related variants carrying different mutation profiles (23). Therefore, heterogeneity of the evolved culture was tested on the 14 single-colony isolates of either species (see above). The different isolates were re-combined in mixed cultures of which acidification and outgrowth was tested. All behaved comparable to the final evolved mixed culture and different from the original mixed culture (data not shown). The same procedures were applied to cultures throughout the evolution process, which showed a step-wise improvement in acidification rate and final CFU counts similar as depicted in Figure 2. This indicates that there was no differentiation in phenotypically variable (sub-) strains in the evolved mixed culture in terms of acidification and growth.

Because not all mutations necessarily confer a benefit, it is possible that, although there was no apparent phenotypical heterogeneity in the evolved culture, there could still be genetic heterogeneity. The same 14 single colony isolates that were used for the growth test were tested for heterogeneity in a systematic analysis of all observed mutations (see below) by sequencing of PCR products. There was no difference in any of the isolates, indicating that the final evolved culture was genetically homogeneous.

Reconstituted mixed cultures of parental and evolved strains.

To further explore the physiological changes in the evolved strains, different combinations of parental and evolved S. thermophilus and L. bulgaricus were prepared and compared to the parental strain combination and the reconstituted mixed culture. Acidification of triplicate cultures was followed for 24 h and the viable count was determined by selective plating (see Figure 4). The mixed culture consisting of evolved S. thermophilus and parental L. bulgaricus showed a similar acidification profile as the reconstituted evolved mixed culture. The mixed culture containing parental S. thermophilus and evolved L. bulgaricus acidified milk with the same kinetics as the culture with both parental strains. Thus, the increased acidification can mainly be attributed to the evolved S. thermophilus. This was also reflected in the final CFU counts: neither S. thermophilus strain was significantly stimulated more by the evolved L. bulgaricus than by the parental L. bulgaricus. The parental L. bulgaricus was stimulated more by the evolved S. thermophilus than by the parental S. thermophilus. Finally, the evolved L. bulgaricus was not significantly differently stimulated by the evolved S. thermophilus strain compared to the parental strain. Remarkably, the mutual stimulatory effect in the evolved mixed culture was larger than in the parental mixed culture for both species as is exemplified by the higher increase in CFUs due to co-cultivation in the reconstituted evolved mixed culture compared to the parental mixed culture.

Survival.

Cells were repeatedly challenged to low pH and high lactic acid concentrations during the propagation. We hypothesized that mutations leading to increased acid resistance improved survival during stationary phase and this may contribute to a fitness increase. Therefore, we grew duplicate parental and evolved mixed cultures in milk for 20 h and subsequently exposed all cultures to the lactic acid concentrations and pH 3.65 encountered during stationary phase in evolved mixed cultures. Viability was tested by plating in triplicate every half hour (see Figure 5). The viability decreased according to exponential decay, which allowed calculating viability coefficients, i.e. the proportion of cells that survives each h (0.19 and 0.69 for the parental and evolved *L. bulgaricus*, respectively, and 0.65 and 0.59 for the parental and evolved *L. bulgaricus*, respectively). Using a pairwise two-tailed t-test, we determined that the evolved *S. thermophilus* was four times more

acid resistant at the used pH than the parental strain. The difference between the parental and evolved *L. bulgaricus* strains was not significant.

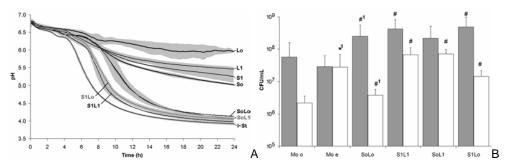


Figure 4. Acidification and final cell density (CFU) in reconstituted cultures. A, Acidification of reconstituted cultures. Grey zones indicate standard deviations of triplicate measurements. Abbreviations: So, parental *S. thermophilus*; S1, evolved *S. thermophilus*; Lo, parental *L. bulgaricus*; L1, evolved *L. bulgaricus*; I-St, commercial starter I-St. B, Colony-forming units after 24 h fermentation of *S. thermophilus* (grey bars) and *L. bulgaricus* (white bars) of the reconstituted cultures. Error bars indicate standard deviations of at least triplicate measurements. Abbreviations: Mo o, parental mono-cultures; Mo e, evolved mono-cultures; other abbreviations like in A. *, significantly different from the corresponding parental culture (two-tailed t-test, p=0.05); #, significantly different from the corresponding mono-culture; ¹, not significant when p=0.05, but significant when p=0.1).

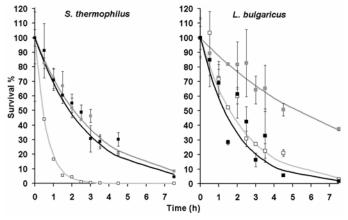


Figure 5. Acid tolerance of the evolved *S. thermophilus* (left) and *L. bulgaricus* (right) isolates compared to parental isolates and the industrial strains *S. thermophilus* Sts and *L. bulgaricus* Ib. The percentage of colony-forming unit counts in mixed cultures acidified to pH 3.65 with lactic acid was determined and compared to the reference (0 h): parental strains (\Box), evolved strains (\blacksquare) and I-St (\blacksquare). Error bars indicate standard deviations of sextuplicate measurements. Lines indicate fitted exponential decay curves used for calculating viability coefficients.

Viscosity and EPS production.

We noticed that the evolved mixed culture and that mono and mixed cultures with the evolved S. thermophilus strain were more viscous when grown in milk than the cultures with parental strains. Therefore, we determined the viscosity of duplicate reconstituted cultures of parental and evolved strains from the evolved culture discussed above and from strains isolated from the independent duplicate evolution experiment. These will be referred to as the second evolved S. thermophilus and L. bulgaricus below. The two evolved S. thermophilus strains displayed a higher viscosity than the parental strain (see Table 3). This was also reflected in the mixed cultures. There was no difference in viscosity between the parental and the two evolved L. bulgaricus mono cultures. In cultures consisting of one parental strain and one evolved strain, viscosity was enhanced by the application of the evolved S. thermophilus, but not by the evolved L. bulgaricus. These results strongly indicate that the increased viscosity in the evolved mixed culture can be attributed to a changed phenotype of the evolved S. thermophilus strains. Indeed, the amount of EPS produced after 24 h culturing was higher in the evolved S. thermophilus culture than in the parental culture. The concentration in the mixed evolved culture more than doubled compared to the reconstituted parental mixed culture. As the increase in biomass of the evolved mixed culture was less than twice that of the parental mixed culture (see Figure 3), the increase in EPS production can not only be attributed to a higher biomass. The evolved L. bulgaricus showed a slight increase when compared to the parental L. bulgaricus culture. It is evident that more EPS was produced in the mixed cultures than in the mono cultures and that in the evolved cultures, especially that of S. thermophilus and the mixed culture, more EPS was produced than in the parental cultures.

Table 3. Viscosity and EPS production in the parental and evolved cultures. P, parental strain(s); E_1 , evolved strain(s) NIZO3938 and/or NIZO3939; E_2 , evolved strain(s) from the duplicate evolved culture; N.D., not determined. Values within parentheses represent standard deviations of duplicate experiments.

	S	S. thermo	ophilus	6	L. bulgaricus				Mixed culture			
	Р	E1	E_2	Sts	Р	E1	E2	lb	Р	E1	E_2	I-St
Viscosity (mPas)	62	158	341	146	194	243	229	187	107	278	300	253
	(8)	(30)	(59)	(8)	(26)	(8)	(10)	(25)	(6)	(30)	(21)	(0)
	0.80	1.35			1.18	1.52			1.46	3.91		
EPS (g/L)	(0.02)	(0.26)	N.D.	N.D.	(0.12)	(0.03)	N.D.	N.D.	(0.04)	(0.48)	N.D.	N.D.

Comparative genome sequence analysis of parental and evolved isolates.

The data presented above clearly indicate that the phenotypic differences between the parental and evolved strains are stable and were caused by mutations in the genomic DNA sequence during the experimental evolution process. Therefore, the genomes of the parental and the evolved strains were sequenced using Illumina Solexa sequencing and compared to the reference sequence. Subsequently, mutations were detected by determining the (gaps in) overlap between the two SNP/INDEL lists (see Table 4).

Table 4. Mutations in the evolved strains *S. thermophilus* NIZO3938 and *L. bulgaricus* NIZO3939 as compared to their parental strains. Mutations that could have an effect based on protein structure are indicated in bold (see text for explanation). The primers used for the PCRs to confirm the presence of mutations in strains NIZO3938 and NIZO3939 and the strains from the duplicate evolved culture are depicted in Supplementary Table 2. N.D., not determined; ^a, according to reference (31), the DegV family protein is involved in fatty acid transport or metabolism; ^b, according to reference (15), the Fic family protein is involved in cell division and is suggested to be involved in the synthesis of 4-aminobenzoic acid or folic acid; ^c, annotation following (17).

	Deee		Tet-		AA	Mutation in duplicate culture		
Position	Base	Locus ID	Total AA	Gene annotation (ERGO)	change	Position	Base	AA
oonion	onungo	Loodo ID	701	Conc annotation (Erroc)	onange	Position	change	change
		IIZO3938						
151195	G>T	str0133 (rpoE)	193	DNA-directed RNA polymerase delta chain (EC 2.7.7.6)	E178>STOP	No		
250442	C>-	str0242 (greA)	160	Transcription elongation factor greA	Q15>N; STOP at 32	No		
289618	C>A	str0303 (dctA)	402	Serine/threonine sodium symporter	L194>I	No		
85740	C>T	str0408 (gor)	450	Glutathione reductase (EC 1.8.1.7)	A138>V	No		
413374	G>T	str0438 (pyrH)	245	Uridylate kinase (EC 2.7.4)	M198>I	No		
586170	C>A	str0625 (rnr)	817	Exoribonuclease II (EC 3.1.13.1)	T180>N	No		
683939	G>C	str0724 (fur)	145	Ferric uptake regulation protein	D46>H	683939 683994	G>A ->A	D46>N 64>D; STOP at 66
725339	T>C	str0770 (pacL1)	878	Calcium-transporting ATPase (EC 3.6.3.8)	K339>E	No		
347292	G>A	str0923 (als)	560	Acetolactate synthase (EC 2.2.1.6)	G417>E	No		
1055098	C>A	str1201 (leuC)	464	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	V172>L	N.D.		
1067308	C>T	str1215	288	Lantibotic precursor	G236>S	No		
1110735	A>G	str1263 (gapN)	477	NADP-dependent glyceraldehyde-3- phosphate dehydrogenase (EC 1.2.1.9)	F228>L	1110738	T>C	N227>H
1182279	G>A	str1336 (rr07)	226	Two-component response regulator	N155>N	No		
1371875	C>A	str1546 (folC2)	420	Folylpolyglutamate synthase (EC 6.3.2.17) / Dihydrofolate synthase (EC 6.3.2.12)	G21>V	No		
425619	G>A	str1601 (dnaQ)	196		A139>V	1425838	G>C	A66>G
. bulgar	icus NIZ	O3939						
61 0 50		LBUL_0063	277	DegV family protein ^a	C62>S	N.D.		
301103		LBUL_0313	483	ATP-dependent RNA helicase	R18>W	No		
33736		LBUL_0343	1221	(EC 2.7.7.6)	R326>L	No		
341010	G>A	231 bp downstr. LBUL_0348		Protein Translation Elongation Factor G (EF-G);		No		
		156 bp upstr. LBUL_0349 (rpsJ)		SSU ribosomal protein S10P				
98290	A>C	LBUL_1085	96	Fic family protein ^b	V28>F	N.D.		
288314	T>C	LBUL_1377	682	Cell division protein Ftsl ^c	E655>G	No		
756309	G>A	LBUL_1933	141	Uncharacterized	R8>W	N.D.		

In *S. thermophilus*, 15 mutations were identified in coding regions, 14 single nucleotide substitutions and one single nucleotide deletion. In the evolved *L. bulgaricus*, there were 7 single nucleotide substitutions compared to the parental strain, of which 6 occurred in coding regions and one in an upstream region. Of all mutations there were 6 in *S. thermophilus* and 2 in *L. bulgaricus* that could have changed the functionality of the enzymes, either by introducing a stop codon or by changing the AA residue in the catalytic site. The discussed mutations are complemented with gene expression data. Global gene expression is discussed below.

Mutations in S. thermophilus. In S. thermophilus, there were four mutations in coding regions that were predicted to affect the catalytic sites of the encoded proteins (GreA, Fur, Als, GapN) and hence could contribute to the observed phenotype. The single nucleotide deletion in greA results in the introduction of a stop codon at the N-terminal part of the encoded transcription elongation factor GreA and renders it non-functional. No orthologues of greB, gfh1 (8) or dksA (24), which are essential for the cleavage of RNA in order to release the transcription machinery when it is locked, have been identified in the genome of S. thermophilus CNRZ1066. Therefore, it is likely that the cleavage of RNA in order to relieve locked transcription processes will be impaired in the evolved strain. Interestingly, the greA gene was lower expressed in the evolved S. thermophilus strain that was isolated from the duplicate experimental evolution culture. The observed missense mutation in the iron-responsive genes transcriptional repressor fur in the evolved S. thermophilus strains may result in a lower affinity as it interfered with the metal binding site 2 of this enzyme (26). A multiple alignment showed that this AA residue is highly conserved among LAB. It is always an asparagine or a glutamate, indicating the importance of a polar hydrophylic AA at that site. If a mutation causes Fur to be less active, it would result in high expression of the genes involved in iron transport genes such as the fatABCD iron ABC transporter and the iron permease feoAB. These genes were much higher expressed in the evolved S. thermophilus compared to the parental strain (respectively 10.4-37.8-fold and 2.5-2.6-fold). Additional information comes from a mutation at the same location in the S. thermophilus isolated from the duplicate experimental evolution culture. Considering the limited number of SNPs in the strains it is highly unlikely that exactly the same nucleotide is mutated in two separate evolved strains. In addition, this strain carried a second mutation in this gene leading to an early stop codon rendering a truncated protein that is likely to be dysfunctional. In this strain, the fatABCD complex was also over expressed 4.7-13.8-fold and the fur gene was 2.3-3.3-fold higher expressed compared to the parental strain.

The gene *als* codes for acetolactate synthase that is involved in the branchedchain amino acid (BCAA) synthesis and the production of diacetyl and acetoin. The *als* gene of the evolved strain contained a missense mutation, changing a glycine in a glutamic acid, at the binding site for the co-factor thiamine pyrophosphate. The exact effect of this mutation is not clear, but it is noteworthy that despite the fact that this gene was 5.0-fold higher expressed in the evolved *S. thermophilus* compared to the parental strain, there was no increase in production of diacetyl (see Table 1). In addition, there was a lower expression of BCAA biosynthesis genes and a higher expression of BCAA import genes in the evolved *S. thermophilus* compared to the parental strain. This all indicates that the mutation in *als* made its gene product less functional.

The observed missense mutation in *gapN* results in a F228L substitution that is located in the NAD binding site of the enzyme in the evolved *S. thermophilus* strain. GapN catalyses an important step in the glycolysis and therefore a mutation in this gene may yield a higher glycolytic flux. Interestingly, the second evolved *S. thermophilus* strain was found to carry a mutation resulting in the N227H substitution, just in the preceding residue. Altogether, this indicates that this region in the *gapN* gene has an important function and is prone to mutation.

Mutations in *L. bulgaricus.* In *L. bulgaricus*, there was one mutation affecting the catalytic site of a protein that could be involved in the interaction between *S. thermophilus* and *L. bulgaricus.* This C62S mutation in *LBUL_0063* was in the fatty acid binding site of the corresponding protein (19). The exact function of this protein of the DegV family is not known, but it is suggested to play a role in fatty acid transport or synthesis as a phosphotransferase (13, 31). Interestingly, the fatty acid metabolism genes were 2.2-3.2-fold lower expressed in the evolved *L. bulgaricus* than in the parental *L. bulgaricus*, except for the 1-acyl-glycerol-3-phosphate acyltransferase *LBUL_0106*, which was 3-fold higher expressed. This also occurred in mixed culture compared to mono culture (29) and suggests that *LBUL_0063* has a function in the acquisition of fatty acids other than *de novo* synthesis. The gene *LBUL_0343* encoding the RNA polymerase beta chain contained a mutation close to its DNA binding site. It is not clear whether this had an effect on the transcription efficiency.

Global changes in gene expression.

Because the evolved mixed cultures grew faster and had mutations that caused this, the effect of the experimental evolution on the global gene expression was tested for both evolved cultures. Presented data focuses on the sequenced evolved culture and is – where appropriate – complemented with data from the

second evolved culture. For an overview of all significantly differential expressed genes, see Supplementary Tables 3 and 4.

S. thermophilus. In the evolved S. thermophilus differential expression compared to the parental strain was mainly in genes involved in the purine and the AA metabolism. For instance, expression of pfl was 2.7-fold higher in the evolved strain in the second exponential phase. This was also the case for the second evolved S. thermophilus and indicates that a higher pyruvate-formate lyase activity is necessary tot sustain a higher growth rate. Interestingly, the gene responsible for CO₂ production from bicarbonate, cah, was lower expressed in both evolved strains compared to the parental strain. This indicates that there was possibly less production of CO₂ that aids in the purine metabolism in *L. bulgaricus* (see below) (9, 29). The lower CO_2 production is likely caused by a lower requirement for de novo biosynthesis of arginine and aspartate (1) due to an 8.2-fold higher expression of the L. bulgaricus exoprotease gene prtB already in the first exponential phase releasing more peptides from casein. The purine biosynthesis genes and those maintaining the C1 pool in the evolved S. thermophilus were higher expressed, but there was no difference in expression of folic acid production genes between the parental and evolved S. thermophilus. The higher expression of most genes in the purine production pathway may be due to the increased growth rate. Indeed genes for peptidoglycan synthesis were higher expressed indicating a higher growth rate. There were a number of remarkable changes in the AA metabolism. The glutamine ABC transport system encoded by str1979, str1580, str1581 and str1582 was higher expressed in the evolved culture compared to the parental culture. This suggests a higher flux through the arginine biosynthesis pathway / urea cycle, although there was no differential expression observed for that pathway. Similarly, the sulfur AA production pathways and BCAA import genes were higher expressed in the evolved strain compared to the parental S. thermophilus, especially in the first exponential phase. In fact, expression of BCAA import genes was reduced in the second exponential phase, probably due to the higher expression L. bulgaricus prtB. Interestingly, the expression of EPS production genes was higher in both evolved S. thermophilus and both evolved L. bulgaricus compared to their parental strains. This may explain the higher EPS production and higher viscosity of the evolved cultures, especially in the S. thermophilus and mixed cultures.

L. bulgaricus. In the evolved *L. bulgaricus* the two lactate dehydrogenases genes were 2.9 and 3.3-fold lower expressed in the first exponential phase compared to the parental strain. In contrast, *LBUL_2034* (pyruvate oxidase), responsible for a large portion of H_2O_2 production by *L. bulgaricus* (10, 29), was

2.7-fold higher expressed. The resulting increased iron catalyzed production of reactive oxygen species (ROS) may be the explanation for the mutations in fur, likely to result in less iron uptake in both evolved S. thermophilus strains. The purine production pathway genes were higher expressed in the evolved strain compared to the parental strain, especially in the first exponential phase. This is in accordance with a higher growth rate resulting in a higher nucleobase requirement. Similarly, the genes for the (incomplete (32)) pathway for folic acid production were higher expressed throughout the fermentation of the evolved culture. We hypothesize that (i) the higher growth rate required more folic acid than could be acquired from the medium while there would be a sufficient amount otherwise (see (29)) or that (ii) the mutation in the evolved S. thermophilus folC2 indirectly led to a lower secretion of folate and a concomitant lower availability to L. bulgaricus. There was a lower expression of sulfur AA biosynthesis genes in both evolved L. bulgaricus strains than in the parental strain. This may be a result of the higher expression of prtB liberating more sulfur AA form casein. BCAA metabolism also showed differential expression in evolved cultures. Adaptation clearly involved an increased supply of BCAA either through increased expression of BCAA biosynthetic genes (strain NIZO3939) or increased expression of the transporter encoded by LBUL 0341 (second evolved L. bulgaricus) (10).

Finally, fatty acid metabolism was affected. The two evolved *L. bulgaricus* strains seem to have found different solutions to increase the supply of long-chain-fatty acids (LCFA) for lipid biosynthesis. The first evolved *L. bulgaricus* lowered the expression of the LCFA biosynthesis genes and increased the expression of 1-acyl-glycerol-3-phosphate acyltransferase gene compared with the parental *L. bulgaricus*. In the second evolved strain, in contrast, expression of the complete biosynthetic pathways increased. Both responses indicate that in the evolved cultures, *L. bulgaricus* required more LCFA in order to sustain a higher growth rate. However, in the first case, *L. bulgaricus* acquires a sufficient amount from the medium and in the second case *L. bulgaricus* acquires more LCFA by *de novo* production.

Comparison of parental and evolved cultures to a commercial yoghurt starter.

Important functionalities in yoghurt of the parental and evolved cultures were bench-marked by comparison with the representative commercial starter I-St. We tested acidification, survival, viscosity and end metabolite profiles (organic acids and flavor compounds) production of *S. thermophilus* Sts, *L. bulgaricus* Ib (both from the commercial starter I-St) and their mixed culture in the same conditions as

in which the other strains were tested. Acidification of I-St was slightly faster (8.5 h to reach pH 4.5) than the evolved mixed culture (10 h) and this was mainly due to the shorter lag phase as the acidification rates in the second exponential phase were comparable (see Figure 4A). In fact, the maximal acidification rate in the evolved culture was higher (25.69±1.28 compared to 21.33±1.03 for I-St). The biomass yield of the evolved strains on lactose improved greatly (see Table 2). Moreover, the yield is significantly higher than that of I-St. In addition, the evolved *S. thermophilus* became much more acid tolerant at pH 3.65 than the original strain and was comparable to Sts (see Figure 5). The production of acetaldehyde, 2-propanone and 2,3-pentatone of the evolved cultures was closer to that of Sts, Ib and I-St than to the corresponding original cultures.

DISCUSSION

In this study, two strains of S. thermophilus and L. bulgaricus were co-evolved. It was shown that the evolved culture acidified faster and produced more EPS than the parental culture. Mutation analysis and gene expression studies showed that the cooperative interactions between the bacteria improved by a few mutations in genes involved in the interactions and fine-tuning gene expression of pathways related to the interactions. It is evident that interactions between consortium members influence the performance of individual bacteria that structures the whole community. In the field of microbial ecology the evolution of stable networks of interacting microorganisms is of great interest. In particular because the occurrence of cooperation is difficult to explain from an evolutionary point of view (5, 34). It was suggested that cooperative behavior, such as that between S. thermophilus and L. bulgaricus, can only occur stably if there is a direct benefit of executing this behavior (34). Moreover, the physical structure of its environment is essential for the performance of a microorganism, i.e. the density of the culture (11) and the dispersal of common goods or secreted products define the extent of interactions (12, 22). In this case, there is a positive feedback loop between the yoghurt bacteria. Because the optimal extent of this cooperative behavior is dependent on the used strains and media (30), it was expected that co-evolving two unfamiliar strains would lead to the optimization of existing interactions (2). Indeed, co-evolving S. thermophilus CNRZ1066 and L. bulgaricus ATCC BAA-365 for 1009 generations led in two independent experiments from a mixed culture that grows relatively slow to a culture that grows and acidifies at rates similar to those of

a commercial starter while approximately maintaining the same ratio between both species.

There were three major improvements in important functionalities of the microorganisms that are likely to increase the fitness: (i) the yield on lactose of the evolved cultures had increased compared to the parental cultures, (ii) the stimulation between the yoghurt bacteria had increased, and (iii) the evolved S. thermophilus showed improved survival at a low pH. The evolved cultures also displayed differences in traits relevant for industrial applications: (i) the evolved mixed culture grew and acidified faster than the parental culture, (ii) the production of EPS was increased in the evolved culture, leading to a higher viscosity and (iii) the production of important flavor components by the evolved mixed culture more resembled that of the commercial starter I-St than that of the parental culture. These improvements could mainly be attributed to the evolved S. thermophilus as the evolved L. bulgaricus was not significantly different from its parental strain in any of the measured properties, except its EPS and volatile production and mutual stimulation with the evolved S. thermophilus. This lack of effective evolution in L. bulgaricus in this study is striking and may be related to the fact that evolution so far shaped a very reduced genome (32) that provides little possibilities for further improvement.

Genetic and regulatory base underlying the adaptations.

There were 15 mutations identified in the evolved *S. thermophilus* and 7 in the evolved *L. bulgaricus* compared to their parental strains. In several cases these mutations could be correlated to differential expression of pathways involved in (or affected by) the interactions and to the found differences in phenotype.

Iron metabolism. The upregulation of the H_2O_2 -producing pyruvate oxidase gene in *L. bulgaricus* was likely the cause of the inactivating mutations in *fur* in *S. thermophilus*, leading to a higher expression of iron-responsive genes such as the *fatABCD* complex. Indeed, *fatA* was reported to be repressed by *fur* in *Vibrio anguillarum* (33). However, why the inactivation of *fur* is favorable remains unclear: a higher presence of ROS will increase the DNA-damaging Fenton reaction making high intracellular levels of iron unfavorable.

AA acquisition. BCAA availability for both bacteria is clearly a key determinant in the adaptation process as is demonstrated by the mutation in *als* in *S. thermophilus*, the increased expression of *prtB* and the BCAA import and *de novo* biosynthesis genes in *L. bulgaricus*. This was also reported before in mixed culture compared to mono culture (29). The higher expression of *prtB* appeared to supply a sufficient amount of sulfur AA for *L. bulgaricus*, but not for *S.*

thermophilus. While the former down-regulated sulfur AA production pathways in the evolved strain, the latter upregulated those pathways in order to achieve the higher growth rate. However, it is anticipated that the higher availability of peptides and of formic acid are the main reasons for the disappearance of the transition phase in co-culture growth (see Figure 3). Addition of these two components was shown to yield an acidification pattern of a parental mixed culture that resembles that of the evolved mixed culture.

LCFA acquisition. For the acquisition of more LCFA *L. bulgaricus* strains in both cultures found different solutions: (i) a higher expression of the LCFA production pathway genes and (ii) a lower expression of this pathways genes with a higher expression of genes involved in LCFA capture from the medium, which was also suggested to occur in mixed cultures compared to mono cultures (29). In the second case, there could be an important function for the mutated protein encoded by *LBUL_0063*, but an exact function of this protein other than fatty acid binding has not been established yet.

EPS production. The production of EPS increased in the evolved cultures as a result of higher expression of EPS production genes. However, it is unclear what triggered this induction as there is no mutation evidently related to EPS production. It could be that the higher EPS synthesis was a response associated with the higher acidification rate, i.e. the higher acidification rate caused a (local) lower pH leading to induction of EPS synthesis (21). That would also explain the lack of extra EPS production by the evolved *L. bulgaricus* in mono culture compared to its parental strain.

In conclusion, our results confirm that interactions between *S. thermophilus* and *L. bulgaricus* involve proteolysis, in particular sulfur AA and BCAA, formic acid, folic acid and EPS. It was shown that these interactions can be fine-tuned by a small number of mutations. This fine-tuning of interactions is relevant for the field of microbial ecology as well as for industry. Using experimental evolution, it is possible to acquire a mixed culture with improved functionalities, such as a higher biomass yield, increased mutual stimulation, a faster acidification, higher survival and more EPS production. It is anticipated that this methodology can be routinely applied as a strategy to improve new combinations of strains in order to develop new starter cultures with interesting traits. More specific, these findings open new possibilities for the development of industrially viable fermented foods containing poor performing probiotic strains or strains with prebiotic properties.

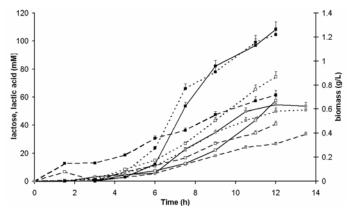
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SUPPLEMENTARY MATERIAL



Supplementary Figure 1. Fermentation profiles of parental, evolved and I-St mixed cultures. The solid lines indicate biomass (g/L); the dashed lines indicate lactose consumption (mM); the dotted lines indicate lactic acid production (mM). \Box , Parental mixed culture; \blacksquare , evolved mixed culture; \blacksquare , I-St. Error bars indicate standard deviations.

Supplementary Table 1. Number of sequenced bases and their coverage as resulting from the Illumina sequencing. P, parental strain; E, evolved strain. *, The most abundant base in the reads was found only in ≤ 0.8 fraction.

	Reads	Bases	Referential bases	Average coverage	Coverage ≤10	Poor quality*	Not covered
S. thermophilus P	5984359	215436924	1796226	120	19	831	13
S. thermophilus E	5614347	202116492	1796226	113	30	929	15
L. bulgaricus P	5083083	182990988	1856951	99	2909	955	2708
L. bulgaricus E	4162688	149856768	1856951	81	5963	1044	5653

Supplementary Table 2. Primers used for confirming SNPs in evolved *S. thermophilus* and *L. bulgaricus* by sequencing of PCR products and for the detection of possible mutations in the strains selected from the duplicate evolved culture. Both primers were used for the PCR amplification and one of the primers for sequencing. The PCR program used was as follows: 1x(94°C, 5 min); 35x(94°C, 30 s; 58°C, 30 s; 72°C, 45 s); 1x(72°C, 5 min; 4°C, hold). N.D., not determined.

Position	Sequence primer 1	Tm	Sequence primer 2	Tm	Product size (bp)
S. therm	ophilus				
151195	AAATGCCTTCATGGATGGTG	60.7	CGTATTCGATAATCAAAATTGTCC	58.9	449
250442	CATGTACTTTGTGGCGGATG	60.0	AAGAACGGGCAATCTTGATG	60.1	317
289618	AGCTACTAAAGCGGCTGCAC	59.8	ACCCATCATCACAAATGCAA	59.8	385
385740	GCGAGTATGGCTTTGATGTG	59.3	ATGGGCGATCCTTACGAAC	59.9	405
413374	CTTTGAAAAAGGGCGTATCG	59.7	GCACGGATAGCTCCAAATTC	59.7	473
586170	CATTGATGGTGACACTGTTGC	60.0	GCCTCTGCTTCAGCCATAAC	60.0	408

683939	AAGAAGAAAGGCGGCGATA	59 Q	AGTGGTCATGCCCCATAAAA	60.2	310
725339	ATCTGGAGCATCGGTTTCAC	60.1	CTCAATGGTGGCTCGATTTT	60.1	306
847292	GTCAGCCTGATGAAGGTACG	58.3	ACCAAAGTCAACCCCAGATG	59.8	401
1055098	N.D.		N.D.		
1067308	CCGTAGCCTGAGTAGCCTTC	59.1	AGGGCAAGTTGTTGCTCTTG	60.4	411
1110735	CGACCAAAGCTGTTACTTTTC	58.1	TGACGTTGTTGCCTTCAAAC	59.7	413
1182279	TTATCCATCATGACGCAACC	59.4	CAATATGGGTGGGGACGAC	61.0	409
1371875	CGCTCAACCAAGCCAAGTAG	61.0	TGGTTGTAGCTAGCAATCTTTGG	60.7	412
1425619	GGGCAGCAAAAGGATTGTTA	60.1	ATAAGATTGCCAAGGCTCCA	59.7	378
L. bulgari	icus				
61050	N.D.		N.D.		
301103	CAGGACATCGTTTTGCTGAA	59.8	GCCAGTTCTCTGGTTGGTTC	59.7	329
333736	TGCTGCAAGAAGCAGTTGAC	60.3	TAACTGAACGGCCGGAGTAG	60.3	171
341010	CCAAGGGAAAGCAATTCCA	61.0	TCATCGAGAATGCTGTGTTCA	60.4	300
998290	N.D.		N.D.		
1288314	ACTTCTGTCGCCACATTCG	59.9	GGCTCTACCAGGTCGTTCAC	59.7	454
1756309	ACTGCACTCTCCTGGTCAGC	60.6	GGCTAATTACCGATCCTTTGG	69.8	444

Supplementary Table 3. Significant (FDR≤0,05) differential expression of *S. thermophilus* genes between parental mixed cultures and evolved mixed cultures, per functional category. Values represent ratios between the first and the second condition. Loci that showed a mutation in the comparative genome sequence analysis are in bold. P, parental culture; E_1 , evolved culture that is used in all analyses; E_2 , duplicate evolved culture.

-		1ª e	xponential p	ohase	2 ^{na} €	exponential	phase	
Locus ID	Locus	E ₁ over P	E ₂ over P	E ₂ over E ₁	E ₁ over P	E ₂ over P	E ₂ over E ₁	Product
Amino aci	d transport a	and metabol	ism					
str0023	prsA1	0.266	0.198			0.453	0.414	ribose-phosphate pyrophosphokinase
str0026	araT	3.216				0.178	0.220	hypothetical protein
str0063	pepS					0.448		aminopeptidase PepS
str0083	cysE1	2.577	2.175			0.387	0.371	serine acetyltransferase
str0125	amiA2	4.728	5.356				0.358	oligopeptide ABC transporter substrate-binding protein
str0150	ilvA		4.225	2.467				threonine dehydratase
str0158	-	2.186	2.598		2.141			amino acid (glutamine) ABC transporter ATP-binding protein
str0159	•	5.305	5.739					amino acid (glutamine) ABC transporter substrate binding protein/permease protein
str0229	pepC				0.430	0.400		cysteine aminopeptidase C
str0283 str0296	ureC	7.213	7.525		8.622	0.468	0.248	urea amidohydrolase (urease) alpha subunit amino acid ABC transporter substrate binding protein, putative
str0298		1.213	2.243		6.053		0.246	succinyl-diaminopimelic descuccinlyasadipeptidase, truncated
str0298	-	4.360	3.360		5.959		0.137	succinyl-diaminopimelic descucciniyasadipeptidase, truncated
str0303	dctA	4.500	5.500		3.333	0.315	0.238	dicarboxylate/amino acid:cation (Na+ or H+) symporter
str0352	metB1		2.214			0.010	0.200	cystathionine gamma-synthase
str0353			2.382		0.348			aminotransferase (class II)
str0359	livJ		2.435		0.010	0.312		branched-chain amino acid ABC transporter substrate-binding protein
str0360	livH		3.123	2.688		0.371		branched-chain amino acid ABC transporter permease protein
str0361	livM		3.380	3.002		0.383		branched-chain amino acid ABC transporter permease protein
str0362	livG		3.958	2.425		0.457		branched-chain amino acid ABC transporter ATP binding protein
str0363	livF			2.206				branched chain amino acid ABC transporter ATP binding protein
str0366	cysM1	5.299	4.428		6.538		0.261	cysteine synthase
str0377	asnA					0.191	0.323	asparagine synthetase AsnA
str0378	lysC		4.757	3.161			0.495	aspartate kinase
str0411	nifS2	2.136						aminotransferase (class V), putative
str0430	gdhA		3.242	3.505				glutamate dehydrogenase
str0454	pepB	2.240				0.338	0.344	oligopeptidase
str0463 str0464	aspC3 argC					0.310	0.275	hypothetical protein N-acetyl-gamma-glutamyl-phosphate reductase
str0466	argB				0.310	0.272		acetylglutamate kinase
str0467	argD				0.510	0.322		acetylomithine aminotransferase
str0469	hom	4.663	9.315			0.0LL	0.387	homoserine dehydrogenase
str0470	thrB	2.554	5.144	2.014			0.354	homoserine kinase
str0526	carA		4.560	4.807				carbamoyl-phosphate synthase small subunit
str0527	carB		4.485	3.841				carbamoyl-phosphate synthase large subunit
str0555	-		2.463		3.533		0.174	alanine dehydrogenase, truncated
str0583	-				6.247		0.219	amino acid permease
str0584	mmuM				8.742		0.162	homocysteine methyltransferase
str0590	bcaT	0.362		2.836	0.428	0.345		branched-chain amino acid aminotransferase
str0629	pepQ						2.290	dipeptidase
str0645	aroA		2.251					3-phosphoshikimate 1-carboxyvinyltransferase
str0646	aroK		2.397			2.230		shikimate kinase
str0755	glyA	4.310	3.666				0.322	serine hydroxymethyltransferase
str0771	pabB		0.240			2.503 0.408	2.212	para-aminobenzoate synthetase component I
str0785	metE		0.240		0.332			5-methyltetrahydropteroyltriglutamatehomocysteine methyltransferase
str0786	metF		0.210	0.224		0.364 0.071	0.160	5,10-methylenetetrahydrofolate reductase cysteine synthase
str0846 str0847	cysM2 metB2		0.310	0.234 0.307	0.425	0.071	0.166	cysteine synthase cystathionine beta-lyase
str0847 str0848	cysE2		0.360	0.307	0.466	0.097	0.207	serine acetyltransferase, putative
str0875	Cyacz		0.420		0.400	0.000	0.398	amino acid (glutamine) ABC transporter, permease protein
str0875 str0876						0.300	0.398	amino acid (glutamine) ABC transporter ATP-binding protein
str0877						0.325	0.000	amino acid (glutamine) ABC transporter, substrate binding protein
str0904						0.402	5.130	hypothetical protein
str0923	als	4.956	6.076				2.021	alpha-acetolactate synthase
2			2.010				2.021	

	adhB dtpT					0.095	2.627 0.115	alcohol dehydrogenase, zinc-containing di-/tripeptide transporter
str0975	-						2.045	ABC transporter substrate binding protein, truncated
str0976 str0977	-		2.566 3.653				2.167 2.273	ABC transporter permease protein, truncated ABC transporter permease protein, truncated
str0984	- dagA		3.003			0.197	0.130	sodium/alanine glycine symporter
str0987	cysD	8.639	13.675		6.101		0.274	O-acetylhomoserine sulfhydrylase
str1007	pepN		3.893			0.354	0.234	lysyl-aminopeptidase, aminopeptidase N
str1061 str1127	- pepV		2.108			7.750	19.076	hypothetical protein dipeptidase
str1139	pepT	0.479	2.100				2.078	peptidase T
str1161	-	0.493			0.463	2.035	4.392	amino acid (glutamine) ABC transporter ATP-binding protein
str1162 str1163	-				0.480	2.310	4.090 4.490	amino acid (glutamine) ABC transporter substrate-binding protein amino acid (glutamine) ABC transporter permease protein
str1163						2.310	4.490	amino acid (glutamine) ABC transporter permease protein amino acid (glutamine) ABC transporter permease protein
str1181	aroH		0.344				0.356	hypothetical protein
str1200	leuD				0.357	0.390		isopropylmalate isomerase small subunit
str1202 str1203	leuB leuA				0.323 0.304	0.281 0.166		3-isopropylmalate dehydrogenase
str1203	metA		0.467		0.304	0.454	0.433	2-isopropylmalate synthase homoserine O-succinyltransferase
str1232	hisK	2.409	2.753			0.101	0.400	hypothetical protein
str1245		2.014						oxidoreductase, DadA family protein/D-amino acid oxidase
str1287 str1297	- dapA	5.552	6.636			0.318	0.427	transcriptional regulator, putative dihydrodipicolinate synthase
str1297	asd	0.002	0.030			0.227	0.427	aspartate-semialdehyde dehydrogenase
str1309	proWX	7.647	3.116		4.669		0.250	proline/glycine betaine ABC transporter
str1310	proV	9.053	6.126		15.640		0.127	proline/glycine betaine ABC transporter ATP-binding protein
str1312 str1316	proWZ sdaB	2.785			16.382	2.716 2.064	0.166 2.451	proline/glycine betaine ABC transporter substrate-binding protein L-serine dehvdratase beta subunit
str1317	sdaA		0.422			3.204	3.240	L-serine dehydratase alpha subunit
str1357	brnQ	4.768		0.260		0.179	0.113	branched chain amino acid transport system II carrier protein
str1361	-		2.266		2.240		0.311	amino acid transporter
str1438 str1439	amiF1 amiE	10.487 14.293	11.719 22.759		2.134 2.004	0.491	0.281 0.245	oligopeptide ABC transporter ATP-binding protein oligopeptide ABC transporter ATP-binding protein
str1439 str1440	amiD	18.279	22.759 24.126		2.004	0.491	0.245	oligopeptide ABC transporter ATP-binding protein
str1441	amiC	16.769	20.785		2.234		0.243	oligopeptide ABC transporter membrane-binding protein
str1443	-	3.384	3.767	0.500			0.450	oligopeptide ABC transporter substrate-binding protein, truncated
str1445 str1447	amiA3	20.191	2.001 31.443	2.506	2.252		0.260	oligopeptide ABC transporter substrate-binding protein oligopeptide ABC transporter ATP-binding protein, truncated
str1447 str1492		20.191	01.440		2.202	0.277	0.260	amino acid (glutamine) ABC transporter substrate-binding protein
str1493	•		0.499					hypothetical protein
str1501	gnIP		0.007	0.400		0.488	0.407	glutamine ABC transporter permease protein
str1517 str1519	- serB	0.388	2.907 0.439	2.198		3.778 2.122	6.485 2.465	permease, putative phosphoserine phosphatase
str1527	serA	5.980	19.856	3.320	0.494	0.346	2.400	D-3-phosphoglycerate dehydrogenase
str1529	serC	6.387	27.583	4.319		0.464		phosphoserine aminotransferase
str1532	gloA		0 70 4			3.381	5.655	glyoxalase l/lactoylglutathione lyase
str1535 str1536	potD potC	2.113	2.794 2.614					spermidine/putrescine ABC transporter periplasmic protein spermidine/putrescine ABC transporter permease protein
str1537	potB		2.312					spermidine/putrescine ABC transporter permease protein
str1545	-					0.408		aminoacid specific permease
str1579		6.405	6.284		9.193		0.138	amino acid (glutamine) ABC transporter substrate binding protein
str1580 str1581		5.346 7.747	4.755 7.211		9.759 3.921		0.127 0.321	amino acid (glutamine) ABC transporter ATP-binding protein amino acid (glutamine) ABC transporter permease protein
str1582		1.141	7.211		8.510		0.163	amino acid (glutamine) ABC transporter permease protein
str1587	trpA		6.597					tryptophan synthase subunit alpha
str1588	trpB		4.580					tryptophan synthase subunit beta
str1589 str1590	trpF trpC		3.389					N-(5'-phosphoribosyl)anthranilate isomerase indole-3-glycerol-phosphate synthase
str1636	aspC2		11.702			0.479		aspartate aminotransferase
str1652	- '		4.195		2.066		0.310	ABC transporter ATP-binding protein, amino acid
str1653		3.008	4.122		2.231		0.283	ABC transporter amino acid permease protein
str1654 str1710	- proA	2.302	3.221				0.324 0.317	ABC transporter substrate-binding protein, amino acid gamma-glutamyl phosphate reductase
str1711	proB					0.318	0.265	gamma-glutamyl kinase
str1728	aroG		2.679					3-deoxy-7-phosphoheptulonate synthase
						0.329 0.266	0.476 0.435	oligopeptide ABC transporter substrate-binding protein, truncated 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase, putative
str1815	dopD					0.200	0.435	pyrroline-5-carboxylate reductase
str1839	dapD	2.540						
str1839 str1852 str1871	proC ilvC	2.540	20.849	8.103				ketol-acid reductoisomerase
str1839 str1852 str1871 str1872	proC ilvC ilvN	2.540	9.738	6.235				ketol-acid reductoisomerase acetolactate synthase small subunit
str1839 str1852 str1871	proC ilvC	2.540	20.849 9.738 11.322	8.103 6.235 8.882				ketol-acid reductoisomerase
str1839 str1852 str1871 str1872 str1873 Carbohyd	proC ilvC ilvN ilvB		9.738 11.322	6.235				ketol-acid reductoisomerase acetolactate synthase small subunit
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114	proC ilvC ilvN		9.738 11.322	6.235				keto-acid reductoisomenase acetolacates ymthase small subunit acetolacate synthase large subunit phosphoglycerate mutase
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191	proC ilvC ilvN ilvB drate transpo gpmB -	rt and metab 0.339	9.738 11.322 olism 0.261	6.235			0.495	ketol-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase large subunit phosphoglycerate mutase PTS glucose-specific enzyme IIABC components, truncated
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191 str0194	proC ilvC ilvN ilvB drate transpo gpmB - pgi	rt and metab	9.738 11.322 olism 0.261 2.586	6.235			0.493	ketot-acid reductoisomenase acetolactate synthase small suburit acetolactate synthase large subunit phosphoglycerate mutase PTS glucose-specific enzyme IIABC components, truncated glucose-6-phosphate isomenase
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191	proC ilvC ilvN ilvB drate transpo gpmB -	rt and metab 0.339	9.738 11.322 olism 0.261	6.235	0.341			ketoi-acid reductoisomenase acetolacates synthase small subunit acetolacates synthase inge subunit phosphoglycerate mutase PTS glucose-cphosphate isomerase transketolase
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191 str0194 str0312 str0333 str0399	proC ilvC ilvN ilvB drate transpo gpmB - pgi tkt manL fruR	rt and metab 0.339 3.798 0.309	9.738 11.322 olism 0.261 2.586 2.124	6.235 8.882 2.275 4.996	0.341		0.493 0.443	ketoi-acid reductoisomenase acetolacates synthase small subunit acetolacates synthase large subunit phosphoglycerate mutase PTS glucose-6-phosphäte isomerase transkrotase mannoce PTS system component IIAB transcriptional greessor
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191 str0194 str0194 str0312 str0333 str0309 str0400	proC ilvC ilvN ilvB drate transpo gpmB - pgi tkt manL	rt and metab 0.339 3.798 0.309 0.463	9.738 11.322 olism 0.261 2.586 2.124	6.235 8.882 2.275 4.996 2.936	0.341		0.493 0.443	ketot-acid reductoisomenase acetolactate synthase small suburit acetolactate synthase large suburit phosphoglycerate mutase PTS glucose-6-phosphate isomerase transketolase mannose PTS system component IIAB transcriptional repressor furctose-1-phosphate kinase
str1839 str1852 str1872 str1873 Carbohyc str0114 str0191 str0194 str0312 str0333 str0339 str0400	proC ilvC ilvN ilvB drate transpo gpmB - pgi tkt manL fruR	rt and metab 0.339 3.798 0.309	9.738 11.322 olism 0.261 2.586 2.124 2.071	6.235 8.882 2.275 4.996 2.936 3.731	0.341	2 928	0.493 0.443 3.555	ketot-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase iarge subunit Phosphoglycerate mutase PTS glucose-specific anzyme ILABC components, truncated ghanketotase mannose PTS system component ILAB transcriptional groressor fructose-1-phosphate kinase PTS fructose-specific enzyme ILABC components, truncated
str1839 str1852 str1871 str1872 str1873 Carbohyd str0114 str0191 str0194 str0333 str0399 str0400 str0401 str0405	proC ilvC ilvN ilvB drate transpo gpmB - pgi tkt manL fruR	rt and metab 0.339 3.798 0.309 0.463	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016	6.235 8.882 2.275 4.996 2.936 3.731 3.086	0.341	2.928	0.493 0.443	ketot-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase iarge subunit PTS glucose-specific argyme IIABC components, truncated glucose-opticate isomerase transcriptional provision fructose-1-phosphate isomerase Truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated
str1839 str1852 str1871 str1872 str1873 Carbohyc str0114 str0191 str0191 str0191 str0192 str0333 str0399 str0400 str0405 str0407	proC ilvC ilvN ilvB drate transpo gpmB - pgi tkt manL fruR	rt and metab 0.339 3.798 0.309 0.463	9.738 11.322 olism 0.261 2.586 2.124 2.071	6.235 8.882 2.275 4.996 2.936 3.731	0.341	2.928	0.493 0.443 3.555 2.109	ketoi-acid reductoisomenase acetolacates synthase small suburit acetolacates synthase mall suburit phosphoglycerate mutase PTS glucose-police naryme IIABC components, truncated glucose-6-phosphate isomerase transketolase mannose PTS system component IIAB transcriptional growsor functione i-phosphate kiname IIABC components, truncated PTS functose-specific anzyme IIABC components, truncated
str1839 str1852 str1871 str1872 str1873 Carbohyc str0194 str0194 str0312 str0312 str0399 str0400 str0405 str0407 str0501	proC ilvC ilvN ilvN gpmB - pgi tkt manL fruB - -	rt and metab 0.339 3.798 0.309 0.463 0.393	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347	6.235 8.882 2.275 4.996 2.936 3.731 3.086		2.928	0.493 0.443 3.555 2.109 0.485	ketot-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase iarge subunit phosphoglycerate mutase PTS glucose-specific anyme IIABC components, truncated glucose-specific anyme IIABC acomponent IIAB mamore PTS anysen component IIAB mamore PTS hystem component IIAB PTS functose-specific enzyme IIABC components, truncated PTS functose-specific enzyme IIABC components, truncated N-acetylglucosamine-6-phosphate deacetylase beta-glucoside-specific PTS system IIABC component, truncated
str1839 str1852 str1871 str1872 str1873 Carbohyco str0114 str0191 str0191 str0191 str0312 str0333 str0309 str0400 str0401 str0405 str0407 str0501 str0512	proC ilvC ilvN ilvN gpmB - pgi tkt manL fruR fruB - - nagA - -	rt and metab 0.339 3.798 0.309 0.463	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092	6.235 8.882 2.275 4.996 2.936 3.731 3.086	0.341 3.190	2.928	0.493 0.443 3.555 2.109 0.485 0.469	ketol-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase inarge subunit phosphoglycarate mutase PTS glucose-phosphate isomerase transketolase mannose PTS system component IIAB transketolase Trautices-phosphate kinase IRAC components, truncated PTS functase-specific enzyme IIABC components, truncated PTS fu
str1839 str1852 str1871 str1872 str1873 Carbohyc str0194 str0194 str0312 str0312 str0399 str0400 str0405 str0407 str0501	proC ilvC ilvN ilvN gpmB - pgi tkt manL fruB - -	rt and metab 0.339 3.798 0.309 0.463 0.393	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347	6.235 8.882 2.275 4.996 2.936 3.731 3.086		2.928	0.493 0.443 3.555 2.109 0.485	ketoi-acid reductoisomenase acetolactate synthase small subunit acetolactate synthase inage subunit phosphoglycerate mutaze PTS glucose-6-phosphate isomerase transketolase mannose PTS system component IIAB transketolase Tructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated Naext/glucosamine-6-phosphate deacet/sae Naext/glucosamine-6-phosphate deacet/sae phosphopyrvate hydratase
str1839 str1852 str1871 str1872 str1873 Carbohyo str0114 str0191 str0194 str0312 str0333 str0339 str0400 str0405 str0407 str0512 str0612 str0635 str0697 str0728	proC iIvC iIvN iIvN iIvB trate transpo gpmB - pgi tkt fruR fruB - nagA - - nagA - - - -	rt and metab 0.339 3.798 0.309 0.463 0.393	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291	6.235 8.882 2.275 4.996 2.936 3.731 3.086		6.603 2.163	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694	ketot-acid reductoisomenaes acetolactae synthase small subunit acetolactae synthase iarge subunit phosphoglycerate mutase PTS glucose-specific anyme IIABC components, truncated glucose-specific anyme IIABC transcriptional tegresco mannose PTS system component IIAB transcriptional tegresco transcriptional tegresco PTS functose-specific enzyme IIABC components, truncated PTS functose-specific enzyme IIABC components, truncated N-acetylglucosamine-6-phosphate deacetylase beta-glucoside-specific PTS system IIABC component, truncated hypothetical protein phosphoglycerate mutase glucose kinae
str1839 str1852 str1872 str1873 Carbohyc str0114 str0191 str0191 str0191 str0312 str0333 str0399 str0400 str0400 str0400 str0407 str0501 str0512 str0512 str0612 str0637 str087 str0878	proC iivC iivN iivB drate transpo gpmB - pgi tkt manL fruB - - - - - eno gpmC glcK	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840	6.235 8.882 2.275 4.996 2.936 3.731 3.086		6.603	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149	ketoi-acid reductoisomense acetolactae synthase small subunit acetolactae synthase small subunit phosphoglycarate mutase PTS glucose-6-phosphate isomerase transketolase mannose PTS system component IIAB transcriptional repressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated phosphopymvate hydratase phosphopymvate hydratase glucose kinase
str1839 str1852 str1871 str1872 str1872 str0114 str0191 str0191 str0191 str0332 str0333 str0400 str0405 str0405 str0405 str0405 str0405 str0512 str0637 str0635 str0635 str0728 str0995 str0995	proC iivC iivC iivR drate transpo gpmB - pgi tikt manL fruB - nagA - - nagA - - supp gpmC gjcK - suhB	rt and metab 0.339 3.798 0.309 0.463 0.393	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523	ketot-acid reductoisomenae acetolactae synthase small subunit acetolactae synthase iarge subunit PTS glucose-specific anyme IIABC components, truncated glucose-specific anyme IIABC components, truncated glucose-specific anyme IIABC transcriptional regressor TST structose-specific anyme IIABC components, truncated PTS functose-specific anyme IIABC components, truncated N-acetylglucosamine-8-phrosphate deacetylase beta-glucoside-specific PTS system IIABC component, truncated hypothetical protein phosphogyuvate hydratase phosphoglycerate mutase glucose kinase transcriptional regulator
str1839 str1852 str1872 str1873 Carbohyc str0114 str0191 str0191 str0191 str0312 str0333 str0399 str0400 str0400 str0400 str0407 str0501 str0512 str0512 str0612 str0637 str087 str0878	proC iivC iivN iivB drate transpo gpmB - pgi tkt manL fruB - - - - - eno gpmC glcK	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840	6.235 8.882 2.275 4.996 2.936 3.731 3.086		6.603 2.163	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694	ketol-acid reductoisomenae acetolactae synthase small subunit acetolactae synthase mall subunit phosphogiverster mutase PTS glucose-6-phosphate isomerase transkrotaes mannose PTS system component IIAB transcriptional repressor fructose-1-phosphate kinase PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated hypothetical protein transcriptional englishers mIABC component, truncated hypothetical protein frustrase protein frustase glucose kinase fruscriptional regulator inositiol monophosphatase family protein glycoagn phosphorylase
str1839 str1852 str1871 str1872 str1872 str0172 str0114 str0194 str0312 str0339 str0339 str0400 str0401 str0401 str0401 str0401 str0401 str0501 str0612 str0651 str0697 str052 str0728 str0999 str017 str1017	proC iivC iivC gpmB - pgi tkt fruR fruR fruR fruR - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523	ketol-acid reductoisomenae acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphoglycarate mutaxe PTIs gluose-specific enzyme IABC components, truncated ytanskrifulae mannose PTS system component IIAB transcriptional greensor fructose-ty-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein phosphogrupate hydratase phosphoglycarate mutaxe phosphoglycarate mutaxe glycoaph notportyholase fmatscriptional engulator inosotio monophorsphatase family protein glycoaph notportein
str1839 str1852 str1871 str1872 str1872 str0114 str0191 str0191 str0191 str0312 str0339 str0400 str0405 str0405 str0405 str0405 str0405 str0612 str0612 str0635 str0699 str10172 str0192	proC iivC iivC iivR drate transpo gpmB - pgi tikt manL fruB - nagA - - nagA - - supp gpmC gjcK - suhB	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113	ketoi-acid reductoisomense acetolactate synthase small suburit acetolactate synthase mall suburit acetolactate synthase mall suburit phosphoglycerate mutase PTS glucose-police naryme IABC components, truncated glucose-phosphate isomerase transketolase mannose PTS system component IAB transcriptional growsor functione - I-phosphate kinane IABC components, truncated PTS functose-specific enzyme IABC component, truncated phosphopyruset hydratase phosphopyruset mutase transcriptional regulator insolatio monophosphatase family protein glycogen phosphorylase malase/maldoaxtin ABC transporter permease protein, truncated hypothetical protein
str1852 str1852 str1871 str1872 str1872 str091 str0194 str0194 str0312 str0333 str0339 str0400 str0401 str0401 str0401 str0401 str0401 str0501 str0501 str0512 str0612 str0697 str052 str0999 str0728 str0999 str077 str01077	proC iivC iivN iivB strate transpo gpmB - pgi kt manL fruB - - - nagA - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 8.815 2.466	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113	ketot-acid reductoisomense acetolactate synthase small subunit acetolactate synthase iarge subunit PTS glucose-specific anyme IABC components, truncated glucose-opticate subunit glucose-opticate subunit manose PTS system component IAB transcriptional regressor fructose-1-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein phosphoglycerate mutase glucose kinase transcriptional regulation transcriptional regulation transcriptional regulation phosphophytase mallose/mallodoxtrin ABC transporter permease protein, truncated hypothetical protein expolysaccharde polymerization protein expolysaccharde polymerization protein phosphophytase
str1839 str1852 str1871 str1872 str1872 str0172 str0114 str0194 str0312 str0339 str0339 str0400 str0401 str0401 str0401 str0401 str0401 str0501 str0612 str0651 str0697 str052 str0728 str0999 str017 str1017	proC iIvC iIvN iIvB drate transpo gpmB rate transpo gpmB tkt manL fruB - - nagA - - eno gpmC glcK - suhB glgP - - - suhB glgP tsl depsL depsI	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphoglycerate mutase PTS glucose-specific enzyme IABC components, truncated glucose-6-phosphate isomerase transketolase mannose PTS system component IAB transketolase PTS futcose-specific enzyme IABC components, truncated PTS futcose-specific enzyme IABC components, truncated Phosphopyruvate hydratase glucose kinase transcriptional regulator inestol monophosphatase family protein glycogen (hosphorylase glucose kinase transcriptional regulator phosphoportymate sugar broksphotransferase system enzyme I
str1839 str1852 str1871 str1873 Carbohyc str0114 str0194 str0194 str0194 str0312 str0323 str0400 str0612 str06512 str0635 str0699 str01728 str019728 str019728 str01928 str01928 str01928 str01928 str01928 str01928 str01928 str0194 str0512 str06512 str06512 str06512 str06512 str0699 str01728 str010728 str01855 str01855 str018555 str018555555555555555555555555555555555555	proC iIvC iIvN iIvB drate transpo gpmB rate transpo gpmB tkt manL fruB - - a a A - - eno gpmC glcK - suhB glgP - - - suhB glgP - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 8.815 2.466 2.013	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365 3.085	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113 2.509	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphoglycerate mutase PTS glucose-phosphate isomerase transketolase mannose PTS system component IIAB transketolase Tructose-specific enzyme IIABC components, truncated PTS furctose-specific enzyme IIABC components, truncated Phosphoglucosamine-6-phosphate deacet/gase Maset/glucosamine-6-phosphate deacet/gase phosphographorytoxet hydratase phosphogonal protein glucose kinase mallose/mallodextin ABC transporter permease protein, truncated hydrotherial protein mallose/mallodextin ABC transporter permease protein, truncated phosphoportorivates mutase phosphoportorivates mutase phosphoportorivates mutase phosphotransferase system enzyme I phosphoportorivates supar phosphotransferase system enzyme I phosphoportorivates supar phosphotransferase system enzyme I phosphocarrier protein HPP (histidine-containing protein)
str1852 str1852 str1871 str1873 Carbohyo str0114 str0194 str0194 str0312 str0312 str0312 str0333 str0400 str0400 str0400 str0400 str0400 str0405 str04	proC iivN iivN drate transpo gpmB - - pgi tkt fruB - - - nagA - - - eno gpmC gjcK - - - - eno gpmC gjcK - - - - - eosL deoB ptsH celB galM	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063 6.693 0.457	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 5.840 2.911 5.840 2.911	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113 2.509	ketol-acid reductoisomense acetolactate synthase small suburit acetolactate synthase inarge suburit phosphoglycerate mutase PTS glucose-poncelic enzyme IABC components, truncated glucose-phosphate isomense transketolase mannose PTS system component IAB transketolase Tructose-poncelic enzyme IABC component, truncated PTS functose-specific enzyme IABC component, truncated phosphopyruvate hydratase phosphopyruvate hydratase glucoside-specific enzyme IABC component, truncated hypothetical protein glycogen phosphorylase matose/maldocatin ABC transporter permease protein, truncated hypothetical protein phosphopentoruutase phosphopentoruutase phosphopentoruutase phosphopentoruutase phosphotransfersas system enzyme I phosphopentoruutase phosphotransfersas system enzyme I
str1852 str1852 str1871 str1873 str1873 carbohyc str0114 str0191 str0191 str0193 str0332 str0339 str0400 str04041 str0405 str0407 str05012 str0632 str0687 str0687 str0693 str012 str012 str0338 str0985 str012 str012 str0395 str012 str0395 str012 str0395 str012 str0395 str012 str0395 str012 str0395 str012 str0395 str012 str0395 str039	proC iivC iivN drate transpo gpmB - p gitte transpo gpmB - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.071 2.016 2.092 0.347 3.291 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365 3.085	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113 2.509	ketol-acid reductoisomenaes acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphogiverare mutase PTS glucose-6-phosphate IABC components, truncated glucose-6-phosphate IABC and the subunit transkrotaes mannose PTS system component IAB transcrotpional repressor fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein transcriptional regulator inesticit monophosphatase family protein glucose kinase mallose/maltedextrin ABC transporter permease protein, truncated hypothetical protein expolysaccharide polymerization protein phosphoendoprovates upp phosphotansferase system enzyme I phosphoendoprovates upper phosphotansferase syste
str1852 str1852 str1852 str1871 str1872 str1873 str0114 str0191 str0191 str0191 str0191 str0332 str0339 str0400 str0401 str0400 str0400 str0400 str0400 str0407 str0512 str0651 str0552 str0652 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str06552 str0177 str0778 str01778 str01778 str01778 str01778 str1264 str1368 str13	proC iivC iivN drate transpo gpmB - pgi tkt fruB - - - nagA - - - eno gpmC gpmC gpmC gpmC gpmC gpmC gpmC gpmS - - - - eosL deoB ptsH celB galM ppnK	rt and metab 0.339 3.798 0.309 0.463 0.393 2.078 2.063 6.693 0.457	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 5.840 2.911 5.840 2.911	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365 3.085	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113 2.509	ketol-acid reductoisomenase acetolacitae synthase small suburit acetolacitae synthase inarge suburit phosphoglycerate mutase PTS glucose-phosphete isomerase transketolase mannose PTS system component IAB transketolase mannose PTS system component IAB transcriptional greensor fructose-t-phosphete kinase PTS fructose-specific enzyme IABC component, truncated PTS fructose-specific enzyme IABC component, truncated phosphoglycare fructions glucose kinase glucose kinase transcriptional regulator phosphopentoriate mutase glucose kinase transcriptional regulator phosphopentoriate for transporter permease protein, truncated hypothetical protein phosphopentoriate polymerization protein phosphocarier protein HPP / histidine-containing protein Phosphopentoriate polymerization protein
str1852 str1872 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str0144 str0141 str0151 str0145 str0407 str040	proC livC livC livB strate transpo gpmB pgi kmanL fruR fruR fruR fruR fruR fruR fruR fruR	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091 8.477 5.901	6.235 8.882 2.275 4.996 2.936 3.731 3.086	3.190	6.603 2.163 4.662 2.365 3.085	0.493 0.443 3.555 2.109 0.485 0.469 2.359 2.359 2.359 2.509 2.506 0.458 6.485	ketol-acid reductoisomense acetolacitae synthase small suburit acetolacitae synthase image suburit phosphoglycerate mutase PTS glucose-ponosphile isomerase transketolase mannose PTS system component IAB transcriptional greessor fructose-phosphate isomerase transcriptional greessor fructose-t-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated beta-glucoside-specific PTS system IABC component, truncated beta-glucoside-specific PTS system IABC component, truncated phosphoprivate hydratase glucose kinase transcriptional regulator insolid moncyhocphatase framity protein insolid moncyhocphatase frams protein phosphopentomutase phosphopentomutase phosphotransferase system enzyme I phosphopentomutase phosphopentomutase pacific IT Camponent aldose T-epinenase aldose I-epinenase aldose I-epine
str1832 str1852 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str0319 str031	proC lik/C lik/D gomB - pgi lkt manL fruB - nagA - - eno gpmC glcK - - eno glcK - - eno glck - - eno glck - - eno glck - - - eno glck - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091 8.476 10.773	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.523 6.113 2.509 2.506 0.458 6.485 3.192	ketol-acid reductoisomenaes acetolactate synthase small subunit acetolactate synthase mail subunit acetolactate synthase mail subunit acetolactate synthase mail subunit phosphoglycarter muzee ITS glucase for phosphate isomerase transcriptional typerssor fructose-t-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein betraglucosite-specific enzyme IABC components, truncated hypothetical protein betraglucosite-specific enzyme IABC component, truncated hypothetical protein phosphopruvate hydratase glucase kinase matose/matodextrin ABC transporter permease protein, truncated hypothetical protein expolysaccharide polymerization protein phosphoenolypruvate-sugar phosphotransferase system enzyme I phosphoenolypruvate-sugar phosphotransferase syst
str1852 str1872 str1872 str1872 str1872 str1872 str1872 str1872 str0114 str0195 str0194 str0195 str019	proC iivC iivC iivB strate transpo gpmB pgi kmanL fruR fruR fruR fruR fruR fruR fruR fruR	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091 8.477 5.901	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041 3.778 3.499	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.523 6.113 2.509 2.506 0.458 6.485 3.192 3.700	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphoglycerate mutase PTS glucose-specific enzyme IABC components, truncated glucose-6-phosphate isomerase transcriptional greessor fructose -1-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated phosphopytwate hydratase glucose kinase transcriptional regulator inositol monophosphatase family protein glycogen phosphorylase mallosetimalcodutin ABC transporter permease protein, truncated expolysoccharde polymerization protein phosphopentomutase phosphocarrier protein HPP, flatidine-containing protein Phosphocarrier protein HPP, flatidine-containing protein phosphocarrier protein HPP, flatidine-containing protein aldoset 1-spinerase inorganic colybropatel/ATP-NAD kinase polysaccharde ABC transporter ATP-binding protein polysaccharde ABC transporter A
str1832 str1852 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str0319 str031	proC lik/C lik/R lik/B strate transpo gpmB - pgi tkt manL fruR fruR fruR fruR fruR fruR glgR - - - eno gpmC glcK - glcK - glk glgP - esoB ptsl tsl galM ppnK deoB ptsl tsl galM ppnK galM ppnK scrA	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091 8.477 5.901	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.523 6.113 2.509 2.506 0.458 6.485 3.192	ketol-acid reductoisomenae acetolactae synthase anal subunit acetolactae synthase mail subunit acetolactae synthase mail subunit acetolactae synthase iarge subunit PTS gluose-specific enzyme IIABC components, truncated yranskrotoae manoces PTS system component IIAB transcriptional greessor fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated hypothetical protein phosphopytrust bydratase phosphopytrust bydratase ghosphopytrust bydratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopytruste updratase phosphopentip entit PHC fructaeted hypothetical protein expolysaccharide polymerization protein phosphopentip Review Phosphotransferase system enzyme I phosphopentip Review Photolise of the component PHC fructaes of PAT Phot inses indicase t-aptimeter Review Photolise permases, putative mannose-d-phosphate isomerase fructokinase sucrose-specific PTS permases, enzyme II
str1852 str1852 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str1873 str0314 str031	proC iivC iivR iivB strate transpo gpmB pgi kmanL fruR fruR fruR fruR fruR fruR fruR fruR	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628	9.738 11.322 olism 0.261 2.586 2.124 2.071 2.016 2.092 0.347 3.291 5.840 2.911 5.840 2.911 8.815 2.466 2.013 2.693 0.396 5.091 8.477 5.901	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041 3.778 3.499	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.529 2.509 2.506 0.458 6.485 3.192 3.700 4.456	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mall subunit acetolactae synthase mall subunit phosphoglycerate mutase PTS glucose-specific enzyme IABC components, truncated glucose-6-phosphate isomerase transcriptional greessor fructose -1-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated phosphopytwate hydratase glucose kinase transcriptional regulator inositol monophosphatase family protein glycogen phosphorylase mallosetimalcodutin ABC transporter permease protein, truncated expolysoccharde polymerization protein phosphopentomutase phosphocarrier protein HPP, flatidine-containing protein Phosphocarrier protein HPP, flatidine-containing protein phosphocarrier protein HPP, flatidine-containing protein aldoset 1-spinerase inorganic colybropatel/ATP-NAD kinase polysaccharde ABC transporter ATP-binding protein polysaccharde ABC transporter A
str1822 str1872 str1872 str1872 str1872 str1872 str1872 str0114 str0191 str0191 str0191 str0191 str0191 str0191 str0191 str0191 str0312 str031	proC iivC iivB iivB gomB - pgi tkt manL fruB - - - eno gbrK - - eno gbrC gbrC - - eno gbrC - - eno gbrC - - eno gbrC - - eno gbrB - - - - eno gbrB - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628 0.207	9.738 11.322 0.261 2.621 2.021 2.021 2.021 2.016 2.024 2.071 3.291 5.040 2.931 5.040 2.931 8.815 2.466 5.040 8.075 2.039 5.091 8.077 3.293 0.0761 0.073 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.07700 0.07700000000	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041 3.778 3.499	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.529 2.509 2.506 0.458 6.485 3.192 3.700 4.456	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mail subunit acetolactae synthase mail subunit acetolactae synthase mail subunit PTS glucose-specific enzyme IABC components, truncated glucose-6-phosphate isomerase transcriptional growsor fructose-1-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC component, truncated Phosphopytwate hydratase phosphopytwate hydratase glucose kinase transcriptional regulator inositol monophosphatase family protein glycogen phosphorylase maitosetimalicodutin ABC transporter permease protein, truncated phosphopenicymutes-sugar phosphotransferase system enzyme I phosphopenicymutes-sugar phosphotransferase system enzyme I phosphopenicymotes ABC inansporter ATP-binding protein phosphocarrier protein HPP, histidine-containing protein phosphocarrier protein HPP, histidine-containing protein phosphocarrier phosphotransferase system enzyme I phosphocarrier phosphotransferase system enzyme I phosphocarrier phosphotase ABC inansporter atTP-binding protein polysaccharide ABC inansporter ATP-binding protein polysaccharide ABC inans
str1852 str1852 str1872 str1872 str1872 str1872 str1872 str0191 str0194 str0191 str0194 str0191 str0194 str0312 str031	proC iivC iivR iivB fate transpo gpmB - pgi tkt fruB - ragA - nagA - nagA - - eno gpmC glcK - - eno glcK - - eno glcK - - - - eno glcK - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628 0.207	9.738 11.322 0.261 2.621 2.021 2.021 2.021 2.016 2.024 2.071 3.291 5.040 2.931 5.040 2.931 8.815 2.466 5.040 8.075 2.039 5.091 8.077 3.293 0.0761 0.073 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.077 0.0761 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.0770 0.07700 0.07700000000	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041 3.778 3.499	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.529 2.509 2.506 0.458 6.485 3.192 3.700 4.456	ketol-acid reductoisomenase acetolacitae synthase small suburit acetolacitae synthase inarge suburit phosphoglycarate mutase PTS glucose-cphosphate isomenase transketolase mannose PTS system component IAB transketolase mannose PTS system component IAB transchiptione Tructose-cphosphate isomenase transchiptione PTS functose-specific enzyme IABC components, truncated PTS functose-specific enzyme IABC component, truncated PTS functose-specific enzyme IABC component, truncated phosphoglycare mutase glucose kinase transcriptional regulator glycogen phosphorylase matose/matodextm ABC transporter permease protein, truncated hypothetical protein phosphoglycaride polymerization protein phosphoglycaride polymerization protein phosphoglycaride ABC transporter Permease protein phosphoglycaride bolymerization protein phosphocariner protein HPP (hittidhe-containing protein) Phosphoglycariner ABC transporter membrane-spanning protein polysaccharide ABC transporter membrane-spanning protein polysaccharide ABC transporter membrane-spanning protein polysaccharide ABC transporter membrane-spanning protein polysaccharide ABC transporter ATP-NAD kinase succese-specific PTS permease, enzyme I I glycose phosphate 3-pipmerase truckinase
str1822 str1872 str1872 str1872 str1872 str1872 str1872 str0114 str0191 str0191 str0191 str0191 str0191 str0191 str0191 str0191 str0312 str031	proC iivC iivB iivB gomB - pgi tkt manL fruB - - - eno gbrK - - eno gbrC gbrC - - eno gbrC - - eno gbrC - - eno gbrC - - eno gbrB - - - - eno gbrB - - - - - - - - - - - - - - - - - - -	rt and metab 0.339 3.798 0.463 0.393 2.078 2.063 6.693 0.457 3.149 7.190 8.628 0.207	9.738 11.322 0.2616 2.966 2.966 2.966 2.967 2.071 2.016 2.062 2.071 3.291 3.291 5.840 2.947 3.291 5.840 2.947 3.291 5.840 2.947 0.34	6.235 8.882 2.275 4.996 2.936 3.731 3.086 5.339	3.190	6.603 2.163 4.662 2.365 3.085 2.041 3.778 3.499	0.493 0.443 3.555 2.109 0.485 0.469 2.359 6.149 2.694 2.694 2.523 6.113 2.509 2.506 0.458 6.485 3.192 3.700 4.456 2.284	ketol-acid reductoisomense acetolactae synthase small subunit acetolactae synthase mail subunit acetolactae synthase mail subunit acetolactae synthase mail subunit PTS glucose-specific enzyme IABC components, truncated glucose-6-phosphate isomerase transcriptional growsor fructose-1-phosphate kinase PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC component, truncated Phosphopytwate hydratase phosphopytwate hydratase glucose kinase transcriptional regulator inositol monophosphatase family protein glycogen phosphorylase maitosetimalicodutin ABC transporter permease protein, truncated phosphopenicymutes-sugar phosphotransferase system enzyme I phosphopenicymutes-sugar phosphotransferase system enzyme I phosphopenicymotes ABC inansporter ATP-binding protein phosphocarrier protein HPP, histidine-containing protein phosphocarrier protein HPP, histidine-containing protein phosphocarrier phosphotransferase system enzyme I phosphocarrier phosphotransferase system enzyme I phosphocarrier phosphotase ABC inansporter atTP-binding protein polysaccharide ABC inansporter ATP-binding protein polysaccharide ABC inans

	- smc	3.200	4.782			0.370		hypothetical protein chromosome segregation SMC protein
str1295 str2002	gidA	3.200	4.702			0.363	0.350	glucose-inhibited division protein A
Cell enve str0020	lope biogenes mreC	sis, outer m	embrane			0.181	0.203	rod shape-determining protein MreC
str0110 str0131	-		0.415 0.405					hypothetical protein mechanosensitive ion channel, putative
tr0163	- rgpG		0.405			0.175	0.217	polysaccharide biosynthesis protein
tr0199 tr0212	eep pbp2A			0.425		0.485		conserved hypothetical protein, putative processing of a peptide sex pheromone penicillin-binding protein 2A
r0230 r0255	pbp1A		0.479				0.496	penicillin-binding protein 1A
r0349	glr murE						2.205	glutamate racemase UDP-N-acetylmuramoylalanyl-D-glutamate2,6-diaminopimelate ligase
r0413 r0563	- gcaD	2.304 4.925	2.033 4.559					glycosyltransferase, putative teichoic acid biosynthesis protein UDP-N-acetylglucosamine pyrophosphorylase
r0636	-	8.339	5.317			0.007	0.440	hypothetical protein
tr0699 tr0721		0.408	0.340			2.697	3.110	endolysin, putative hypothetical protein
tr0762 tr0764	dltB dltD	3.429	5.159 2.608					integral membrane protein extramembranal protein
tr0873	glmS	6.381	3.348				0.284	D-fructose-6-phosphate amidotransferase
tr1046 tr1058		0.428	0.107				0.489	endolysin, putative, truncated D-alanyl-D-alanine-carboxypeptidase, penicillin-binding protein, truncated
tr1073 tr1077	epsX epsL	0.421 6.693	0.307 8.815			0.339	0.488	lipopolysaccharide 1,6-galactosyltransferase exopolysaccharide polymerization protein
tr1080	epsl	3.632	3.946				0.491	exopolysaccharide biosynthesis protein, sugar transferase
tr1082 tr1083	epsG -	3.687	5.565				0.453 0.480	exopolysaccharide biosynthesis protein, glycosyltransferase exopolysaccharide biosynthesis protein, UDP-galactopyranose mutase, truncated
tr1084 tr1085	epsF epsE		2.346 2.001					exopolysaccharide biosynthesis protein exopolysaccharide biosynthesis protein
tr1167	murA		0.413				0.372	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
tr1169 tr1277	galE2	0.367 2.049	0.350 3.937					UDP-glucose 4-epimerase sortase, truncated
tr1278	- don ĉ	2.881	5.505				0.427	sortase, truncated
tr1297 tr1311	dapA proWY	5.552 2.848	6.636		21.241		0.103	dihydrodipicolinate synthase proline/glycine betaine ABC transporter membrane-spanning protein
tr1373 tr1392	2	2.215	2.579			3.654	2.848	UDP-glucose 4-epimerase, truncated glycosyl transferase
tr1467	rgpF	4.280	3.554				0.407	polysaccharide biosynthesis protein
tr1468 tr1469	rgpE rgpD	10.199 7.190	10.390 8.476				0.497	polysaccharide biosynthesis protein/putative glycosyltransferase polysaccharide ABC transporter ATP-binding protein
tr1470 tr1471	rgpC rgpB	8.628 4.430	10.773 4.419				0.458	polysaccharide ABC transporter membrane-spanning protein polysaccharide biosynthesis protein/putative rhamnosyl transferase
tr1472	rgpA	2.553	2.237			0.345	0.289	polysaccharide biosynthesis protein/putative rhamnosyl transferase
tr1476 tr1478		2.792 2.713	2.207 2.177			0.406 0.320	0.384 0.379	glycosyl transferase glycosyl transferase, truncated
tr1479 tr1485		5.892	4.978			0.288 0.352	0.283 0.366	glycosyl transferase glycosyl transferase, family 2
tr1560	murZ		2.156			0.272	0.281	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
str1576 str1629	murF -	2.346	2.254		2.814		0.326	UDP-N-acetylmuramoylalanine-D-glutamyl-lysineD-alanyl-D-alanine ligase hypothetical protein
tr1726	alr	2.263 2.820	2.408 2.981					alanine racemase
tr2006	pbp1B -	0.463	2.901	2.314		0.456	0.469	penicillin-binding protein 1B conserved hypothetical protein, LysM domain protein
Cell motil	ity and secreti	ion						
str0117 str0196	mur3 yajC	0.427 2.120	0.349			0.380	0.448	peptidoglycan hydrolase preprotein translocase, YajC subunit, putative
tr0245	-	2.120				0.389	0.391	OxaA-like protein precursor
tr0356 tr0496	clpP mur1				0.362	0.439	4.182	ATP-dependent Clp protease proteolytic subunit peptidoglycan hydrolase
str0624 str0889	secG ffh	5.131	4.181			0.340	0.401	translocase signal recognition particle
str1730	secA	2.403	2.097			0.464		translocase
str1810 str1860		3.540	2.750 0.249			0.328	0.290	hypothetical protein competence protein, putative
str1862 str1863	comGD comGC		0.191 0.177				2.055	competence protein late competence protein, exogenous DNA-binding protein
str1864	comGB		0.135		5.866	5.329		late competence protein, ABC transporter subunit
str1865 str1914	comGA secY	0.432 3.057	0.206 3.463			0.389	0.371	late competence protein, ABC transporter subunit preprotein translocase SecY
Coenzym	e metabolism							
str0092	panE					0.336		2-dehydropantoate 2-reductase (ketopantoate reductase)
str0123 str0226	thiD pncB				0.490	0.457	0.420	phosphomethylpyrimidine kinase nicotinate phosphoribosyltransferase
str0227 str0409	nadE folC1					3.431	0.429 4.554	NAD(+) synthetase folylpolyglutamate synthase / dihydrofolate synthase
tr0412	thil		2.424			3.431	4.304	thiamine biosynthesis protein Thil
str0545 str0579	- folA		0.323	0.441	0.357			molybdopterin biosynthesis protein (HesA/MoeB/ThiF family protein), putative, truncated dihydrofolate reductase
str0590	bcaT	0.362	2.652	2.836	0.428 2.259	0.345	0.430	branched-chain amino acid aminotransferase
tr0611 tr0771	folD pabB		2.002		2.259	2.503	2.212	methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase para-aminobenzoate synthetase component l
tr0826	ptpS als	4.956	6.076			0.142	0.113 2.021	6-pyruvoyl tetrahydrobiopterin synthase, putative alpha-acetolactate synthase
tr0996	ribC					2.878		riboflavin kinase/flavin adenine dinucleotide synthase
tr1009 tr1172	lpIA metK	2.339	0.392 2.176			3.076 0.181	4.610 0.189	lipoate-protein ligase S-adenosylmethionine synthetase
tr1173 tr1527	birA serA	5.980	19.856	3.320	0.494	0.346	2.186	biotinprotein ligase D-3-phosphoglycerate dehydrogenase
tr1529	serC	6.387	27.583	4.319	0.434	0.464		phosphoserine aminotransferase
str1546 str1796	folC2		0.396			0.365		folylpolyglutamate synthase / dihydrofolate synthase hypothetical protein
str1871 str1873	ilvC ilvB		20.849	8.103 8.882				ketol-acid reductoisomerase
			11.322	0.002				acetolactate synthase large subunit
	mechanisms -					2.545	3.376	hypothetical protein
tr0009	- labC	4.438	0.199					bacteriocin self-immunity protein, putative, truncated lantibiotic biosynthesis protein
str0009 str0071	murO		0.199			0.440		peptidoglycan branched peptide synthesis protein, alanine adding enzyme, putative
str0009 str0071 str0099 str0348	maro	8.263				0.204	0.219	ABC transporter ATP binding protein ABC transporter ATP binding/permease protein
str0009 str0071 str0099 str0348 str0434	-					0.134	0.135	ABC transporter ATP binding/permease protein
str0009 str0071 str0099 str0348 str0348 str0434 str0538 str0539	-							ABC transporter ATP binding protein type I restriction-modification system restriction subunit
str0009 str0071 str0099 str0348 str0434 str0538 str0539 str0546 str0705	- - - hsdR1	11.232	2.459 8.490					
str0009 str0071 str0099 str0348 str0434 str0538 str0539 str0539 str0546 str0705 str0708	- - - hsdR1 hsdS1	11.232	8.490			2.545	2 4RF	type I restriction-modification system specificty subunit
str0009 str0071 str0099 str0348 str0434 str0538 str0539 str0546 str0705 str0708 str0708 str0711 str0758	- - - hsdR1	5.677	8.490 3.871 4.553			3.267	2.486 0.333	type I restriction-modification system specificty subunit type I restriction-modification system methyltransferase subunit ABC transporter ATP-binding/permease protein
str0009 str0071 str0099 str0348 str0434 str0538 str0539 str0546 str0705 str0708 str0711	- - - hsdR1 hsdS1		8.490 3.871		2.033	2.545 3.267 0.358		type I restriction-modification system specificty subunit type I restriction-modification system methyltransferase subunit

						2.283		ABC transporter ATP binding protein
str1342 str1375	norM sthll	0.482 3.868	0.456			0.356	0.270	MATE efflux family protein (Na(+)/drug antiporter) type II restriction-modification system restriction subunit
str1411	-					0.284	0.326	ABC transporter, truncated
str1436	-						3.222	ABC transporter ATP binding protein
str1660 str1667	-		0.464	0.301		0.470	0.387	type I restriction-modification system specificty subunit, truncated hypothetical protein
str1693	-			0.301		0.494	0.382	ABC transporter ATP-binding/permease protein
DNA repli	cation, recom	bination and	d repair					to a second second second in a factor
str0006 str0013	trcF	0.411	0.479 3.579					transcription repair coupling factor IS1167, transposase, ISL3 family, truncated
str0019			0.070				4.077	IS861, transposase (orf2), IS3 family, truncated
str0027	recO	3.790		0.294		0.230	0.255	DNA repair protein RecO
str0050	mutS1		2.018					DNA mismatch repair protein
str0056 str0060	ruvA recA		0.491			0.351	0.437	Holliday junction DNA helicase motor protein recombinase A
str0062	polC					0.278	0.407	DNA polymerase III subunit alpha
str0067	-						5.257	ISSpn1, transposase, IS3 family, truncated
str0069 str0107	-		0.401			5.906 0.371		ISSpn1, transposase, IS3 family, truncated truncated IS1216 transposase
str0107 str0108	-		0.401			0.371		truncated IS1216 transposase
str0126	-		3.180				2.492	truncated IS1193 transposase
str0136	-			0.449				MutT/nudix family protein, truncated
str0234 str0237	- snf	2.074				0.427	0.493	hypothetical protein
str0259	xer2	2.074				2.915	2.917	ATP-dependent RNA helicase tyrosine recombinase
str0320	dnaB		0.435			0.413	0.421	chromosome replication initiation / membrane attachment protein DnaB
str0321	dnal					0.458	0.457	primosomal protein Dnal
str0326 str0396	- tnp1216		0.185			0.221	2.573 0.379	truncated IS1191 transposase IS1216 transposase
str0490	dnaH	0.495	0.306			0.221	0.575	DNA polymerase III subunit delta
str0588	parE	2.256				0.399	0.333	DNA topoisomerase IV subunit B
str0589	parC	5.397	5.515				0.390	DNA topoisomerase IV subunit A
str0601 str0614	- recR	0.480	0.289			0.302	0 202	conserved hypothetical protein, MutT/nudix family protein
str0614 str0620	mutM		2.314			0.302	0.392	recombination protein RecR formamidopyrimidine-DNA glycosylase
str0658	-		2.014			0.405		hypothetical protein
str0719	holA	0.371	0.223					DNA polymerase III subunit delta
str0783	int2	0.455	0.235				0.405	integrase/recombinase, phage associated
str0796 str0813	tnpSth1 dinG	4.221	4.125				2.425	ISSth1, transposase (orf2), IS3 family ATP-dependent DNA helicase
str0822	-						2.041	truncated IS1193 transposase
str0885	sthIM	10.363	10.162					type III restriction-modification system methylation subunit
str0894 str0986	rnhB pcrA	2.637 2.358	3.148 2.218			2.428 0.396	2.214 0.399	ribonuclease HII ATP-dependent DNA helicase
str1055	ung	2.300	2.720	3.808		0.390	0.399	uracil-DNA glycosylase
str1126	-						0.438	hypothetical protein
str1198	dnaE					3.462	2.536	DNA polymerase III subunit alpha
str1221 str1224	dnaD recJ	4.045	0.495 4.550			0.380	0.488	DNA replication protein dnaD single strand DNA-specific exonuclease
str1261	deaD	4.043	4.000			2.910	2.279	ATP-dependent RNA helicase
str1274	-		2.063					ISSth5, transposase, IS110 family, truncated
str1279	gyrA	2.177	3.324					DNA gyrase subunit A
str1300 str1304	alkD					0.281 2.468	0.225 3.945	DNA alkylation repair protein truncated IS1193 transposase
str1306	uvrC					2.400	2.045	excinuclease ABC subunit C
str1375	sthll	3.868						type II restriction-modification system restriction subunit
str1394	sbcC					2.759	2.342	ATP-dependent dsDNA exonuclease
str1425	pknB dnaG	2.344				0.477 0.283	0.407 0.395	protein kinase DNA primase
str1489 str1526	-		8.791	2.463	0.480		0.385	
str1526 str1550	- exoA		8.791	2.463 0.399	0.480	0.392		methylguanine-DNA methyltransferase, truncated 3'-exo-deoxyribonuclease
str1526 str1550 str1568	- exoA rheA	0.092	2.286	2.463 0.399			0.395	methylguanine-DNA methyltransferase, truncated 3'-exo-deoxyribonuclease ATP-dependent RNA helicase
str1526 str1550 str1568 str1601	- exoA	0.082 0.214	2.286 0.045	2.463 0.399	0.495	0.392 0.446	0.275	methylguanine-DNA methyltransferase, truncated 3'exco-deoxyribonuclease ATP-dependent RNA helicase DNA polymerase III subunit epsilon
str1526 str1550 str1568	- exoA rheA dnaQ - -	0.082 0.214	2.286	2.463 0.399		0.392 0.446 2.185	0.275 9.580 2.088	methydjuanine-DNA methyltransferase, truncated 3'exx-dexythonuclease ATP-dependent RNA helicase DNA polymersell I subunit epsilon ISSht, transposase, If30 family, truncated ISSht, transposase (orf1), ISS Jamik, truncated
str1526 str1550 str1568 str1601 str1638 str1677 str1699	- exoA rheA dnaQ - - rheB		2.286 0.045	2.463 0.399	0.495	0.392 0.446 2.185 2.799	0.275 9.580 2.088 2.783	methylguanine-DNA methyltransferase, truncated 3'-avoc doxyrthonuclease ATP-dependent RNA helicase DNA polymorase III subunit epsilon ISSith, transposae, IS30 family, truncated ISSith, transposaes (arth), IS3 family, truncated ATP-dependent RNA helicase
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716	- exoA rheA dnaQ - - rheB rexA		2.286 0.045	2.463 0.399	0.495	0.392 0.446 2.185 2.799 0.368	0.275 9.580 2.088 2.783 0.446	methydjuanine-DNA methyltransferase, truncated 3'exo-dexoyribonuclease ATP-depondent RNA helicase DNA polymersell il subunit epsilon ISSht3, transposase, IS30 family, truncated ISSht1, transposase (orth), IS3 family, truncated ATP-depondent RNA helicase ATP-depondent exonuclease, subunit A
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716 str1717	- exoA rheA dnaQ - rheB rexA rexB	0.214	2.286 0.045 0.213	2.463 0.399	0.495	0.392 0.446 2.185 2.799 0.368 0.300	0.275 9.580 2.088 2.783 0.446 0.395	methylguanine-DNA methyltransferase, truncated 3'-exo-dexoyribnouclease ATP-dependent RNA helicase DNA polymerase III subunit epsilon ISSIh3, transposaes (350 family, truncated ISSIh1, transposaes (arth), IS3 family, truncated ATP-dependent RNA helicase ATP-dependent exonucleases, subunit A ATP-dependent exonucleases, subunit A
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716 str1717 str1753 str1753	- exoA rheA dnaQ - - rheB rexA		2.286 0.045 0.213 11.995	2.463 0.399	0.495	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415	methylguanine-DNA methyltransferase, truncated 3'-exo-deoxythonuclease ATP-depondent RNA holicase DNA polymerse III subunit epsilon IISSIn3, transposase, IS30 family, truncated ISSIn3, transposase, IG31, IS31 family, truncated ATB-dispondent exo-truncated ATB-dispondent exo-truncated ATP-dispondent exo-truncates, subunit B single-strand DNA-binding protein DNA mismatch repair protein
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716 str1717 str1753 str1762 str1765	- exoA rheA dnaQ - rheB rexA rexB ssbB	0.214 6.554 2.013	2.286 0.045 0.213 11.995 2.022	2.463 0.399	0.495	0.392 0.446 2.185 2.799 0.368 0.300 0.397	0.275 9.580 2.088 2.783 0.446 0.395 0.311	methydjuanine-DNA methyltransferase, truncated 3'exx-dexyrhonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSht), transposase, IS30 family, truncated ISSht), transposase (orf1), IS3 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein DNA mismatch repair protein
str1526 str1550 str1568 str1601 str1638 str1677 str1639 str1716 str1717 str1753 str1762 str1765 str1800	- exoA rheA dnaQ - - rheB rexA rexB ssbB mutS2 rnhB -	0.214	2.286 0.045 0.213 11.995 2.022 0.458	2.463 0.399	0.495	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415	methylguanine-DNA methyltransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSIh3, transposase, IS30 family, truncated ISSIh1, transposase (ATI), IS3 family, truncated ATP-dependent RNA helicase ATP-dependent RNA helicase ATP-dependent exonuclease, subunit A angle-stand DNA-binding protein DNA mismatch repair protein DNA mismatch repair protein
str1526 str1550 str1568 str1601 str1638 str1677 str1639 str1716 str1717 str1753 str1762 str1765 str1800	- exoA rheA dnaQ - - rheB rexA rexB ssbB mutS2	0.214 6.554 2.013 0.473	2.286 0.045 0.213 11.995 2.022 0.458 0.381	2.463 0.399	0.495 0.228	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415	methylguanine-DNA methyltransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSh1, transposase, IS30 family, truncated ISSh1, transposase (orf1), IS3 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein Dboruclease HIII Dipolosiase HIII Bioformane Septimase deoxythonuclease, IS300 family
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716 str1717 str1753 str1765 str1800 str1801 str1807 str1845	- exoA rheA dnaQ - rheB rexA rexB ssbB mutS2 rnhB - tatD	0.214 6.554 2.013	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098	0.399	0.495	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415	methydjuanine-DNA methyltransferase, truncated 3'exx-dexythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSht, transposase, IS30 family, truncated ISSht, transposase, fort1), IS3 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein Disomerase/primase decoyribounclease, putative IS667, transposase, IS200 family single-strand DNA-binding protein
str1526 str1550 str1568 str1601 str1638 str1677 str1639 str1716 str1717 str1753 str1762 str1705 str1800 str1801 str1801 str1845	- exoA rheA dnaQ - rheB rexA rexB ssbB mutS2 rnhB - tatD tnp657	0.214 6.554 2.013 0.473 0.140	2.286 0.045 0.213 11.995 2.022 0.458 0.381	2.463 0.399 0.423	0.495 0.228 0.373	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497	methylguanine-DNA methyltransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismach repair protein DNA mismach repair protein ES657, transposase, IS300 family single-strand DNA-binding protein hypothelical protein
str1526 str1550 str1568 str1601 str1638 str1677 str1699 str1716 str1717 str1753 str1765 str1800 str1801 str1807 str18458 str1904	- exoA rheA dnaQ - rheB rexA rexB ssbB mutS2 rnhB - tatD tnp657	0.214 6.554 2.013 0.473 0.140	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098	0.399	0.495 0.228 0.373	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192	0.275 9.580 2.088 2.783 0.346 0.395 0.311 2.415 0.497 0.152	methylguanine-DNA methyltransferase, truncated 3'-exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIht, transposae, IS30 family, truncated ISSIht, transposae, IS30 family, truncated
str1526 str1550 str1568 str1601 str1638 str1677 str1639 str1716 str1717 str1753 str1762 str1705 str1800 str1801 str1801 str1845	- exoA rheA dnaQ - rheB rexA rexB ssbB mutS2 rnhB - tatD tnp657	0.214 6.554 2.013 0.473 0.140 2.507	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098	0.399	0.495 0.228 0.373	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497	methylguanine-DNA methyltransferase, truncated 3'-exo-deoxythonuclease ATP-depondent RNA holicase DNA polymerse III subunit epsilon IISSIn1, transposase, IS30 family, truncated ISSIn1, transposase, IS30 family, truncated ATM-depondent RNA holicase ATM-depondent RNA holicase ATM-depondent exoruclases, subuni A ATM-depondent exoruclases, subuni A ATM-depondent exoruclases, subuni A Single-strand DNA-binding protein DNA mismatch-spirimase deoxytibonuclease, IS200 family trupcisonerasese, IS200 family single-strand DNA-binding protein SiSht, transposase, IS30 family, truncated ISSIht, transposase, IS30 family, truncated
str1526 str1526 str1560 str1560 str1601 str1609 str1716 str1717 str1765 str1776 str1775 str1765 str1800 str1800 str1807 str1805 str1936 str1936	- exoA rheA dnaQ - - rheB rexA rexA rexB ssbB mutS2 rmhB - tatD tnp657 ssbA - - - - - ruvB	0.214 6.554 2.013 0.473 0.140	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098	0.399	0.495 0.228 0.373	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210	methydguanine-DNA methyttransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymersell il subunit epsilon ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein Ibonuclease Hill topolsomerase/primase deoxythonuclease, prataine leagestand DNA-binding protein Phytophetical protein ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ISSh4, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB
str1526 str1550 str1560 str1601 str1603 str1603 str1639 str1716 str1775 str1765 str1705 str1765 str1807 str1807 str1807 str1807 str1805 str1805 str1904 str1936 str1936	- exoA rheA dnaQ - rheB rexA rexB ssbB mut52 rmhB - tatD tmp657 ssbA - ruvB - cshA	0.214 6.554 2.013 0.473 0.140 2.507	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.307 0.397 2.076 0.452 5.192 2.473	0.275 9.580 2.083 0.446 0.395 0.341 2.415 0.497 0.152 2.972	methylguanine-DNA methyltransferase, truncated 3'-exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIn1, transposase, IS30 family, truncated ISSIn1, transposase, IS30 family, truncated ATP-dependent RNA helicase ATP-dependent exoruclases, subuni A Single-stand DNA-binding protein DNA mismatch repair protein riboruclease HIII topoisomersse/primase deoxytiboruclease, IS200 family single-stand DNA-binding protein DS67, transposae, IS30 family, truncated ISSIn1, transposae, IS30 family, truncated ISSIn4, transposae, IS30 family, truncated ISSIn4, transposae, IS30 family, truncated ISSIn4, transposae, IS30 family, truncated Holiday juncito DNA helicase Ru/B hypothetical protein
str1526 str1526 str1560 str1560 str1601 str1609 str1716 str1717 str1765 str1776 str1775 str1765 str1800 str1800 str1807 str1805 str1936 str1936	- exoA rheA dnaQ - - rheB rexA rexA rexB ssbB mutS2 rmhB - tatD tnp657 ssbA - - - - - ruvB	0.214 6.554 2.013 0.473 0.140 2.507	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462	0.399	0.495 0.228 0.373	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210	methydguanine-DNA methyttransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymersell il subunit epsilon ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein Ibonuclease Hill topolsomerase/primase deoxythonuclease, prataine leagestand DNA-binding protein Phytophetical protein ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ISSh4, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB
str1526 str1526 str1568 str1663 str1663 str1677 str1638 str1677 str1776 str1776 str1775 str1775 str1775 str1775 str1780 str1807 str1807 str1807 str1807 str1808 str1905 str1905 str1935 str1935 str1957 str2015 Energy pt	- exxA theA dnaQ theB ssbB multS2 mhB - tatD tmp657 ssbA - cshA - cshA recF routhan - coshA	0.214 6.554 2.013 0.473 0.140 2.507 0.289	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.307 0.397 2.076 0.452 5.192 2.473	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210	methydjuanine-DNA methyttransferase, truncated 3'exo-deoxyribonuclease ATP-dependent RNA helicase DNA polymersell i subunit epsilon ISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA helicase Hill topoisomerase/primase deoxyribonuclease, pitalive ISSH2, transposase, IS30 family, truncated ISSH4, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB Hyothesical protein chromosome segregation helicase recombination protein F
str1526 str1526 str1568 str1568 str1661 str1637 str1699 str1716 str1716 str1716 str17176 str1775 str1762 str1780 str1775 str1782 str1782 str1782 str1904 str1904 str1904 str1904 str1905 str1904 str1905 str19	- exoA maA dnaQ rexA rexA rexB ssbB - tatD - tatD - ruvB - csbA recF coshA recF coduction and acyP	0.214 6.554 2.013 0.473 0.140 2.507 0.289	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.307 0.397 2.076 0.452 5.192 2.473	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210 2.719	methylguanine-DNA methyltransferase, truncated 3*exo-deoxyltronuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSh1, transposase, IS30 family, truncated ISSh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B ATP-dependent exonuclease, subunit B ATP-dependent exonuclease, subunit B DNA mismatch regain protein PNA mismatch regain protein PNA mismatch regain protein Ptopolomerasese, IS300 family, truncated ISSh4, transposase, IS30 family, truncated ISSh4, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB Holiday junction DNA helicase RuvB Holiday junction DNA helicase RuvB Holiday junction protein F
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str1526 str1526 str1550 str167 str1638 str1677 str1639 str1716 str1753 str1776 str1775 str1775 str1775 str1775 str1775 str1780 str1801 str1801 str1803 str1904 str1805 str1904 str1936 str1945 str1945 str1945 str1957 str2015	- exoA rheA dnaQ rheB ssbB rexA rexA rexA rexA rexA rexA rexA rexB mHS2 - tatD tmp657 ssbA - - cshA recF coluction and acyP	0.214 6.554 2.013 0.473 0.140 2.507 0.289	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.300 0.300 0.307 2.076 0.452 5.192 2.473 0.307 0.307	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210 2.719	methyguanine-DNA methytransferase, truncated 3*exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSIh3, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein Dobuclease HIII proteina 19657, transposase, IS30 family, truncated ISSIh4, transposase, IS30 family, truncated ISSIh4, transposase, IS30 family, truncated ISSIh4, transposase, IS30 family, truncated ISSIh4, transposase, IS30 family, truncated Hallday junction DNA helicase Rv/B hypothetical protein Chromosome sagregation helicase recombination protein F
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str1526 str1526 str1550 str1678 str1671 str1639 str1677 str1639 str1776 str1773 str1776 str1773 str17762 str1780 str1780 str1807 str1805 str1807 str1805 str1805 str1905 str1948 str1948 str1948 str1948 str1948 str1955 str1948 str1948 str1955 str10557 str0578 str10557	- exxA rheA drhaQ drhaQ - rexA rexA rexA rexA rexA rexA rexB rexA rexB rexA rexB rexB rexB rexB rexB rexB rexB rexB	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334 0.230 3.771	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192 2.473 0.307 0.452	0.275 9.580 2.088 2.783 0.446 0.385 0.391 0.446 0.395 0.497 0.152 2.972 2.210 2.719 0.446 11.305	methyguanine-DNA methytransferase, truncated 3'exo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSIh3, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein TPK-typer and the subunit B single-strand DNA-binding protein hypothesical protein ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB hypothesical protein chromosome segregation helicase recombination protein F
str1526 str1526 str1550 str1663 str167 str1669 str1717 str1699 str1716 str1717 str1753 str1762 str1780 str1780 str1780 str1807 str1803 str1805 str1805 str1805 str1805 str1805 str1936 str1936 str1937 str0246 str037 str0562 str0758	- exxA rhaA dmaQ dmaQ - rhaB rexB ssbB rmhB - tatD rmb57 ssbA - tatD rmp657 ssbA - c - c tatD rmp657 ssbA - c - c - ruvB - c - c - c - c - c - c - c - c - c -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.998 0.462 0.334 0.334 0.230 3.771 2.158	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.300 0.300 0.307 2.076 0.452 5.192 2.473 0.307 0.307	0.275 9.580 2.088 2.783 0.446 0.395 0.311 2.415 0.497 0.152 2.972 2.210 2.719 0.446	methylguanine-DNA methyltransferase, truncated 3'rexo-deoxyltronuclease ATP-dependent RNA helicase DNA polymerse III subunit tepsilon IISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ATP-dependent RNA helicase ATP-dependent RNA helicase ATP-dependent sconuclease, subunit A B single-stand DNA-binding protein DNA mismatch repair protein PDA mismatch repair protein PDA mismatch repair protein Ptopicomerase/primase deoxyltopuclease, Iptative IS657, transposae, IS300 family single-stand DNA-binding protein Hypothetical protein SISIhi, transposae, IS300 family, truncated ISSIH, transposae, IS300 family, truncated ISSIH, transposae, IS300 family, truncated Holiday junciton DNA helicase recombination protein F acylphosphatase putative manganese-dependent inorganic pyrophosphatase protom-transiccaling ATPaea, c subunit protom-tansiccaling ATPaea, c subunit
str1526 str1526 str1550 str1663 str167 str1669 str1717 str1699 str1716 str1717 str1753 str1762 str1800 str1807 str1803 str1803 str1803 str1803 str1803 str1803 str1936 str1936 str1936 str1936 str1937	- exxA rheA dmaQ dmaQ rheB rexB ssbB ssbB mut52 rhhB - tatD mut52 rbhB - tatD - tatD - c - c - c - c - c - c - c - c - c -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.381 0.381 0.384 0.334 0.334 0.230 3.771 2.158 0.459	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192 2.473 0.307 0.427 9.011 3.813 0.439 2.312 0.230	0.275 9.580 2.088 2.783 0.446 0.385 0.391 0.446 0.395 0.497 0.152 2.972 2.210 2.719 0.446 11.305	methylguanine-DNA methyltransferase, truncated 3*exo-deoxyltronuclease ATP-dependent RNA helicase DNA polymerse III subunit tepsilon ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit A Arg-dependent exonuclease, subunit B Arg-dependent exonuclease, subunit B BSB-dt, transposase, IS30 family, truncated ISSIH4, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB Hotmossome segregation helicase eccombination protein F acylphosphatase putative manganese-dependent inorganic pyrophosphatase proton-translocating ATPase, c subunit pyridine nucleotide-disulfide oxidoreductase isopenteryl pyrophosphat isomerase phosphenor(pyruvate carboxylase asionic detyrophosphat isomerase aphosphenor(pyruvate carboxylase asionic detyrophosphat
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str1526 str1526 str1558 str1663 str1663 str1673 str1673 str1673 str1773 str1775 str1775 str1775 str1780 str1780 str1801 str1801 str1803 str1804 str1804 str1804 str1804 str1805 str1845 str1904 str1845 str1904 str1805 str1904 str1805 str1904 str1805 str1904 str1807 str1845 str1904 str1807 str1845 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1904 str1905 str1024 str1022 str122 str222	- exxA rheA dmaQ dmaQ rheA rexB ssbB ssbB mut52 rhhB - tatD rpp657 ssbA - - - tatD rpp657 ssbA - - - - - - - - - - - - - - - - - - -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334 0.230 3.771 2.158 0.459 0.335	0.399	0.495 0.228 0.373 4.025	0.392 0.446 2.185 2.799 0.368 0.300 0.397 2.076 0.452 5.192 2.473 0.307 0.427 9.011 3.813 0.439 2.312 0.230	0.275 9.580 2.088 2.783 0.395 0.395 0.497 0.152 2.972 2.210 2.719 0.446 11.305 2.294	methyguanine-DNA methytransferase, truncated 3*exo-dexythorouclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ATP-dependent RNA helicase ATP-dependent RNA helicase Attransposae, IS30 family, truncated ISSIH, transposae, IS30 family, truncated ISSIH, transposae, IS30 family, truncated Heliday junction DNA helicase RwB Helicase RwB Helicase RwB Helicase RwB Atomosome segregation helicase recombination protein F acytphosphatase phospheorolpyrurate catooxytase phospheorolpyrurate catooxytase ADP-dependent glycerafdebyde3-sphosphate dehydrogenase
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str1526 str1526 str1568 str1633 str1633 str1633 str1633 str1765 str1776 str1775 str1775 str1785 str1776 str1785 str1800 str1800 str1800 str1800 str1800 str1805 str1948 str1905 str1948 str1905 str1948 str1905 str1948 str1905 str1948 str1905 str1948 str1905 str1948 str1905 str1948 str1955 str1948 str1955 str1948 str1955 str1255 str057	- exoA rheA drhaQ drhaQ rexA ssbB rexA ssbB mut52 rmhB - tatD tmp657 ssbA - - ruvB - cshA recF - ruvB - cshA recF - idi ppc acoA fer nfrA gapN - pta	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.995 2.022 0.458 0.381 0.098 0.462 0.334 0.230 3.771 2.158 0.459 0.335 2.884 8.495	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 0.300 0.300 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.231 0.281	0.275 9.580 2.088 2.783 0.395 0.395 0.497 0.152 2.972 2.210 2.719 0.446 11.305 2.294	methylguanine-DNA methyltransferase, truncated 3'rexo-deoxyltransferase, truncated STexo-deoxyltransferase, truncated ISSIn1, transposase, IS30 family, truncated ISSIn1, transposase, transposase
str1526 str1526 str1568 str1650 str1668 str1677 str1677 str1775 str17555 str17555 str17555 str17555 str17555 str17555 str17555 str17555 str17555 str15555 str15555 str15555 str155555 str155555 str1555555555555555555555555555555555555	- exxA rheA dmaQ dmaQ - rheB resA esbB resA esbB rmNB - tatD rmNB - tatD rmNB - csbA - c csbA - c csbA - csbA - csbA - csbA - c csbA - c c csbA - c csbA - c c c csbA - c c csbA - c csbA - c c csbA - c csbA - c c c c c c c c c c c c c c c c c c	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.395 2.022 0.459 0.381 0.098 0.462 0.334 0.334 0.334 0.334 0.334 0.334 0.334 0.335	0.399	0.495 0.228 0.373 4.025 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.397 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 3.813 3.813 3.813 0.439 2.312 0.281 0.281 0.281	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.152 2.2712 2.719 0.446 111.305 2.294 0.324	methyguanine-DNA methytransferase, truncated 3*exo-dexythorouclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon ISSIh1, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit A ATP-dependent exonuclease, subunit B subunit and the source of the subunit A ATP-dependent exonuclease, subunit B subunit SISH, transposase, IS30 family, truncated ISSIh1, transposase, IS30 family, truncated Holiday junction DNA helicase RuvB hypothetical protein thypothetical protein econtination protein F acylphosphatase putative manganese-dependent inorganic pyrophosphatase proton-transiccating ATPase, c subunit pyridine nucleotide-disulfide oxidoreductase ispenteryl pyrophosphate isomerase phosphenolypruvate carboxylase aceclini delytdrogenase B-isoprogryminate dehydrogenase ADD(P)H niroveductase, putatve phosphate acetyltransferase pyrvate formate-lysase
str1526 str1526 str1568 str1663 str1663 str1663 str167 str1716 str17716 str1776 str1776 str1776 str1776 str1776 str1780 str1801 str1801 str1801 str1801 str1801 str1803 str1965 str1948 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1448 str1448 str1448 str1448 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1948 str1948 str1448 str1948 str1448 str1948 str1448 str1948 str1448 str1448 str1948 str1448 str1948 str1448 str1948 str144	- exxA rhaA dmaQ dmaQ dmaQ roxA roxA roxA roxA ssbB roxA roxA tatD tmp657 ssbA - tatD tmp657 ssbA - ctatD tmp657 ssbA - ctatD ctatD ctatD ruvB - ctatA recA ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ctatA recA - ruvB - ru - ru - ru - ruvB - ru - ru - ru - ruB - ru - ru - ru r	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2.286 0.045 0.213 11.995 2.022 0.458 0.0381 0.098 0.462 0.334 0.334 0.334 0.334 0.334 0.337 1 2.158 0.459 0.335 2.884 4.895 0.355	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 0.300 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.323 0.281	0.275 9.580 2.088 2.783 0.446 0.397 0.446 0.397 2.415 0.497 0.152 2.972 2.210 2.719 0.446 11.305 2.294 0.324	methyguanine-DNA methyltransferase, truncated 3'exo-deoxythoruclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ISSIh, transposae, IS30 family, truncated ISSI h, transposae, transposae
str1526 str1526 str1568 str1663 str1663 str1663 str1663 str1671 str1771 str1775 str1775 str1776 str1776 str1776 str1780 str1800 str1800 str1800 str1800 str1805 str1948 str194	- exxA rheA dmaQ dmaQ - rheB resA esbB resA esbB rmNB - tatD rmNB - tatD rmNB - csbA - c csbA - c csbA - csbA - csbA - csbA - c csbA - c c csbA - c csbA - c c c csbA - c c csbA - c csbA - c c csbA - c csbA - c c c c c c c c c c c c c c c c c c	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274	2 286 0.045 0.213 11.995 2.022 0.459 0.381 0.086 0.462 0.384 0.384 0.384 0.384 0.384 0.385 0.462 0.334 0.335 0.335 2.884 2.884 0.335	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.397 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 3.813 3.813 3.813 0.439 2.312 0.281 0.281 0.281	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.152 2.2712 2.719 0.446 111.305 2.294 0.324	methyguanine-DNA methyltransferase, truncated 3'rew-dexythorouclease ATP-dependent RNA helicase DNA polymerse III subunit tepsilon IISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ISSIh, transposae, IS30 family, truncated ISSIh transposae, IS30 family, truncated ISSI transposae, tran
str1526 str1526 str1568 str1669 str1667 str1667 str1677 str1773 str1773 str1775 str1775 str1775 str1775 str1775 str1785 str1880 str1717 str1775 str1785 str1885 str1885 str1890 str1994 str1995 str1994 str1995 str1995 str1994 str1995 str1995 str1994 str1995 str199	- exxA rheA draQ draQ draQ - rexA ssbA - tap657 ssbA - - - ruvB - csbA - csbA - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - cbC - csbA - cbC - c - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC cbC - c cbC cbC - c cbC cbC - c cbC cbC cbC cbC cbC cbC cbC cbC cbC c	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274 0.383	2.286 0.043 0.213 11.995 2.022 0.455 0.381 0.098 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.335 2.884 4.859 0.335 2.884 0.459 0.335 2.884 0.459 0.352 0.452 0.452 0.453	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.281 0.281 0.385 0.200	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.311 2.719 0.446 11.305 2.294 0.324	methylguanine-DNA methyltransferase, truncated 3-rexo-deoxythoruclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISsins, transposae, IS30 family, truncated IISsins, transposae, IS30 family, truncated IISsins, transposae, IS30 family, truncated ATP-dependent exoruclease, subunit A ATP-dependent exoruclease, subunit B single-strand DNA-binding protein DNA mismatch repair protein PNA mismatch repair protein PISof, transposae, IS30 family, truncated IISsins, transposae, IISsins, truncated IISsins, transposae, IIS
str1526 str1526 str1568 str1663 str1663 str167 str167 str1771 str1771 str1775 str1775 str1775 str1776 str1801 str1801 str1803 str1805 str1845 str1948 str1845 str1948 str1948 str195 str10246 str10372 str10246 str10372 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str10245 str12855 str1285 str1885str1885 str1885 str1885str1885 str1885 str1885str1885 str1885 str1885str1885 str1885 str1885str1885 str1885str1885 str1885 str1885 str18	- exxA rheA draQ draQ draQ - rexA ssbA - tap657 ssbA - - - ruvB - csbA - csbA - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - cbC - csbA - cbC - c - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC cbC - c cbC cbC - c cbC cbC - c cbC cbC cbC cbC cbC cbC cbC cbC cbC c	0.214 6.554 2.013 0.473 0.140 2.507 0.289 0.289 0.383 0.383	2 286 0.045 0.213 11.995 2 0.22 0.459 0.381 0.096 0.462 0.334 0.334 0.334 0.334 0.334 0.334 0.334 0.335 2.884 8.459 0.352 0.252 0.352 0.252 0.352 0.252 0.355	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.281 0.281 0.385 0.200	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.311 2.719 0.446 11.305 2.294 0.324	methyguanine-DNA methytransferase, truncated 3'rexo-dexythorouclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ATP-dependent RNA helicase ATP-dependent RNA helicase Attransposae, IS30 family, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated
str1526 str1526 str1568 str1633 str1633 str1633 str1633 str1765 str1765 str1775 str1775 str1775 str1785 str1840 str1775 str1840 str1945 str1840 str1945 str1845 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1945 str1265 str1945 str1265 str1945 str1265 str1945 str126	- exxA rheA draQ draQ draQ - rexA ssbA - tap657 ssbA - - - ruvB - csbA - csbA - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - csbA - cbC - cbC - csbA - cbC - c - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC - c cbC cbC - c cbC cbC - c cbC cbC - c cbC cbC cbC cbC cbC cbC cbC cbC cbC c	0.214 6.554 2.013 0.473 0.140 2.507 0.289 conversion 5.373 2.274 0.383	2.286 0.043 0.213 11.995 2.022 0.455 0.381 0.098 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.381 0.335 2.884 4.859 0.335 2.884 0.459 0.335 2.884 0.459 0.352 0.452 0.452 0.453	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.281 0.281 0.385 0.200	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.311 2.719 0.446 11.305 2.294 0.324	methylguanine-DNA methyltransferase, truncated 3-rexo-deoxythoruclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISMn1, transposae, IS30 family, truncated ISSM1, transposae, IS30 family, truncated ISSM1, transposae, IS30 family, truncated AT-dependent RNA helicase and the subunit of the subunit of the subunit of the subunit single-strand DNA-binding protein DNA mismatch repair protein DNA mismatch subunit B Single-strand DNA-binding protein DNA mismatch subunit B Single-strand DNA-binding protein DNA mismatch subunit B Single-strand DNA-binding protein DSM, subunit B Single-strand DNA-binding protein DNA mismatch subunit B Single-strand DNA-binding protein DNA-binding protein DNA-binding protein F Single-strand DNA-binding protein DNA-binding protein F subjects are subunit hypothesical protein F subunit subunit subunit subunit single-strand DNA-binding subunit single-strand DNA-binding subunit single-strand DNA-binding subunit hypothesical protein F subunit subunit subunit single-subunit s
str1526 str1526 str1568 str1633 str1633 str1633 str1633 str1765 str1776 str1775 str1785 str1775 str1785 str1785 str1785 str1880 str1948 str1905 str1948 str1905 str1948 str1948 str1905 str1948 str1948 str1905 str1948 str1948 str195 str1883 str1948 str195 str1883 str1948 str1955 str1883 str1948 str1955 str1883 str1985 str1885str1885 str1885	- exxA rheA draQ draQ - - - - - - - - - - - - - - - - - - -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 0.289 0.383 0.383	2,286 0,0213 11,395 2,022 0,458 0,0381 0,098 0,462 0,334 0,230 0,334 0,459 0,335 2,884 8,495 0,355 2,884 8,495 0,355 2,884 0,355	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.281 0.281 0.385 0.200	0.275 9.580 2.088 2.783 0.446 0.395 0.431 2.415 0.497 0.311 2.719 0.446 11.305 2.294 0.324	methyguanine-DNA methytransferase, truncated 3'rexo-dexythorouclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ISSIh1, transposae, IS30 family, truncated ATP-dependent RNA helicase ATP-dependent RNA helicase Attransposae, IS30 family, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated ISSIh1, transposae, truncated
str1526 str1526 str1568 str1668 str1668 str1677 str168 str1777 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1785 str1885 str1885 str1885 str1885 str1905	- exxA rheA driaQ driaQ driaQ - rexB rexA rexB rexA rexB ssbB - ctaD trp657 ssbA - - revB - rexB ssbA - - revB taD trp657 ssbA - - - revB taD trp657 ssbA - - - - - - - - - - - - - - - - - - -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 0.289 0.289 0.383 2.274 0.383	2,286 0,0213 11,395 2,022 0,458 0,0381 0,098 0,462 0,334 0,230 0,334 0,459 0,335 2,884 8,495 0,355 2,884 8,495 0,355 2,884 0,355	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.230 0.281 0.285 0.200 0.456	0.275 2.088 2.083 0.395 0.395 0.395 0.397 0.152 2.210 2.719 0.446 11.305 2.294 0.324 0.324	methylguanine-DNA methyltransferase, truncated 3-rexo-deoxyltronuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISsins, transposase, IS30 family, truncated IISsins, transposase, IIS30 family, truncated IISSINs, transposase, truncated IISS
str1526 str1526 str1568 str1663 str1663 str1663 str1716 str1776 str1776 str1776 str1776 str1776 str1776 str1780 str1776 str1800 str1800 str1800 str1800 str1800 str1800 str1800 str1800 str1985 str1985 str1985 str1985 str1985 str1985 str1985 str1765 str1276 str1776 str1765 str1800 str1985 str1985 str1985 str1985 str1985 str1765 str1765 str1765 str1775 str1785 str1785 str1875 str1875 str1875 str1875 str1875 str1875 str1875 str1875 str188	- exxA rheA draQ draQ - - - - - - - - - - - - - - - - - - -	0.214 0.554 2.013 0.473 0.140 2.507 0.289 0.289 0.289 0.289 0.383 0.383	2 286 0.045 0.213 11.995 2.022 0.458 0.459 0.334 0.230 0.3771 2.158 0.459 0.335 2.884 2.884 0.459 0.335 2.884 0.459 0.335	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 0.300 0.300 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.281 0.320 0.281	0.275 9.580 2.783 0.395 0.395 0.395 0.497 0.152 2.210 2.210 2.719 0.446 111.305 2.294 0.324 0.324 0.324 0.351	methyguanine-DNA methyltransferase, truncated 3-rexo-deoxythonuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISMI, transposae, IS30 family, truncated ISSMI, transposae, ISSMI, truncated ISSMI, transposae, truncated ISSMI, truncated, ISSMI ISSMI, truncated ISSMI, truncated, ISSMI ISSMI, truncated ISSMI,
str1526 str1526 str1568 str1668 str1668 str1677 str168 str1777 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1778 str1785 str1885 str1885 str1885 str1885 str1905	- exxA rheA driaQ driaQ driaQ - rexB rexA rexB rexA rexB ssbB - ctaD trp657 ssbA - - revB - rexB ssbA - - revB taD trp657 ssbA - - - revB taD trp657 ssbA - - - - - - - - - - - - - - - - - - -	0.214 6.554 2.013 0.473 0.140 2.507 0.289 0.289 0.289 0.383 2.274 0.383	2,286 0,0213 11,395 2,022 0,458 0,0381 0,098 0,462 0,334 0,230 0,334 0,230 0,335 2,884 8,495 0,355 2,884 8,495 0,355 2,884 0,355 2,884 0,355 2,684 0,413 0,355 2,022 0,335	0.399 0.423 2.012 2.073	0.495 0.228 0.373 4.025 0.478 0.478	0.392 0.446 2.185 2.799 0.368 0.300 0.307 0.452 5.192 2.473 0.307 0.452 0.307 0.427 9.011 3.813 0.439 2.312 0.230 0.281 0.230 0.281 0.285 0.200 0.456	0.275 2.088 2.083 0.395 0.395 0.395 0.397 0.395 0.397 2.2415 2.2415 2.2410 2.2710 2.719 0.454 0.324 0.324	methylguanine-DNA methyltransferase, truncated 3-rexo-deoxyltronuclease ATP-dependent RNA helicase DNA polymerse III subunit epsilon IISsins, transposase, IS30 family, truncated IISsins, transposase, IIS30 family, truncated IISSINs, transposase, truncated IISS

str0124																
					0.427		2.931	hypothetical protein								
str0254 str0260	- scpA	0.407	0.337			3.440	3.049	hypothetical protein segregation and condensation protein A								
str0268	- -					0.084	0.106	hypothetical protein								
str0276				0.429		0.262	0.284	membrane protein								
str0306		0.346	0.085					hypothetical protein								
str0340			2.136			0.334	0.456	hypothetical protein								
str0427 str0503	•		0.182		0.241 0.330		2.597	hypothetical protein hypothetical protein, truncated								
str0503		0.359	0.182		0.330			hypothetical protein, truncated								
str0552	-	0.000	0.100		0.448	0.252		hypothetical protein								
str0587	-		0.388					hypothetical protein								
str0595	-						0.493	hypothetical protein								
str0632	•	0.191	0.305			2.430 4.196	3.153 3.433	hypothetical protein								
str0634 str0643	-					2.066	3.433	hypothetical protein hypothetical protein								
str0652	mip		3.069		7.075	2.000	0.147	macrophage infectivity potentiator-related protein, putative								
str0657	-			2.053		0.401		hypothetical protein								
str0661						2.585	3.081	hypothetical protein								
str0698	-					5.230	5.492	transcriptional regulator								
str0830 str0884	- sthIR	9.108	11.074				2.278	hypothetical protein DNA endonuclease, type III restriction and modification system								
str0888	-	4.185	2.700				0.464	hypothetical protein								
str0993			0.143					hypothetical protein								
str1063	-	0.385				2.636	7.822	hypothetical protein								
str1157	-		3.698			2.296		hypothetical protein								
str1248 str1256	-		3.148	2.514	2.108	2.870 3.839	4.288	hypothetical protein hypothetical protein								
str1250	-	2.715	3.148	0.479		0.462	4.288	hypothetical protein								
str1422		2.715		0.473		0.350	0.385	conserved hypothetical protein, putative transporter								
str1425	pknB	2.344				0.477	0.407	protein kinase								
str1458	-			0.422		0.332	0.425	hypothetical protein								
str1459	•	5.252	6.147					GTP pyrophosphokinase, putative								
str1466 str1551	-	10.249	9.188 0.458	0.409				hypothetical protein hypothetical protein, citrulline cluster-linked gene								
str1555		4.178	0.400	0.409			0.403	membrane protein								
str1723	-	2.765	2.051					conserved hypothetical protein, Cof family								
str1768	-		0.452					hypothetical protein								
str1778						0.262	0.220	hypothetical protein								
str1795 str1961		0.421	0.427 0.211					hypothetical protein hypothetical protein								
str1968		2.428	2.165				0.386	hypothetical protein								
str1982		0.498	2.100		0.383	3.568	9.327	hypothetical protein								
str1993	-		0.391			0.165	0.308	hypothetical protein								
str1996			0.376			0.187	0.246	hypothetical protein								
str2011	-		0.355	0.495		0.497		hypothetical protein								
str2014 str2019	-			0.318	0.449	0.242 0.332	0.396	hypothetical protein								
5112019	-			0.310		0.332	0.390	hypothetical protein								
General fr	unction pred	liction only														
str0022	pcsB	0.384				0.289	0.389	glucan binding protein								
str0059	cinA					0.309	0.358	competence damage-inducible protein A								
str0066	•			0.449		0.491		hypothetical protein MuT/oudir family protein transated								
str0136 str0193	÷			0.449		0.370		MutT/nudix family protein, truncated hypothetical protein								
str0201			3.161	3.119		0.239	0.274	ABC transporter permease protein								
str0202						0.305	0.318	ABC transporter ATP binding protein								
str0231	recU						0.407	hypothetical protein								
str0248 str0249	-					3.077 3.037	4.369 4.158	conserved hypothetical protein, putative hydrolase								
str0249	÷					2.520	2.342	conserved hypothetical protein, membrane protein hypothetical protein								
str0258						2.473	2.260	hypothetical protein								
str0316	-	2.683				0.423	0.299	hypothetical protein								
str0336	-	3.214	2.571			0.221	0.130	conserved hypothetical protein, xanthine/uracil permease family								
str0364	-	0.419				3.548	5.144	acetoin utilization protein, truncated								
str0375 str0379	recX					2.228	3.974 2.026	RecA regulator RecX								
str0385	- fabK		0.441			0.484	2.020	beta-phosphoglucomutase, putative trans-2-enoyl-ACP reductase II								
str0397	-					0.437	0.323	hypothetical protein								
str0443	-	0.372				0.311	0.459	glucan binding protein								
str0451	metG					0.436	0.377	methioninetRNA ligase								
str0455 str0462	-					0.449	0.209									
			0.000					methyltransferase, putative								
		2.792	3.062					hypothetical protein								
str0471	-	2.792 5.751 3.095	3.062 10.869 2.856					hypothetical protein membrane protein								
	-	5.751	10.869 2.856					hypothetical protein								
str0471 str0474 str0548 str0554	- - - hipO1	5.751 3.095 2.629 3.883	10.869 2.856 10.259	2.642	3.071		0.199	hypothetical protein membrane protein hypothetical protein hypothetical protein aminoacylaseN-acyl-L-amino acid amidohydrolase/hippurate hydrolase								
str0471 str0474 str0548 str0554 str0575	- - - hipO1 hlyIII	5.751 3.095 2.629	10.869 2.856	2.642	3.071 0.337	0.360		hypothetical protein membrane protein hypothetical protein hypothetical protein aminoacy/ase/N-acy/L-amino acid amidohydrolase/hippurate hydrolase similar to hemolysin III								
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str1190								
301130	-	4.000	3.927	0.237		0.444	0.000	ABC transporter substrate binding protein
str1225 str1226	- elaC	4.028 3.889	4.113			0.414 0.357	0.260 0.290	oxidoreductase, short chain dehydrogenase/reductase family ribonuclease Z
str1228	hflX					0.320	0.293	GTP-binding protein
str1232	hisK	2.409	2.753					hypothetical protein
str1257 str1281	- nox	4.987	11.654	2.337	2.167	4.204 2.160	3.773	hypothetical protein NADH oxidase (H2O-forming)
str1282	-	4.907	2.438	2.331	3.376	2.100	0.258	ABC transporter ATP binding protein
str1307	-	5.134	4.806		3.268	2.813		hydrolase, haloacid dehalogenase-like family
str1324	-						0.401	ABC transporter ATP binding protein, truncated
str1330 str1363	-		8.534	5.936	0.341 0.428		2.201	Na+-dependent transporter, putative
str1363 str1371	-	2.019		0.425	0.428	0.398		hypothetical protein oxidoreductase, aldo/keto reductase family
str1425	- pknB	2.344		0.420	0.403	0.398	0.407	protein kinase
str1433	-	2.088						conserved hypothetical protein, Cof family
str1480	-	4.781	4.477			0.253	0.304	polysaccharide/teichoic acid transporter, putative
str1504	obg	3.122	2.508					GTP-binding protein, GTP1/Obg family
str1517	-		2.907	2.198	0.404	3.778	6.485	permease, putative
str1524 str1547	-				0.484	0.401 0.405	0.320	hypothetical protein hypothetical protein
str1605	2					4.415	2.414	hypothetical protein
str1615	-	0.333						hypothetical protein
str1616	-	0.430	0.424					hypothetical protein
str1641	hlyX					0.263	0.287	hemolysin, putative hypothetical protein
str1665 str1666	-	2.367				0.259	0.267	ABC transporter ATP binding protein
str1723	2	2.765	2.051			0.200	0.230	conserved hypothetical protein, Cof family
str1775	-	0.442	0.338					glucan-binding protein
str1798	-		0.486					ribosome-associated GTPase
str1802			0.257			0.356	0.383	hypothetical protein
str1809	jag	0.445	0.050		0.404	0.475		conserved hypothetical protein, Jag protein
str1836 str1838	- hipO3	0.445	0.252		0.481	0.365		hypothetical protein aminoacylase/N-acyl-L-amino acid amidohydrolase/hippurate hydrolase
str1847	-	2.112		0.459	3.298	0.303	0.180	permease, putative
str1848	-						0.396	phenylalanyl-tRNA synthetase homolog
str1853	-					2.421	2.946	hypothetical protein
str1875	-					0.280	0.300	hypothetical protein
str1948 str1951	-	0.289	0.334	0.343				hypothetical protein
str1951 str1965		2.185		0.343				hypothetical protein acetyltransferase, GNAT family
str2012		2.105	0.484	0.396		0.305	0.414	peptidase
str2013	-					0.207	0.366	protease, putative
str2016	guaB	3.169		0.253		0.207	0.290	inositol-5-monophosphate dehydrogenase
str2020	-	2.798		0.414				ABC transporter ATP-binding protein
Inorganic	ion transport	and metabo	nlism					
str0061	spxA	0.240	10111	2.700	0.237		2.339	transcriptional regulator Spx
str0264	trkH1	3.598	2.740					potassium Trk transporter membrane-spanning protein
str0265	trkA1	3.019	2.226			0.400	0.347	potassium Trk transporter NAD+ binding protein
str0288	cbiM	2.376	3.325					cobalt transport protein CbiM
str0289 str0290	cbiQ cbiO	2.396	3.741 3.344					cobalt ABC transporter permease protein cobalt ABC transporter ATP-binding protein
str0297	-	3.228	2.170		5.772		0.170	ABC transporter substrate binding protein
str0301	-	5.550	3.885		4.469		0.130	ABC transporter ATP binding protein
str0302	-	5.088	4.537		3.798	0.496	0.131	ABC transporter permease protein
str0308	-	0.369	0.098			0.230		ABC transporter ATP binding protein
str0310	-		0.271			2.833		ABC transporter permease protein cation transporter P-type ATPase, truncated
str0351 str0498						2.833		Na/Pi cotransporter II-related protein, truncated
str0499	-		0.405		0.375	0.362		Na/Pi cotransporter II-related protein, truncated
str0608	feoB				2.582		0.377	ferrous ion transport protein B
str0677	mntH		2.372					manganese transport protein, NRAMP family
str0720	sodA	0.070			0.477		4.027	superoxide dismutase (Mn)
str0723 str0724	dpr fur	0.279		2.337	0.064 0.378	4.020 3.151	63.262 8.328	peroxide resistance protein, non-heme iron-containing ferritin
str0745		0.458	2.712	5.919	0.378	3.131	0.320	ferric transport regulator protein hypothetical protein
str0840	copB	0.100	0.390	0.010	0.372		2.580	cation transporting ATPase, copper transport
str0860	adcA		2.441		2.267	0.359	0.158	zinc ABC transporter substrate binding protein
str0874	phnA					0.305	0.247	conserved hypothetical protein, PhnA protein
								phosphate ABC transporter substrate binding protein
str1001	pstS		2.125					abarahata ADC transmission and in
str1002	pstC1		2.347					phosphate ABC transporter permease protein
str1002 str1003					16 904	3 182	0 188	phosphate ABC transporter permease protein phosphate ABC transporter permease protein
str1002	pstC1		2.347		16.904 9.424	3.182	0.188 0.174	phosphate ABC transporter permease protein
str1002 str1003 str1022 str1023 str1024	pstC1 pstC2 -		2.347 2.247		9.424 14.007	3.182	0.174 0.170	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein hypothetical protein
str1002 str1003 str1022 str1023 str1024 str1025	pstC1 pstC2 - - fatB	10.846	2.347 2.247 9.884		9.424 14.007 24.748	3.182	0.174 0.170 0.212	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein ferrichrome ABC transporter, substrate-binding protein
str1002 str1003 str1022 str1023 str1024 str1025 str1026	pstC1 pstC2 - - fatB fatA	10.406	2.347 2.247 9.884 10.717		9.424 14.007 24.748 32.109	3.182	0.174 0.170 0.212 0.211	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein terrichrome ABC transporter, substrate-binding protein ferrichrome ABC transporter, ATP-binding protein
str1002 str1003 str1022 str1023 str1024 str1025 str1026 str1027	pstC1 pstC2 - fatB fatA fatC	10.406 15.104	2.347 2.247 9.884 10.717 13.797		9.424 14.007 24.748 32.109 37.808	3.182	0.174 0.170 0.212 0.211 0.159	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein ferrichrome ABC transporter, substrate-binding protein ferrichrome ABC transporter, ATP-binding protein ferrichrome ABC transporter, premease protein
str1002 str1003 str1022 str1023 str1024 str1025 str1026 str1027 str1028	pstC1 pstC2 - - fatB fatA	10.406 15.104 11.262	2.347 2.247 9.884 10.717 13.797 8.874		9.424 14.007 24.748 32.109		0.174 0.170 0.212 0.211 0.159 0.174	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein hypothetical protein environme ABC transporter, substrate-binding protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein
str1002 str1003 str1022 str1023 str1024 str1025 str1026 str1027 str1028 str1056 str1116	pstC1 pstC2 - fatB fatA fatC fatD -	10.406 15.104	2.347 2.247 9.884 10.717 13.797		9.424 14.007 24.748 32.109 37.808	3.182 0.189	0.174 0.170 0.212 0.211 0.159	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein typothetical protein typothetical protein ferrichrome ABC transporter, a Pholending protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein cation effux protein chioride channel protein, truncated
str1002 str1003 str1022 str1023 str1024 str1025 str1026 str1027 str1028 str1056 str1116	pstC1 pstC2 - fatB fatA fatC	10.406 15.104 11.262 7.257	2.347 2.247 9.884 10.717 13.797 8.874 4.731 2.806	0.423	9.424 14.007 24.748 32.109 37.808	0.189	0.174 0.170 0.212 0.211 0.159 0.174 0.213	phosphate ABC transporter permease protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein ferrichrome ABC transporter, substrate-binding protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein cation efflux protein chioride channel protein, truncated calcium transporter P-ype ATPase
str1002 str1022 str1023 str1024 str1025 str1026 str1027 str1028 str1056 str1116 str1150 str1180	pstC1 pstC2 - fatB fatA fatC fatD -	10.406 15.104 11.262 7.257	2.347 2.247 9.884 10.717 13.797 8.874 4.731	0.423 0.467	9.424 14.007 24.748 32.109 37.808	0.189	0.174 0.170 0.212 0.211 0.159 0.174	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein terrichrom ABC transporter, substrate-binding protein ferrichrome ABC transporter, APD-binding protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein cation effux protein chloride channel protein, truncated calcum transporter P-type ATPase conserved hypothetical protein, voltage-gated chloride channel family
str1002 str1003 str1022 str1023 str1024 str1025 str1026 str1027 str1028 str1056 str1116 str1180 str1180	pstC1 pstC2 - fatB fatA fatC fatD -	10.406 15.104 11.262 7.257	2.347 2.247 9.884 10.717 13.797 8.874 4.731 2.806	0.423 0.467	9.424 14.007 24.748 32.109 37.808	0.189 0.311 0.394	0.174 0.170 0.212 0.211 0.159 0.174 0.213	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein ferrichrome ABC transporter, substrate-binding protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein ferrichrome ABC transporter, permease protein cation efflux protein chioride channel protein, truncated calcium transporter P-type ATPase conserved hypothetical protein, voltage-gated chloride channel family chloride channel protein
str1002 str1022 str1023 str1024 str1025 str1026 str1027 str1028 str1056 str1116 str1150 str1180	pstC1 pstC2 - fatB fatA fatC fatD -	10.406 15.104 11.262 7.257	2.347 2.247 9.884 10.717 13.797 8.874 4.731 2.806	0.423 0.467	9.424 14.007 24.748 32.109 37.808	0.189	0.174 0.170 0.212 0.211 0.159 0.174 0.213	phosphate ABC transporter permease protein phosphate ABC transporter permease protein hypothetical protein hypothetical protein terrichrome ABC transporter, substrate-binding protein terrichrome ABC transporter, premease protein terrichrome ABC transporter, premease protein terrichrome ABC transporter, premease protein terrichrome ABC transporter, premease protein terlichrome ABC transporter, premease protein conserved hypothetical protein, voltage-gated chloride channel family chloride channel protein.
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Mixed culture experimental evolution

str0763 str0910	dltC	3.815	4.082				0.483	D-alaninepoly(phosphoribitol) ligase subunit 2 acetoin reductase, truncated
str1305	cls					2.864	2.885	cardiolipin synthetase
str1563	· _	2.877	3.012					1-acyl-sn-glycerol-3-phosphate acyltransferase, putative
str1727	acpS	3.473	3.215					4'-phosphopantetheinyl transferase
Not in COO	Gs							
str0003	-	0.388	0.302					hypothetical protein
str0005	pth	0.401	0.372					peptidyl-tRNA hydrolase
str0021 str0030	mreD purC		0.330		3.909	0.185	0.180	rod shape-determining protein MreD phosphoribosylaminoimidazole-succinocarboxamide synthase
str0034	purN		0.000		4.446		0.360	phosphoribosylglycinamide formyltransferase
str0035	purH				4.538		0.385	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
str0043	-				2.865		0.411	hypothetical protein
str0044					2.894		0.471 3.786	hypothetical protein
str0051 str0053		2.031		0.285		0.308	0.422	hypothetical protein hypothetical protein
str0057	-	2.001	0.478	0.200		0.000	0.4LL	3-methyladenine DNA glycosylase I, truncated
str0073	rpsB		5.906				0.442	30S ribosomal protein S2
str0074	tsf	3.625	4.801					elongation factor Ts
str0075 str0082	qacE	2.956	0.493			0.441	0.304	small multidrug export related protein, putative hypothetical protein
str0086		2.382				0.469	0.309	hypothetical protein
str0087	-	4.332					0.269	hypothetical protein
str0091	-			0.477				hypothetical protein 50S ribosomal protein L13
str0093 str0094	rpIM		2.072			0.473	0.489	50S ribosomal protein L13 20E ribosomal protein E0
str0094 str0097	rpsl		2.072		0.223	0.473	0.440	30S ribosomal protein S9 hypothetical protein, putative bacteriocin
str0098	-				0.425	0.305		lantibiotic biosynthesis protein, truncated
str0109	-		0.404					hypothetical protein, truncated
str0111	·		0.108					hypothetical protein
str0116 str0135	dacB	0.450 2.112	0.323	0.397				D-alanyl-D-alanine-carboxypeptidase hypothetical protein
str0146	dtd	2.112	0.448	0.331				D-tyrosyl-tRNA deacylase
str0147	-	0.262	0.105					1,6-alpha-glucanhydrolase (dextranase), truncated
str0148		0.474	0.238					1,6-alpha-glucanhydrolase (dextranase), truncated
str0149 str0151	- def	0.487	0.129 0.419				2.113	1,6-alpha-glucanhydrolase (dextranase), truncated
str0151 str0153	msf	0.437	0.419	0.312			2.113	peptide deformylase major facilitator superfamily transporter, efflux protein
str0154	rpsO	2.407	2.383					30S ribosomal protein S15
str0155	-					0.218	0.307	hypothetical protein
str0156	-					0.219	0.384	hypothetical protein
str0160 str0161	uppP		3.813			9.591	0.323 10.455	undecaprenyl pyrophosphate phosphatase hypothetical protein
str0162	mecA		0.385			0.166	0.238	adaptor protein
str0182	-					0.360	0.396	positive transcriptional regulator MutR family
str0184	-					0.392	0.387	conserved hypothetical protein, peptide-efflux protein homolog
str0192 str0195	-	2.283				0.429 0.368	0.472 0.425	PTS glucose-specific enzyme IIABC components, truncated hypothetical protein
str0208		0.435	0.244			0.186	0.282	hypothetical protein
str0209	-	0.359	0.295			0.167	0.243	hypothetical protein
str0210	-	0.476	0.347			0.293	0.376	hypothetical protein
str0216	-		0.350			0.310	0.324	hypothetical protein
str0232 str0241	- pabC		0.350			0.488	0.486	hypothetical protein aminodeoxychorismate lyase
str0261	scpB					3.983	3.390	segregation and condensation protein B
str0263	-					3.825	2.851	hypothetical protein
str0270	plcR		0.370	0.407		0.186	0.239	transcriptional regulator
str0280 str0281	urel ureA					0.480		urease accessory protein, putatuve transport protein urea amidohydrolase (urease) gamma subunit
str0282	ureB					0.386	0.481	urea amidohydrolase (urease) beta subunit
str0287	ureD		2.735					urease accessory protein
str0299	-	3.449	2.671		6.639		0.133	succinyl-diaminopimelic descuccinlyasadipeptidase, truncated
str0304 str0319	-		0.232 0.411			0.217	0.232	hypothetical protein hypothetical protein
str0323		0.240	0.253			0.468	0.381	hypothetical protein
str0325	-		0.461					hypothetical protein
str0328	-					6.101	6.636	hypothetical protein
str0331 str0332	manN manM		4.936 4.055	3.109 2.625	0.401 0.387		3.728 3.949	mannose PTS system component IID mannose PTS system component IIC
str0354	-		4.000	2.025	0.307		3.201	hypothetical protein
str0365						5.117	5.236	acetoin utilization protein, truncated
str0394	-	0.414					2.026	
	- luxS							S-ribosylhomocysteinase
str0395	- luxS -	0.414 0.415	0.135			0.260	0.313	S-ribosylhomocysteinase type I restriction modification system specificity subunit, truncated
str0402	- luxS - -	0.415	0.135	4.886				S-ribosylhomocysteinase type I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IIABC components, truncated
str0402 str0403	luxS - -		0.135	4.886 2.441		0.260 2.077	0.313	S-ribosyfhomocysteinase type I restriction modification system specificity subunit, truncated PTS furctose-specific enzyme IIABC components, truncated PTS furctose-specific enzyme IIABC components, truncated
str0402 str0403 str0404 str0410	- luxS - - -	0.415 0.339		4.886 2.441		0.260		S-ribosylhomocysleinase type I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated hypothetical protein
str0402 str0403 str0404 str0410 str0414	- luxS - - - -	0.415 0.339 3.362	2.446			0.260 2.077	0.313	S-ribosylhomocysteinase type I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated hypothetical protein
str0402 str0403 str0404 str0410 str0414 str0415	- luxS - - - - -	0.415 0.339 3.362 2.848				0.260 2.077	0.313	S-ribosylhomocysleinase type I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated hypothetical protein hypothetical protein, truncated
str0402 str0403 str0404 str0410 str0414 str0415 str0416 str0417	- - - - - - rpIU	0.415 0.339 3.362	2.446 2.906 3.198			0.260 2.077	0.313	S-ribosylhomocysleinase type I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated hypothetical protein hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated
str0402 str0403 str0404 str0410 str0414 str0415 str0416 str0417 str0418	- - - - -	0.415 0.339 3.362 2.848 2.264	2.446 2.906 3.198 2.073			0.260 2.077	0.313	S-ribosylhomocysleinase bype I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein truncated hypothetical protein, truncated 50S ribosomal protein, 121 50S ribosomal protein L21
str0402 str0403 str0404 str0410 str0414 str0415 str0415 str0416 str0417 str0418 str0435	- - - - - rpIU rpmA -	0.415 0.339 3.362 2.848	2.446 2.906 3.198			0.260 2.077 2.146	0.313 2.194 2.801	S-ribosylhomocysleinase type I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated hypothetical protein hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated SoS ribosomal protein L27 SoS ribosomal protein L27
str0402 str0403 str0404 str0410 str0414 str0415 str0415 str0416 str0417 str0418 str0435	- - - - - - rpIU	0.415 0.339 3.362 2.848 2.264	2.446 2.906 3.198 2.073			0.260 2.077	0.313	S-ribosylhomocysleinase ybe I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein protein function biosomal protein L27 hypothetical protein truncated hypothetical protein hypothetical prot
str0402 str0403 str0404 str0410 str0410 str0415 str0415 str0416 str0417 str0418 str0435 str0439 str0444 str0446	- - - - - rpIU rpmA -	0.415 0.339 3.362 2.848 2.264 4.257	2.446 2.906 3.198 2.073 2.850			0.260 2.077 2.146 0.402	0.313 2.194 2.801	S-ribosylhomocysleinase ype I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein truncated protein hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated SS ribosoma protein ZZ SS ribosoma protein ZZ hypothetical protein truncated IS1193 transposose surface immunogenic protein, truncated
str0402 str0403 str0404 str0410 str0414 str0415 str0416 str0416 str0417 str0418 str0435 str0439 str0444 str0448	- - - - - rpIU rpmA -	0.415 0.339 3.362 2.848 2.264	2.446 2.906 3.198 2.073 2.850 0.097			0.260 2.077 2.146 0.402 2.409	0.313 2.194 2.801 0.346	S-ribosylhomocysleinase yber I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme ILABC components, truncated PTS fructose-specific enzyme ILABC components, truncated PTS fructose-specific enzyme ILABC components, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated SoS ribosomal protein L27 Hypothetical protein truncated STIS transposse surface immunogenic protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein
str0402 str0403 str0404 str0410 str0414 str0415 str0416 str0417 str0418 str0435 str0439 str0444 str0446 str0449	- - - - - rpIU rpmA -	0.415 0.339 3.362 2.848 2.264 4.257	2.446 2.906 3.198 2.073 2.850 0.097 0.148			0.260 2.077 2.146 0.402 2.409	0.313 2.194 2.801 0.346	S-ribosylhomocysleinase S-ribosylhomocysleinase Ype I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated hypothetical protein hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated SS ribosomal protein, truncated SS ribosomal protein L27 ribosome releasing factor truncated IS1193 transposase surface immunogenic protein hypothetical protein hypothetical protein surface immunogenic protein, truncated hypothetical protein
str0402 str0403 str0404 str0410 str0410 str0415 str0415 str0415 str0417 str0418 str0435 str0435 str0439 str0444 str0448 str0448 str0449 str0449	- - - - rpiU rpmA - frr - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229			0.260 2.077 2.146 0.402 2.409 0.271	0.313 2.194 2.801 0.346 0.346	S-ribosylhomocysleinase yber I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein, truncated hypothetical protein, truncated S0S ribosomal protein L21 S0S ribosomal protein functional IS1 faraposea truncated IS1 f3S (ransposea truncated IS1 f3S (r
str0402 str0403 str0404 str0410 str0414 str0415 str0415 str0416 str0417 str0418 str0435 str0439 str0434 str04446 str0448 str0448 str04450 str0456	- - - - - rpIU rpmA -	0.415 0.339 3.362 2.848 2.264 4.257	2.446 2.906 3.198 2.073 2.850 0.097 0.148			0.260 2.077 2.146 0.402 2.409 0.271 0.205	0.313 2.194 2.801 0.346 0.346 0.346	S-ribosylhomocysleinase S-ribosylhomocysleinase Yrps I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IIABC components, truncated PTS fructose-specific enzyme IIABC components, truncated hypothetical protein hypothetical protein, truncated hypothetical protein, truncated SOS ribosomal protein, truncated SOS ribosomal protein, truncated SOS ribosomal protein L27 hypothetical protein fructure surface immunogenic protein, truncated hypothetical protein truncated IS1193 transposses surface immunogenic protein, truncated hypothetical protein hypothetical
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str0402 str0403 str0404 str0410 str0414 str0415 str0415 str0415 str0418 str0418 str0418 str0418 str0435 str0439 str0448 str0448 str0448 str0445 str0456 str0459 str0459 str0468	- - - - rpiU rpmA - frr - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.386			0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.163 4.452	0.313 2.194 2.801 0.346 0.346 0.210 5.120 5.933 4.599	S-ribosylhomocysleinase ybe I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated PTS fuctose-specific enzyme IIABC components, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated SOS ribosomal protein L27 hypothetical protein truncated STI SI ransposase surface truncation hypothetical protein protein protein protein hypothetical protein protein hypothetical protein hypothetical
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str0402 str0403 str0404 str0410 str0411 str0415 str0415 str0415 str0417 str0418 str0448 str0448 str0448 str0448 str0448 str0448 str04450 str0450 str0455 str0455 str0455 str0455 str0455 str0455 str0455 str0455 str0455 str0473 str0473 str0477 str0477 str0477 str0478	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.386 4.958	2.441		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.163 4.452 0.330 0.442	0.313 2.194 2.801 0.346 0.346 0.210 5.120 5.933 4.599 0.396 2.556	S-ribosylhomocysleinase yber I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein truncated Devices of the system of the system of the system hypothetical protein, truncated SOS ribosomal protein L21 SOS ribosomal protein L27 hypothetical protein truncated IS1183 transposase truncated IS1183 transposase truncated IS1183 transposase hypothetical protein hypothetical protein proteinese maturation protein precursor protease maturation protein precursor cell wall protein precursor, similar to choline binding protein, truncated hypothetical protein protease maturation protein all wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated hypothetical protein hypothetical protein ATP synthase subunit A ATP synthase subunit A
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str0402 str0403 str0404 str0410 str0414 str0414 str0415 str0418 str0418 str0418 str0418 str0418 str0418 str04435 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0472 str0458 str0460 str0451 str0472 str0479 str0450 str0540 str0540 str0542 str0542 str0542 str0542 str0540 str0542 str05	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402 2.393	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.386 4.958 4.953 2.572	2.441		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.163 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.346 0.210 5.933 4.599 0.396 2.556 0.419 0.371 0.490	S-ribosylhomocysleinase yber I restriction modification system specificity subunit, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated PTS fuctose-specific enzyme IABC components, truncated hypothetical protein, truncated SoS ribosomal protein, truncated SoS ribosomal protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein truncated protein hypothetical protein truncated protein hypothetical protein hypothetical protein protease maturation protein precursor cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated hypothetical protein ATP synthase subunit A ATP synthase subunit A ATP synthase subunit A ATP synthase subunit A ATP synthase protein hypothetical protein
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str0402 str0404 str0404 str0410 str0411 str0411 str04116 str04116 str04118 str0418 str0418 str0418 str0418 str0448 str0448 str0448 str04445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0445 str0472 str0472 str0479 str0479 str0479 str0479 str0479 str0479 str0516 str0547 str0547 str0571 str0571	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402 2.393	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.366 4.953 2.572 0.355 2.678 2.726	2.441		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.210 5.933 4.599 0.396 2.556 0.419 0.391 0.439	S-ribosylhomocysleinase ybe I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein hypothetical protein hypothetical protein truncated SOS ribosomal protein L21 SOS ribosomal protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein L27 hypothetical protein hypothetical pro
str0403 str0404 str0404 str0410 str0411 str0415 str0415 str0415 str0417 str0418 str0448 str0448 str0448 str0448 str0448 str0449 str04460 str0450 str0550 str05	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402 2.393 4.151	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.386 4.953 2.572 0.355 2.618 2.726 4.055 2.431 0.435	0.463		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.163 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.346 0.346 0.346 0.346 0.346 0.396 2.556 0.419 0.391	S-ribosylhomocysleinase yber I etsriction modification system specificity subunit, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein, truncated So Sribosomal protein, truncated SOS ribosomal protein, truncated SOS ribosomal protein, truncated hypothetical protein, truncated hypothetical protein, truncated hypothetical protein and truncated IS1193 transposase surface immunogenic protein, truncated hypothetical protein precursor protease maturation protein precursor protease maturation protein precursor proteinal protein hypothetical protein
str0402 str0404 str0404 str0410 str0414 str0411 str04116 str04116 str0418 str0418 str0418 str0418 str0448 str0448 str0448 str0448 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0447 str0472 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0516 str0516 str0547 str0574 str0577 str0577 str0577	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402 2.393 4.151	2.446 2.996 3.199 2.073 2.850 0.097 0.148 0.229 2.386 4.958 4.953 2.572 0.355 2.618 2.726 4.055 2.728 4.055 2.431 0.230	0.463		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.210 5.933 4.599 0.396 2.556 0.419 0.391 0.439 0.391 0.439	S-ribosylhomocysleinase yei le ristriction modification system specificity subunit, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein hypothetical protein truncated Developments, truncated hypothetical protein DSS ribosomal protein SA TH Synthase subunit A ATP synthase subunit A ATP synthase subunit A ATP synthase subunit A DSS ribosomal protein hypothetical protein hypothetical protein hypothetical protein DSS ribosomal protein Hypothetical p
str0402 str0404 str0404 str0410 str0414 str0411 str0415 str0416 str0416 str0416 str0416 str0418 str04403 str0443 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str0448 str04472 str0450 str0458 str0472 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0510 str0510 str0574 str0574 str0574 str0578	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.848 2.264 4.257 0.402 2.393 4.151	2.446 2.906 3.198 2.073 2.850 0.097 0.148 0.229 2.386 4.958 4.953 2.572 0.355 2.618 2.726 4.055 2.431 0.435 0.290 3.191	0.463		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.210 5.120 5.933 0.396 2.556 0.459 0.371 0.371 0.490 0.371 0.490 0.371	S-ribosylhomocysleinase yber I restriction modification system specificity subunit, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein, truncated So Sribosomal protein, truncated SOS ribosomal protein, truncated SOS ribosomal protein, truncated hypothetical protein, truncated SOS ribosomal protein L21 SOS ribosomal protein L27 hypothetical protein truncated IS1193 transposase surface immunogenic protein, truncated hypothetical protein proteosase maturation protein precursor protease maturation protein precursor proteinase protein ATS syntase subusit asion hypothetical protein hypothetical protein proteosase maturation protein scheme binding protein, truncated cell wall protein precursor, similar to choline binding protein, truncated hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein proteoses abusit asion ATS syntase subusit asion hypothetical protein hypothetical protein S-adenosylmethionins:RNA ribosyltransferase-isomerase sensor histidine kinase, truncated ABC transporter permease protein hypothetical prote
str0402 str0404 str0404 str0410 str0414 str0411 str04116 str04116 str0418 str0418 str0418 str0418 str0448 str0448 str0448 str0448 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0446 str0447 str0472 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0479 str0516 str0516 str0547 str0574 str0577 str0577 str0577	- - - - - - - - - - - - - - - - - - -	0.415 0.339 3.362 2.264 4.257 0.402 2.393 4.151 2.978 4.847	2.446 2.996 3.199 2.073 2.850 0.097 0.148 0.229 2.386 4.958 4.953 2.572 0.355 2.618 2.726 4.055 2.728 4.055 2.431 0.230	0.463		0.260 2.077 2.146 0.402 2.409 0.271 0.205 3.508 4.452 0.330 0.442 0.330 0.442 0.284 0.391	0.313 2.194 2.801 0.346 0.346 0.210 5.933 4.599 0.396 2.556 0.419 0.391 0.439 0.391 0.439	S-ribosylhomocysleinase yei le ristriction modification system specificity subunit, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated PTS fructose-specific enzyme IABC components, truncated hypothetical protein hypothetical protein truncated Developments, truncated hypothetical protein DSS ribosomal protein SA TH Synthase subunit A ATP synthase subunit A ATP synthase subunit A ATP synthase subunit A DSS ribosomal protein hypothetical protein hypothetical protein hypothetical protein DSS ribosomal protein Hypothetical p

str0593						0.367	0.416	hypothetical protein
str0594	-					0.355	0.394	hypothetical protein
str0598 str0599	-					0.407 0.286	0.433 0.305	oxidoreductase, truncated oxidoreductase, truncated
str0600		0.462	0.250			0.200	0.305	hypothetical protein
str0607	feoA	0.402	0.200		2 548		0.329	ferrous ion transport protein A
str0609	-				2.641		0.234	hypothetical protein
str0610	-				2.078		0.318	hypothetical protein
str0618	dgk		3.941				2.033	diacylglycerol kinase
str0622	pmrA		3.220					multi-drug resistance efflux pump
str0631	·	0.370	0.319			2.601	2.835	hypothetical protein
str0633	grk	0.379	0.404				2.260	glycerate kinase, putative
str0641 str0648	aroF		2.208			2.028 2.393	2,117	chorismate synthase negative transcriptional regualtor-PBP synthesis, truncated
str0650	- eetB		2.200		8.729	2.393	0.229	exfoliative exotoxin B, putative
str0654			3.379		0.725		0.220	hypothetical protein
str0656						0.301	0.480	hypothetical protein
str0660						0.317		hypothetical protein
str0664			6.512			2.067		hypothetical protein
str0667	lgt		2.068			2.509	2.357	prolipoprotein diacylglyceryl transferase
str0669	-					2.042	2.853	hypothetical protein
str0670	-	4.953	5.959			0.248	0.335	hypothetical protein
str0675		0.289	0.370			0.346		hypothetical protein
str0685 str0690	-	2.428	2.073 0.455				2.152	hypothetical protein hypothetical protein
str0690			0.400				2.102	hypothetical protein
str0700			0.411			6.257	6.773	hypothetical protein
str0701		8,746	11.248			0.201	0.110	hypothetical protein
str0702						2.655	3.997	hypothetical protein
str0703							3.183	hypothetical protein
str0707	-	3.800	2.448			2.137		hypothetical protein
str0709	-	3.554	3.500			2.498		hypothetical protein
str0710	-		2.375			2.406		hypothetical protein
str0713			2.998					deoxyribonuclease
str0717	-		0.489			2 000	2.595	hypothetical protein
str0727 str0744						2.000 2.420	2.595	hypothetical protein truncated IS1193 transposase
str0747	apbE	0.312	0.234			2.420		lipoprotein involved thiamine biosynthesis
str0756		7.194	6.972			0.482	0.290	hypothetical protein
str0757		2.948	2.397			0.402	0.294	hypothetical protein, RAS-related protein
str0760	dltX	2.725	2.524					component involved in D-alanylation of teichoic acids, putative
str0766						2.808		IS861, transposase (orf2), IS3 family, truncated
str0782	-	0.474	0.238					unknown protein, phage associated
str0784	-		0.222					unknown protein, phage associated
str0793		0.047	0.029			0.421	0.379	sensor histidine kinase (homolog to ciaH Spn), truncated
str0794	•	0.049	0.033					sensor histidine kinase (homolog to ciaH Spn), truncated
str0798	rpsT				0.047	0.399		30S ribosomal protein S20
str0819 str0820	-				2.017	3.105	3.277	hypothetical protein truncated IS1193 transposase
str0820						2.288	2.600	truncated IS1193 transposase
str0838	cspB	0.368	0.378			0.383	2.000	cold shock protein B
str0861	-	0.241	0.234			0.346	0.340	hypothetical protein
str0862			0.037					hypothetical protein
str0868						0.291	0.395	hypothetical protein
str0906	ndk				0.474			nucleoside diphosphate kinase
str0912	-	0.459						hypothetical protein
str0913	-		0.277					hypothetical protein
str0914		0.227	0.199				2.544	hypothetical protein
str0922		0.394	0.405			0.357	4.872	hypothetical protein
str0930 str0934		0.394	0.405			4.664	2.313	hypothetical protein ferrochelatase, truncated
str0935			2.258				2.010	ferrochelatase, truncated
str0951			3.544				0.381	hypothetical protein
str0952			5.151				0.001	hypothetical protein
str0969		0.244	0.097			2.367		amidase, truncated
str0978			4.003				3.600	hypothetical protein
str0980	-		5.759			3.619	3.744	hypothetical protein
str0981						5.512	7.344	transcriptional regulator, AraC family, truncated
str0982	-	0.107				3.155	3.586	transcriptional regulator, AraC family, truncated
str0992		0.467	0.224					hypothetical protein
str0998 str1013	- malQ	0.267	2.652	4.462	0.221	2.197	9.940	hypothetical protein 4-alpha-glucanotransferase
str1013	tatA	0.207		4.402	24.584	2.197	0.181	Sec-independent protein translocase protein tatA, putative
str1020	tatC				21.304		0.186	Sec-independent protein translocase protein tatis, putative
str1037		0.253	0.236				2.806	hypothetical protein
str1038		0.291	0.264				2.502	hypothetical protein
str1044			0.150					positive transcriptional regulator MutR family
str1047	-	0.475	0.102					hypothetical protein
str1052	-			3.818				hypothetical protein, truncated
str1053	-	7 404	44.040	4.722			0.404	hypothetical protein, truncated
str1078 str1079	epsK epsJ	7.424	11.246				0.481 0.461	exopolysaccharide gene claster protein exopolysaccharide polymerization protein
str1118	-		2.312				0.401	hypothetical protein, truncated
str1125		4.964	3.721				0.453	hypothetical protein
str1129			0.234					hypothetical protein
str1130		0.376	0.076			0.304		IS657, transposase, IS200 family, truncated
str1132	rpIT		3.826	2.400		0.438	0.382	50S ribosomal protein L20
str1136	·	0.310	0.409			0.074		hypothetical protein
str1140	sipB		0.415			3.674	5.104	signal peptidase I conserved hypothetical protein, TPR domain protein
str1141 str1151			0.415			3.248	3.214	hypothetical protein
str1153						2.863	0.214	hypothetical protein, acetyltransferase, truncated
str1165	endA					2.500	0.364	competence associated membrane nuclease
str1166	epuA					0.327	0.273	conserved hypothetical protein, competence associated
			0.471			0.389	0.315	hypothetical protein
str1168	-					0.177	0.275	hypothetical protein
str1168 str1170	-					0.384	0.296	50S ribosomal protein L19
str1170 str1179	- - rpIS	2.305	3.945	0.077		0.349	0.492	hypothetical protein
str1170 str1179 str1184	- rpIS -	2.305 4.036	3.945	0.286		0.040		
str1170 str1179 str1184 str1193	1		3.945	0.286	0 000		3.195	surface-associated protein cshA precursor, truncated
str1170 str1179 str1184 str1193 str1201	- rpIS - IeuC	4.036		0.286	0.382	0.374	3.195	isopropylmalate isomerase large subunit
str1170 str1179 str1184 str1193 str1201 str1208	- - leuC -	4.036	0.072	0.286	0.382 0.284		3.195	isopropylmalate isomerase large subunit hypothetical protein
str1170 str1179 str1184 str1193 str1201 str1208 str1209	1	4.036 0.059 0.351	0.072 0.473	0.286	0.382 0.284	0.374 0.432		isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein
str1170 str1179 str1184 str1193 str1201 str1208	- - leuC -	4.036	0.072	0.286	0.382 0.284	0.374	3.195 0.374	isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein hypothetical protein
str1170 str1179 str1184 str1193 str1201 str1208 str1209 str1227	- - leuC -	4.036 0.059 0.351	0.072 0.473 2.821	0.286	0.382 0.284	0.374 0.432		isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein hypothetical protein hypothetical protein
str1170 str1179 str1184 str1193 str1208 str1209 str1227 str1233 str1239 str1240	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115	0.286	0.382 0.284	0.374 0.432		isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1170 str1179 str1184 str1193 str1201 str1208 str1209 str1227 str1233 str1239 str1240 str1241	- - leuC -	4.036 0.059 0.351 2.967 0.102	0.072 0.473 2.821 2.045 0.089 0.115 0.152	0.286	0.382 0.284	0.374 0.432		isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1170 str1179 str1184 str1193 str1201 str1208 str1209 str1227 str1233 str1239 str1240 str1241 str1250	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115	0.286	0.382 0.284	0.374 0.432 0.438		IsopropyImalate isomerase large subunit hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein, GrA family
str1170 str1179 str1184 str1193 str1201 str1208 str1209 str1227 str1233 str1239 str1240 str1241 str1250 str1253	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377		0.382 0.284	0.374 0.432		isopropylmalate isomerase large subunit hypothetical protein histone-like DNA-binding protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein, GTA family hypothetical protein
str1170 str1179 str1184 str1193 str1208 str1209 str1227 str1233 str1239 str1240 str1240 str1241 str1253 str1253 str1283	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377 6.255	6.327	0.382 0.284	0.374 0.432 0.438 4.442		isopropyimalate isomerase large subunit hypothetical protein hypothetical protein
str1170 str1179 str1184 str193 str1208 str1209 str1227 str1233 str1239 str1240 str1240 str1241 str1250 str1283	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377		0.382 0.284	0.374 0.432 0.438 4.442 0.278	0.374	isopropylmalate isomerase large subunit hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein, GTA family hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1170 str1179 str1184 str1193 str1208 str1209 str1227 str1239 str1239 str1240 str1240 str1241 str1250 str1253 str1285 str1285	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377 6.255		0.382 0.284	0.374 0.432 0.438 4.442	0.374	isopropyimalate isomerase large subunit hypothetical protein hypothetical protein
str1170 str1179 str1184 str1203 str1208 str1209 str1227 str1233 str1233 str1240 str1241 str1250 str1253 str1283 str1285 str1286 str1291	- - leuC -	4.036 0.059 0.351 2.967 0.102 0.269	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377 6.255		0.382 0.284	0.374 0.432 0.438 4.442 0.278	0.374 0.342 2.074	isopropylmalate isomerase large subunit hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein, CHA family hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein
str1170 str1179 str1184 str1193 str1208 str1209 str1227 str1239 str1239 str1240 str1240 str1241 str1250 str1253 str1285 str1285	- leuC - hstH - - - - - - - - - - - - - - - - - - -	4.036 0.059 0.351 2.967 0.102 0.269 0.226	0.072 0.473 2.821 2.045 0.089 0.115 0.152 2.377 6.255 3.911	6.327	0.284	0.374 0.432 0.438 4.442 0.278	0.374	isopropyimalate isomerase large subunit hypothetical protein hypothetical protein

str1314	-				17.738	2.746	0.155	hypothetical protein
str1315	hutU	8.369	4.237		6.335		0.174	urocanate hydratase
str1329 str1332		2.943	3.210				3.435	hypothetical protein hypothetical protein
str1343	msrA1	0.129	3.210			44.088	18.265	bifunctional methionine sulfoxide reductase A/B protein
str1349	-	0.120		0.041		-11.000	10.200	hypothetical protein
str1360			0.169	0.328	0.334	0.465		hypothetical protein
str1370					0.435	0.472		hypothetical protein
str1378		0.160				5.889	8.639	hypothetical protein
str1387					0.290			hypothetical protein
str1393			0.032			0.440	0.450	hypothetical protein
str1407 str1408	-					0.410 0.334	0.452 0.350	zinc metalloprotease ZmpB, truncated
str1408	-					0.334	0.350	zinc metalloprotease ZmpB, truncated ABC transporter, putative ATP binding protein, truncated
str1412						0.211	0.432	ABC transporter, putative ATP binding protein, truncated ABC transporter, truncated
str1423				0.407		0.159	0.149	potassium channel protein, truncated
str1424		2,108		0.354		0.224	0.228	potassium channel protein, truncated
str1437	-	4,192	4.731				2.313	ABC transporter permease protein
str1450	OXIT	0.102	0.160		2.953		0.245	oxalate:formate antiporter
str1474	-		2.088			0.492		glycosyltransferase, putative teichoic acid biosynthesis protein
str1475	-	2.666	3.101			0.347	0.391	hypothetical protein
str1477	-	3.122	2.582			0.309	0.342	glycosyl transferase, truncated
str1487	-					0.278	0.359	hypothetical protein
str1499	-					0.225	0.491	hypothetical protein hypothetical protein
str1500 str1503	-	3.018 2.966	2.693	0.284		0.228	0.491	hypothetical protein
str1503		2.900	0.137					hypothetical protein
str1510	-		0.405					hypothetical protein
str1515			0.405			2.723		hypothetical protein
str1518		0.343	0.211			2.120		hypothetical protein
str1523		0.456			0.463			hypothetical protein
str1528		7.255	21.065	2.904		0.407		acetyltransferase, GNAT family
str1542	amyL		0.492					cytoplasmic alpha-amylase
str1548	rpsP		2.700			0.488	0.463	30S ribosomal protein S16
str1552	-						2.127	ISSth2, transposase, IS5 family, truncated
str1564	-		0.440					peptidoglycan GlcNAc deacetylase, truncated
str1570	-		0.255	0.433				hypothetical protein
str1572	-		0.000			0.000	0.419	positive transcriptional regulator MutR family
str1573 str1575	-		0.298			0.399 0.435		macrolide-efflux protein, putative hypothetical protein
str1595						0.435	3.144	hypothetical protein
str1602		0.275	0.244				3.144	hypothetical protein
str1604	ilvD1	0.388				0.366		dihydroxy-acid dehydratase
str1608	-	3.924	2.259				0.370	ABC transporter permease protein
str1611	-						2.412	hypothetical protein
str1626	gatA	2.758	3.480					glutamyl-tRNA amidotransferase subunit A
str1628					5.941		0.206	hypothetical protein
str1630	-				4.193		0.240	6-phospho-beta-glucosidase, truncated
str1631	-				4.214		0.272	6-phospho-beta-glucosidase, truncated
str1632	msrA2				5.599	2.340	0.418	methionine sulfoxide reductase A
str1635	codY		2.779	4.359			2.058	transcriptional repressor CodY
str1639 str1651	-		0.258				0.343	hypothetical protein hypothetical protein
str1655		7.816					0.343	hypothetical protein
str1658	- cah	0.040	0.022		0.211			carbonate dehydratase
str1659	-	0.039	0.049		0.337			hypothetical protein
str1662	-					0.458	0.404	plasmid mobilization protein, truncated
str1663	int3					0.188	0.167	integrase/recombinase plasmid associated, putative
str1664						0.294	0.273	hypothetical protein
str1668	cppA	4.255	3.649			0.355	0.294	C3-degrading proteinase glycerol uptake facilitator protein
str1671	gla						0.327	
str1672	pepXP					2.710	2.334	x-prolyl-dipeptidyl aminopeptidase
str1685	blpK		0.419		0.430		2.325	pore-forming peptide, putative bacteriocin
str1702	ftsL		0.475 0.436	0.400			0.470	cell division protein
str1703	mraW		0.436	0.403 0.134		0.237	0.470	S-adenosyl-methyltransferase MraW
str1718 str1719			0.185	0.134		0.257	0.360	hypothetical protein hypothetical protein
str1735	scrB	2.252	0.100	0.201	0.460	0.001	0.000	sucrose-6-phosphate hydrolase
str1750	-		2.521					hypothetical protein
str1751			0.497					hypothetical protein
str1752	rpsR	7.072	15.726	2.224		0.419	0.280	30S ribosomal protein S18
str1755	-		0.424			0.352		hypothetical protein
str1756	-		0.286		0.414	0.366		hypothetical protein
str1763						0.435		hypothetical protein
str1773						0.495		hypothetical protein
str1776	gnlA					0.418		glutamine synthetase
str1791 str1804	rpsL	2.970	4.364 0.355	0.406			0.480	30S ribosomal protein S12
str1808	- rpmH		4.900	0.400				hypothetical protein 50S ribosomal protein L34
str1816	-		4.000			0.269	0.420	oligopeptide ABC transporter substrate-binding protein, truncated
str1817	rpIA	5.380	10.177			0.416	0.387	50S ribosomal protein L1
str1818	rplK		7.898			0.466	0.389	50S ribosomal protein L11
str1820	-					0.460		hypothetical protein
str1824	dut						0.477	deoxyuridine 5'-triphosphate nucleotidohydrolase
str1831	-	4.002	0.000		0.450	2.359		hypothetical protein
str1837 str1842	- rrmA		0.328		0.450 0.273	0.282 0.276		hypothetical protein rRNA (guanine-N1-)-methyltransferase
str1850	IIIIA				0.275	0.399	0.361	hypothetical protein
str1859			0.287			0.399	0.301	hypothetical protein
str1861			0.287					hypothetical protein
str1866	-	0.431	0.407			3.107	3.851	hypothetical protein
str1876	asp					0.244	0.298	alkaline-shock protein
str1883	- 1		0.150					alcohol-acetaldehyde dehydrogenase, truncated
str1886	-	0.254	0.067					trehalose-6-phosphate hydrolase, truncated
str1887	-	0.076	0.087					trehalose-6-phosphate hydrolase, truncated
str1888	-	0.086	0.042					trehalose-6-phosphate hydrolase, truncated
str1889	-	0.115	0.011					PTS trehalose-specific IIBC component, truncated
str1890 str1891	-	0.073	0.049					PTS trehalose-specific IIBC component, truncated
str1891 str1894		0.113	0.026 0.200			0.453		PTS trehalose-specific IIBC component, truncated hypothetical protein
str1894 str1895		0.299	0.200			0.453		hypothetical protein
str1896		0.389	0.291			0100		hypothetical protein
str1920	- rpsH	3.832	4.871			0.393	0.348	30S ribosomal protein S8
str1920	rpIN	4.578	6.740			0.383	0.348	50S ribosomal protein L14
str1926	romC	4.085	5.907			0.359	0.298	50S ribosomal protein L29
str1929	rpIV	3.456	4.397			0.374	0.317	50S ribosomal protein L22
str1933	rpID	3.810	5.529			0.316	0.281	50S ribosomal protein L4
str1934	rpIC	3.643	8.128			0.346	0.299	50S ribosomal protein L3
str1947	-						2.543	positive transcriptional regulator MutR family
str1950	-			0.309				positive transcriptional regulator MutR family, truncated
str1956	2	0.345	0.443		0.340	0.466		hypothetical protein
str1959 str1960	:	0.415 0.429	0.213 0.200			0.395 0.467		hypothetical protein Holliday junction resolvase-like protein
str1960 str1962		0.429	0.200	0.490		0.467		hypothetical protein
			0.020	0.400		0.002		

str1964 str1970		2.630				0.450	0.434	hypothetical protein
301370		2.788	2.948			0.489	0.465	hypothetical protein
str1977 str1983			0.182		0.288	3.222	11.174	hypothetical protein
str1983		0.388			0.288	3.457	10.811	hypothetical protein hypothetical protein
str1986	-	0.285			0.306	3.783	12.374	hypothetical protein
str1987	-				0.401	4.621	11.524	hypothetical protein
str2004 str2005		0.323	0.353			0.186	0.318	hypothetical protein hypothetical protein
str2021		0.525		0.353		0.100	0.510	ABC transporter permease protein
Nucleotid	e transport and	metabolisn	n					
str0023	prsA1	0.266	0.198			0.453	0.414	ribose-phosphate pyrophosphokinase
str0031	purL				3.864		0.360	phosphoribosylformylglycinamidine synthase II (FGAM synthetase)
str0032 str0033	purF purM				3.952 4.276		0.340 0.310	amidophosphoribosyltransferase phosphoribosylaminoimidazole synthetase
str0040	purD		0.487		2.729		0.342	phosphoribosylamineglycine ligase
str0041	purE				2.749		0.404	phosphoribosylaminoimidazole carboxylase catalytic subunit
str0042	purK				2.668		0.432	phosphoribosylaminoimidazole carboxylase
str0045 str0134	purB1 pyrG				2.331	0.234	0.468 0.201	adenylosuccinate lyase CTP synthetase
str0139	-		0.156			0.204	0.345	cyclo-nucleotide phosphodiesterase, truncated
str0140	-		0.094					cyclo-nucleotide phosphodiesterase, truncated
str0141 str0142			0.204					cyclo-nucleotide phosphodiesterase, truncated cyclo-nucleotide phosphodiesterase, truncated
str0144	nrdl		0.105	0.476		0.430	0.344	hypothetical protein
str0256	-	0.418	0.410			3.158	2.451	putative deoxyribonucleotide triphosphate pyrophosphatase/unknown domain fusion prote
str0355	upp	3.369	2.379			0 404	0.070	uracil phosphoribosyltransferase
str0438 str0489	pyrH tmk	0.495	2.098 0.293			0.434	0.376	uridylate kinase thymidylate kinase
str0523	pyrR	0.100	2.246	3.346		0.352	0.439	pyrimidine regulatory protein PyrR
str0524	pyrP		2.868	3.722		0.411		uracil permease
str0525 str0526	pyrB carA		2.942 4.560	4.205 4.807				aspartate carbamoyltransferase catalytic subunit
str0526 str0527	carA carB		4.560	3.841				carbamoyl-phosphate synthase small subunit carbamoyl-phosphate synthase large subunit
str0551		5.149		0.261	0.438	0.110	0.250	phosphorylase, Pnp/Udp family, putative
str0566	pfs		2.104					5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
str0750 str0751	add tdk	2.655	2.009	0.498		0.403	0.376	adenosine deaminase thymidine kinase
str0791	fhs	0.426	0.297				0.283	formate-tetrahydrofolate ligase
str0801	-	0.460				3.223	3.360	pyrimidine-nucleoside phosphorylase, truncated
str0802 str0803	-	0.435		2.548		3.409 3.565	3.443 3.567	pyrimidine-nucleoside phosphorylase, truncated pyrimidine-nucleoside phosphorylase, truncated
str0803		0.332		2.340		3.849	4.222	pyrimdine-nucleoside phosphorylase, truncated
str0805	-	0.337				8.001	5.826	deoxyribose-phosphate aldolase, truncated
str0806	-	0.005		0.574		8.323	6.657	deoxyribose-phosphate aldolase, truncated
str0807 str0886	cdd guaA	0.305 0.391	0.413	2.571		7.450 2.411	5.934	cytidine deaminase bifunctional GMP synthase/glutamine amidotransferase protein
str0941	-	0.001	0.410			0.279		phosphorylase, Pnp/Udp family
str0955	pyrDb		2.217	3.452				dihydroorotate dehydrogenase
str0967 str0968	pyrF pyrE	0.466	3.036	5.043 3.301				orotidine 5'-phosphate decarboxylase orotate phosphoribosyltransferase
str1054	pyrC	0.400	2.629	2.496				dihydroorotase
str1113	deoD	3.474	5.441					purine nucleoside phosphorylase (family 1)
str1114	gat		2.211					glutamine amidotransferase
str1117 str1135	punA cmk	0.298	2.369 0.265					purine nucleoside phosphorylase cvtidvlate kinase
str1207	pyrDa	5.938	2.484	0.418		0.424		dihydroorotate dehydrogenase
str1223	apt					0.389	0.333	adenine phosphoribosyltransferase
str1270	nrdE	2.072				0.279	0.162	ribonucleotide-diphosphate reductase alpha subunit
str1289 str1339					2.157		2.559	hypothetical protein nucleobase:cation symporter for xanthine, truncated
str1340	-		0.376		2.475			nucleobase:cation symporter for xanthine, truncated
str1341	-		0.358					nucleobase:cation symporter for xanthine, truncated
str1698	-		0.293			3.891 0.473	2.690 0.399	hypothetical protein cytidine/deoxycytidylate deaminase family protein, putative
						0.185	0.178	adenylate kinase
str1844	- adk	3.292	4.451					
str1844 str1913 str1963	- adk nrdD		4.451			0.365	0.396	anaerobic ribonucleoside triphosphate reductase
str1844 str1913	- adk nrdD guaB	3.292 3.169	4.451	0.253		0.365 0.207	0.396 0.290	
str1844 str1913 str1963 str2016 Posttrans	nrdD guaB lational modific	3.169	4.451		s	0.365 0.207	0.290	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase
str1844 str1913 str1963 str2016 Posttrans str0119	nrdD guaB lational modific grpE	3.169	4.451		s	0.365 0.207 4.078	0.290	anaerobic ribonudeoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin
str1844 str1913 str1963 str2016 Posttrans str0119 str0120	nrdD guaB lational modific grpE dnaK	3.169	4.451 in turnover,		s	0.365 0.207	0.290 6.289 5.260	anaerobic ribonudeoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132	nrdD guaB lational modific grpE dnaK dnaJ	3.169	4.451		s	0.365 0.207 4.078 4.444	0.290 6.289 5.260 4.176 0.249	anaerobic ribonudeoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor
str1844 str1913 str2016 Posttrans str0119 str0120 str0121 str0132 str0164	nrdD guaB lational modific grpE dnaK dnaJ tig	3.169	4.451 in turnover,			0.365 0.207 4.078 4.444 3.496 0.259	0.290 6.289 5.260 4.176 0.249 2.216	anaerobic ribonucleoside triphosphate reductase inositeJ-S-monophosphate dehydrogenase heat shock gratelin, chaperonin molecular chaperonin Doak heat shock protein, chaperonin trigger factor ABC transporter ATP binding protein
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132 str0164 str0203	nrdD guaB lational modific grpE dnaK dnaJ tig - groES	3.169	4.451 in turnover,		0.361	0.365 0.207 4.078 4.444 3.496 0.259 3.005	0.290 6.289 5.260 4.176 0.249 2.216 8.328	anaarobic ribonudeoxide triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor ABC transporter ATP binding protein co-chaperonin GroES
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132 str0164 str0203 str0204	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL	3.169	4.451 in turnover, 2.041			0.365 0.207 4.078 4.444 3.496 0.259	0.290 6.289 5.260 4.176 0.249 2.216	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK molecular chaperone DnaK ABG transporter ATP binding protein co-chaperonin GroEL chaperonin GroEL
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132 str014 str0203 str0204 str0285 str0285	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL ureF clpP	3.169 ation, prote	4.451 in turnover,	, chaperone	0.361	0.365 0.207 4.078 4.444 3.496 0.259 3.005	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin heat shock protein, chaperonin AsiC transport. ATP binding protein co-chaperonin GroES chaperonin GroEL urease accessory protein ATP-dependemic Elp protease proteolytic subunit
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132 str0132 str014 str0203 str0204 str0204 str0285 str0265 str0515	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL ureF clpP ppiA	3.169	4.451 in turnover, 2.041 2.088		0.361 0.330 0.362	0.365 0.207 4.078 4.444 3.496 0.259 3.005	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959	anaarobic ribonudeoxide triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor ABC transporter ATP binding protein co-chaperonin GroES chaperonin GroEL urease accessory protein ATP-dependent Cip protease proteolytic subunit peptidyl-prot/ ice-strans isomerase
str1844 str1913 str1963 str2016 Postrans str0119 str0121 str0120 str0121 str0132 str0204 str0285 str0204 str0285 str02515 str0515	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL ureF clpP ppiA clpX	3.169 ation, prote	4.451 in turnover, 2.041	, chaperone	0.361 0.330 0.362 0.480	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor ABC transporter ATP binding protein ochtaperonen CE urease accessory protein ATP-dependent Cip protease proteolytic subunit peptidiy-protyl cis-trans isomerase ATP-dependent protease ATP-binding subunit
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0132 str0132 str014 str0203 str0204 str0204 str0285 str0265 str0515	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL ureF clpP ppiA	3.169 ation, prote	4.451 in turnover, 2.041 2.088	, chaperone	0.361 0.330 0.362	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369	anaarobic ribonudeoxide triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor Vitiger factor ABC transporter ATP binding protein co-chaperonin GroES chaperonin GroEL urease accessory protein ATP-dependent Cip protease proteolytic subunit ATP-dependent protease ATP-binding subunit ATP-dependent Cip protease
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0120 str0121 str0164 str0203 str0204 str0203 str0204 str0205 str02515 str0515 str0515 str0622 str0626	nrdD guaB lational modific grpE dnaK dnaJ tig groES groEL ureF clpP ppiA clpZ clpE ssrA ppIB	3.169 ation, prote	4.451 in turnover, 2.041 2.088	, chaperone	0.361 0.330 0.362 0.480	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369 0.481	anaarobic ribonucleoside triphosphate reductase inosito-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperonin Dack heat shock protein, chaperonin trigger factor ABC transporter ATP binding protein co-chaperonin GroEL urease accessory protein a Chaperonin GroEL urease accessory proteins protein/protein consese proteolytic subunit ATP-dependersi Cap protease proteolytic subunit ATP-dependersi Cap protease proteolytic subunit ATP-dependersi Cap protease proteolytic subunit ATP-dependersi Cap protease ATP-abrinding subunit ATP-dependersi Cap protease SarA-binding protein peptidyl-profit ciertans isomerase
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0122 str0164 str0203 str0204 str0205 str0356 str0356 str0551 str0602 str0626 str06715	nrdD guaB lational modific grpE dnaK dnaJ tig - groES groEL ureF clpP ppiA clpX clpX clpE ssrA	3.169 ation, prote	4.451 in turnover. 2.041 2.088 0.355	0.426	0.361 0.330 0.362 0.480	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369	anaarobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor drigger factor ABC transporter ATP binding protein oc-chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES schaperonin protein ATP-dependent protease ATP-binding subunit ATP-dependent protease SAX-binding protein peptidy-protein peptidy-protein HbX
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0121 str0120 str0121 str0164 str0203 str0204 str0203 str0204 str0205 str02515 str0515 str0515 str0622 str0626	nrdD guaB lational modific grpE dnaK dnaJ tig groES groEL ureF clpP ppiA clpZ clpE ssrA ppIB	3.169 ation, prote	4.451 in turnover, 2.041 2.088	, chaperone	0.361 0.330 0.362 0.480	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369 0.481	anarócióc ribonucleosiók triphosphate reductase inositol-5-monophosphate dehydrogenase hade shock protein, chaperonin maleulaic haperone Drak maleulaic haperone Drak Maleulaic haperone Drak Albor transport ATP binding protein co-chaperonin GroEL urease accessory protein ATP-dependent Cip protease proteolytic subunit paptidy-i-proly cla-strans isomerase ATP-dependent protease ATP-binding subunit ATP-dependent protease ATP-binding subunit ATP-dependent Gratrans isomerase heat shock protein HIpX glutathione 5-transferase family
str1844 str1913 str1963 str2016 Posttrans str0119 str0120 str0120 str0121 str0132 str0164 str0204 str0204 str0285 str0515 str0581 str0626 str0626 str0627 str0749 str0827	nrdD guaB lational modific grpE dnaK dnaJ tig groES groEL ureF clpP ppiA clpZ clpE ssrA ppIB	3.169 ation, prote	4.451 in turnover. 2.041 2.088 0.355	0.426	0.361 0.330 0.362 0.480	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115	0.290 6.289 5.260 4.176 8.328 7.959 4.182 0.391 8.936 0.391 8.936 0.481 2.510 0.089 0.304	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin Abs/t pransport ATP binding protein co-chaperonin GroEs ABS/transport ATP binding protein co-chaperonin GroEs HTP-dependent Clip protease proteolytic subunit ATP-dependent Clip protease ATP-dependent protease ATP-dependent protease ATP-dependent protease ATP-dependent protease ATP-dependent Sprotease Sark-binding protein past shock protein HDX glutathions S-transferase family hypothetical protein, conzyme PQQ synthesis homologue thiol peroxidase
str1844 str1913 str1963 str2016 Posttrans str0119 str0121 str0121 str0120 str0124 str0203 str0204 str0204 str0205 str0285 str0356 str0515 str0627 str0627 str0715 str0749 str0827 str0390 str1185	nrdD guaB lational modific grpE dnaK dnaK dnaJ tig - groES groEL ureF cipP cipX cipE ssrA pplB htpX - - tpx -	3.169 ation, prote	4.451 in turnover. 2.041 2.088 0.355	0.426	0.361 0.330 0.362 0.480 0.297	0.365 0.207 4.078 4.444 3.496 0.259 0.259 0.259 2.628 2.655 0.389 0.480 0.325 0.115 0.304	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369 0.481 2.510 0.089 0.304 0.438	anaarobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin trigger factor Utigger factor ABC transporter ATP binding protein oc-chaperonin GroES chaperonin GroES chaperonin GroES chaperonin GroES Hore and the striphosphate of the striphosphate ATP-dependent protease proteolytic subunit ATP-dependent protease proteolytic subunit ATP-dependent protease proteolytic subunit ATP-dependent protease BTP-dependent protease Stri-binding protein peptidy-protein HpX glutathione S-transferase family hypothetical protein, conzyme PQQ synthesis homologue thiol peroxidase
str1844 str1913 str1963 str2016 Posttrans str0119 str0121 str0121 str0122 str0164 str0203 str0204 str0203 str0204 str0205 str0515 str0515 str0581 str0626 str0627 str0627 str0749 str0790 str049 str0490 str1269	nrdD guaB lational modific grpE dnaK dnaJ tig groES groEL ureF cipP ppiA tip cipX cipP ppiA htpX - - tpX - tpx - tpx - rdH - tpx - rdH - tpy - - - - - - - - - - - - - - - - - - -	3.169 ation, prote	4.451 in turnover. 2.041 2.088 0.355	0.426	0.361 0.330 0.362 0.480 0.297	0.365 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115	0.290 6.289 5.260 4.176 0.249 2.216 8.328 7.959 4.182 0.391 8.936 0.369 0.481 2.510 0.089 0.304 0.304 0.304 0.446	anaerobic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone DnaK heat shock protein, chaperonin Asic transport. ATP binding protein co-chaperonin GroES chaperonin GroEL urease accessory protein ATP-dependent Clp protease proteolytic subunit ATP-dependent protease Pro-binding subunit ATP-dependent protease Sark-binding protein paptidy-protyl cis-trans isomerase heat shock protein HBX ATP-dependent Clp protease Sark-binding protein paptidy-protyl cis-trans isomerase heat shock protein HBX how the transport of the transport of the transport of the transport protein HBX how the transport of the transp
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stri 844 stri 913 stri 963 str2016 Posttrans str0112 posttrans str0112 str0124 str0124 str0124 str0124 str0264 str0255 str0276 str0275 str0276 str0275 str0276 str0275 str0276 str0275 str0276 str0275	nrdD guaB lational modific grafic driau ig groEL	2.365 2.365 3.382 0.327 6.934 0.319 essynthesis 0.468 2.630	4.451 2.041 2.088 0.355 0.305 0.305 0.305 0.209 0.262 2.259 3.622 0.196 t;transport 4.037	0.426 0.410 5.172 0.255	0.361 0.330 0.362 0.480 0.297 2.259 0.336 2.188 0.361	0.365 0.207 4.078 4.444 3.496 0.259 2.655 0.389 0.480 0.325 0.115 0.304 0.257 15.718 2.276 0.385 0.200 0.456	0.290 6.289 5.260 4.176 8.328 7.959 4.182 0.391 8.936 0.389 0.481 2.510 0.489 0.304 0.339 0.304 0.334 0.342 0.344 0.332 0.344 0.342 0.344 0.345 0.325 0.351 0.321 0.321	anarcicic ribonucleoside triphosphate reductase inosito-5-monophosphate dehydrogenase
str1844 str1913 str1963 str1963 str2016 Posttrans str0110 str0121 str0121 str0121 str0121 str0121 str0121 str0122 str0122 str0122 str0122 str0222 str0221 str0222 str0	nrdD gua8 lational modific grpE groEL groE	2.365 2.365 3.382 6.934 0.319 0.368	4.451 . 1 unover 2.041 2.088 0.355 0.305 0.209 0.262 0.403 2.259 0.403 3.622 0.196 transport 0.131	0.426 0.410 5.172 0.255	0.361 0.330 0.362 0.480 0.297 2.259 0.336 2.188 0.361	0.385 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115 0.304 0.325 15.718 2.276 0.385 0.200 0.456 0.243	0.290 6.289 5.260 0.249 4.176 0.249 4.172 0.391 4.182 0.391 0.481 0.369 0.481 0.369 0.481 0.369 0.484 0.369 0.484 0.369 0.484 0.348 0.369 0.484 0.348 0.342 0.347 4.720 0.347 0.	anaroticic ribonucleoside triphosphate reductase inositol-5-monophosphate dehydrogenase heat shock protein, chaperonin molecular chaperone Dnak heat shock protein, chaperonin heat shock protein, chaperonin heat shock protein, chaperonin ABC transporter ATP binding protein co-chaperonin GroEL urease accessory protein ATP-dependent Clp protease proteolytic subunit ATP-dependent Clp protease Sark-binding protein ATP-dependent Clp protease proteinase glutarboots T-caraferase family hypothetical protein, Caraferase family hypothetical proteins ATP-binding subunit ATP-dependent Clp protease SPFH domant/Band 7 family protein SPFH domant/Band 7 family protein SPFH domant/Band 7 family protein ATP-dependent clp protease SPFH domant/Band 7 family protein ATP-dependent clp proteins ATP-dependent proteinses SPFH domant/Band 7 family protein ATP-dependent classes ATP-dependent classes
str1913 str1913 str1963 str1963 str0165 str0116 str0116 str0116 str0116 str0116 str0116 str0204 str0204 str0205 str0204 str0205 str0204 str0205 str0204 str0205 str0204 str0205 str020	nrdD gua8 lational modific grpE draal draal grpE groEL	2.365 2.365 3.382 0.327 6.934 0.319 iosynthesis 0.468 0.468 3.3815	4.451 1.00000000000000000000000000000000000	0.426 0.410 5.172 0.255	0.361 0.330 0.362 0.480 0.297 2.259 0.336 2.188 0.361	0.385 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115 0.304 0.325 15.718 2.276 0.385 0.200 0.456 0.243	0.290 6.289 5.260 0.249 4.176 0.248 8.328 0.394 4.182 0.394 4.82 0.394 0.384 2.510 0.084 0.347 46.723 0.347 46.723 0.347 46.223 0.347	anarcicic ribonucleoside triphosphate reductase inosito-5-monophosphate dehydrogenase
stri 844 stri 913 stri 963 stri 9163 stri 9163 stri 9163 stri 9163 stri 9163 stri 917 stri 91	nrdD guaB lational modific grafic driau ig groEL	2.365 2.365 3.382 0.327 6.934 0.319 essynthesis 0.468 2.630	4.451 in turnover, 2.041 2.088 0.355 0.305 0.305 0.209 0.262 0.305 0.209 0.262 0.403 2.522 0.196 transport 0.131 4.032	0.426 0.410 5.172 0.255	0.361 0.330 0.362 0.480 0.297 2.259 0.336 2.188 0.361	0.385 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115 0.304 0.325 15.718 2.276 0.385 0.200 0.456 0.243	0.290 6.289 5.260 0.249 4.176 0.249 4.172 0.391 4.182 0.391 0.369 0.481 0.369 0.481 0.369 0.484 0.327 0.	anaroticic ribonucleoside triphosphate reductase inosito-5-monophosphate dehydrogenase head shock protein, chaperonin meleulaic toperone Drak meleulaic toperone Drak Alb transport ATP binding protein co-chaperonin GroEL urease accessory protein ATP-dependent Cip protease proteolytic subunit pertidy-proly cla-stans isomerase ATP-dependent Cip protease proteolytic subunit ATP-dependent Cip protease and ATP-binding subunit ATP-dependent Cip protease and ATP-binding subunit ATP-dependent Cip protease and ATP-binding subunit has shock protein HIpX glutathione S-transferase family hypothetical protein reductase SPFH domain/Band 7 family protein ATP-dependent proteinase ATP-binding subunit provate-formate lyase activating enzyme thioredoxin reductase ATP-dependent proteinas ATP-binding subunit provate-formate lyase activating enzyme thioredoxin reductase ASV carrier protein ATP-dependent protein ATP-binding subunit provate-formate lyase activating enzyme thioredoxin regulator, putative transcription regulator, putative transcription regulator, putative and protein ATP-binding subunit 2 abina-acortologin regulator, putative Datamenter-Datanyl carrier protein ligase D-atamine-Datanyl carrier protein ligase applica-acortolariate decatboxylase hypothetical protein
str1913 str1913 str1963 str1963 str0165 str0116 str0116 str0116 str0116 str0116 str0116 str0204 str0204 str0205 str0204 str0205 str0204 str0205 str0204 str0205 str0204 str0205 str020	nrdD gua8 lational modific grpE draal draal grpE groEL	2.365 2.365 3.382 0.327 6.934 0.319 iosynthesis 0.468 0.468 3.3815	4.451 1.00000000000000000000000000000000000	0.426 0.410 5.172 0.255	0.361 0.330 0.362 0.480 0.297 2.259 0.336 2.188 0.361	0.385 0.207 4.078 4.444 3.496 0.259 3.005 2.628 2.655 0.389 0.480 0.325 0.115 0.304 0.325 15.718 2.276 0.385 0.200 0.456 0.243	0.290 6.289 5.260 0.249 4.176 0.248 8.328 0.394 4.182 0.394 4.82 0.394 0.384 2.510 0.084 0.347 46.7238 0.344 0.347 46.7238 0.347	anarotic ribonucleoside triphosphate reductase inosito-5-monophosphate dehydrogenase

Signal tran	asduction m	nechanisms						
str0112	-	ICCI di IISTI S				0.413	0.318	hypothetical protein
str0145	relA			0.397	0.407	0.363	0.366	(p)ppGpp synthetase
str0152 str0159	2	5.305	0.389 5.739	0.437	0.497			transcriptional regulator, putative
str0159 str0296		7.213	7.525		8.622		0.248	amino acid (glutamine) ABC transporter substrate binding protein/permease prol amino acid ABC transporter substrate binding protein, putative
str0317	rr01	7.210	1.020		0.0LL	0.297	0.291	response regulator (homolog to csrR/covR Spy)
str0318	hk01	2.784	2.527			0.220	0.208	sensor histidine kinase (homolog to csrS/covS Spy)
str0401	-	0.393		3.731				PTS fructose-specific enzyme IIABC components, truncated
str0437	•	4.150	2.810					sensor histidine kinase, uncoupled, truncated
str0543 str0665	rr02	0.467	0.328	0.388	0.175	0.179	0.239 6.877	response regulator hypothetical protein
str0666	- ptsK	0.407			0.175	2.021	2.221	HPr kinase/ohosphorvlase
str0729	typA	0.440		2.169		2.021	2.221	GTP-binding protein TypA/BipA (tyrosine phosphorylated protein A)
str0792	-	0.059	0.027	2.100				response regulator (homolog to ciaR Son), truncated
str0795		0.049	0.041					sensor histidine kinase (homolog to ciaH Spn), truncated
str0877						0.492		amino acid (glutamine) ABC transporter, substrate binding protein
str0975	-						2.045	ABC transporter substrate binding protein, truncated
str1162 str1335	- bk07	6 077	2 575		0.480		4.090	amino acid (glutamine) ABC transporter substrate-binding protein
str1335	hk07	6.277 0.117	3.575 0.215		0.363	5.809	16.007	sensor histidine kinase (homolog to HK01Spn & Sth) response regulator (homolog to RR08 Spn) uncoupled, truncated
str1381		0.137	0.220		0.303	8.149	17.564	response regulator (homolog to RR08 Spn) uncoupled, truncated
str1420	rr08					0.491		response regulator (homolog to RR03 Spn)
str1421	hk08	2.623				0.332	0.411	sensor histidine kinase (homolog to HK03 Spn)
str1425	pknB	2.344				0.477	0.407	protein kinase
str1426 str1492	pppL					0.428 0.277	0.419 0.450	phosphoprotein phosphatase amino acid (glutamine) ABC transporter substrate-binding protein
str1501	- gnIP					0.488	0.407	alutamine ABC transporter permease protein
str1579	-	6.405	6.284		9.193	0.400	0.138	glutamine ABC transporter permease protein amino acid (glutamine) ABC transporter substrate binding protein
str1637		0.233	0.352		0.274	2.315	8.443	hypothetical protein
str1654		2.302	3.221				0.324	ABC transporter substrate-binding protein, amino acid
str1939			0.239					protein-tyrosine phosphatase
str1948	-	0.289	0.334			0.000	0.000	hypothetical protein
str2001	-					0.330	0.393	hypothetical protein
Transcript	ion							
str0006	trcF	0.411	0.479					transcription repair coupling factor
str0065	-					0.415		transcriptional regulator, MarR family, truncated
str0101			0.301					hypothetical protein
str0118	hrcA					3.325	5.108	heat-inducible transcription repressor
str0133	rpoE	0.432	0.364	0.397		0.371	0.362	DNA-directed RNA polymerase subunit delta
str0145 str0185	relA adcR	3.105		0.397		0.363	0.366	(p)ppGpp synthetase zinc transport transcriptional repressor
str0215	nusG	3.105				0.359	0.384	transcription antitermination protein NusG
str0237	snf	2.074						ATP-dependent RNA helicase
str0242	greA		0.418	0.452				transcription elongation factor GreA
str0317	rr01					0.297	0.291	response regulator (homolog to csrR/covR Spy)
str0341	nusA		2.129			0.390	0.439	transcription elongation factor NusA
str0342			2.255			0.405	0.464	hypothetical protein
str0399 str0452	fruR	0.309 2.684		4.996	4.401		0.471	transcriptional repressor transcriptional regulator, LysR family
str0520		2.505	3.134		4.401		0.471	transcriptional regulator, LysR family
str0543	rr02	2.000	0.328	0.388		0.179	0.239	response regulator
str0615			0.106			0.268		transcriptional antiterminator (BgIG family), truncated
str0616			0.117			0.301		transcriptional antiterminator (BgIG family), truncated
str0625	rnr					0.495	0.401	exoribonuclease R
str0630 str0649	ccpA		2.338			2.029 2.373	2.705	catabolite control protein
str0649	- tex	4.884	2.338			2.373	2.118 2.116	negative transcriptional regualtor-PBP synthesis, truncated transcriptional regulator, putative
str0665	-	0.467	5.514		0.175	2.203	6.877	hypothetical protein
str0728	glcK					2.163	2.694	glucose kinase
str0792	-	0.059	0.027					response regulator (homolog to ciaR Spn), truncated
str0813	dinG	4.221	4.125					ATP-dependent DNA helicase
str0887		2.987	0.440	0.442				transcription regulator GntR family
str0892	•		0.443			4 000	0.500	transcriptional regulator
str0895 str0916		0.318	5.840 0.264			4.662	2.523	transcriptional regulator transcriptional regulator
str0931		0.510	0.499			4.193	3.259	transcriptional regulator, TetR family
str0950	fbp					0.493	0.410	fibronectin-binding protein-like protein A
str1173	birA						2.186	biotinprotein ligase
str1261	deaD					2.910	2.279	ATP-dependent RNA helicase
str1287	•	e				0.318		transcriptional regulator, putative
str1296	rncS	5.126 3.868	4.661					ribonuclease III tune II section medification sustem sectricition subunit
str1375 str1380	sthll	3.868 0.117	0.215		0.363	5.809	16.007	type II restriction-modification system restriction subunit
str1381		0.137	0.215		0.000	8.149	17.564	response regulator (homolog to RR08 Spn) uncoupled, truncated response regulator (homolog to RR08 Spn) uncoupled, truncated
str1403	galR	0.436	0.449			2.140	2.234	galactose operon repressor
str1420	rr08					0.491		response regulator (homolog to RR03 Spn)
str1425	pknB	2.344				0.477	0.407	protein kinase
str1488	rpoD		0.000			0.299	0.350	RNA polymerase sigma factor
str1568 str1586	rheA		2.286 8.458	5.665	0.367	0.446 9.972	0.275 27.158	ATP-dependent RNA helicase
str1586 str1600	copY -	0.059	8.458 0.052	0.000	0.307	3.312	21.108	negative transcriptional regulator - copper transport operon transcriptional regulator, MerR family
str1600	- rheB	0.009	0.002			2,799	2.783	ATP-dependent RNA helicase
str1733	scrK					3.499	3.700	fructokinase
str1736		2.283			0.369		2.074	sucrose regulon regulatory protein, truncated
str1737	-	2.025						sucrose regulon regulatory protein, truncated
str1867 str1868	rpoC		2.972			0.000		DNA-directed RNA polymerase beta' subunit
str1868 str1908	rpoB rpoA		4.270			0.386	0.247	DNA-directed RNA polymerase beta subunit
str1908 str1948	-	0.289	0.334			0.201	0.247	DNA-directed RNA polymerase alpha subunit hypothetical protein
str1946		0.289	0.368					transcriptional regulator, TetR/AcrR family
tr2025	spoJ	0.385	0.172					chromosome segregation protein
	n, ribosoma	al structure an	d biogenes	is	e (= :			
str_r03		0.441			0.451			
tr_r05 tr_r09		2.272			0.491			
tr_r09 tr_t01		2.086	2.214		0.491	0.164	0.368	
tr_t01 tr_t02		2.086	2.214 2.942		0.440	0.164 0.262	0.368	
		0.075	3.073	2.547	0.422	0.251	0.400	
str_t02			2.721	2.347	0.422	0.231		
tr_t03			4.430	3.142	0.316	0.181		
tr_t03 tr_t04					0.363	0.290		
tr_t03 tr_t04 tr_t05		5.799	4.349		0.450	0.389		
tr_t03 tr_t04 tr_t05 tr_t06 tr_t07		2.441	2.813		0.479	0.342		
str_t03 str_t04 str_t05 str_t06 str_t07 str_t08			5.603		0.321	0.346		
str_t03 str_t04 str_t05 str_t06 str_t06 str_t07 str_t08 str_t09		3.733			0.108	0.177		
str_t03 str_t04 str_t05 str_t06 str_t07 str_t08 str_t08 str_t09 str_t10			8.052	8.718	0.108	0.111		
str_t03 str_t04 str_t05 str_t06 str_t06 str_t07 str_t08 str_t09 str_t10 str_t10 str_t11		3.733 4.250	8.052 2.489	8.718	0.108			
str_t03 str_t04 str_t05 str_t06 str_t06 str_t07 str_t08 str_t09 str_t10 str_t10 str_t11 str_t13		4.250	2.489	8.718	0.108	0.386	0.400	
ttr_t03 ttr_t04 ttr_t05 ttr_t05 ttr_t06 ttr_t07 ttr_t08 ttr_t08 ttr_t09 ttr_t10 ttr_t11 ttr_t13 ttr_t13		4.250 3.593	2.489 3.108		0.108		0.428	
str_t03 str_t04 str_t05 str_t06 str_t06 str_t07 str_t08 str_t09 str_t09 str_t10 str_t10 str_t10 str_t11		4.250	2.489	8.718	0.108	0.386	0.428	

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str_t23		4.354	3.029			0.297	0.401	
str t27						0.472		
str t30					0.413	0.290		
str_t44		3.059			0.410	0.256	0.470	
str_t46		3.998	3.338			0.317	0.350	
						0.458	0.330	
str_t52		2.143	2.062					
str_t55		2.407				0.413		
str_t58		8.853	3.793					
str_t60							4.028	
str0007	-		0.441				3.078	conserved hypothetical protein, S4 domain protein
str0081	pnpA	2.891				0.414	0.336	polynucleotide phosphorylase, (PNPase)
str0084	cysS	2.964	2.415			0.486	0.330	cysteinyl-tRNA synthetase
str0122	truA	2.001	2.410		0.449	0.400	0.000	tRNA pseudouridine synthase A
str0122	prmA	2.012			0.449			ribosomal protein L11 methyltransferase
str0181	nifR	2.388				0.376	0.334	possible transcriptional regulator
str0211	-							ribosomal large subunit pseudouridine synthase, RluD subfamily
str0220	leuS	2.564				0.406	0.355	leucyl-tRNA synthetase
str0247	spoU					2.124	2.504	rRNA methyltransferase
str0262	rluB					3.658	3.257	ribosomal large subunit pseudouridine synthase B
str0267			2.344			0.135	0.121	rRNA methyltransferase, TrmH family
str0329	serS		2.419					servi-tRNA synthetase
str0343	-		2.410			0.430	0.494	hypothetical protein
str0345	rbfA	2.076	2.433			0.326	0.416	ribosome-binding factor A
str0370	IDIA	0.381	0.416			0.020	0.410	nicosome on tanga tactor A
	•							ribosomal subunit interface protein, ribosomal protein S30AE family
str0419	-	0.145	0.089		0.142	0.318		acetyltransferase, GNAT family, truncated
str0420	-	0.130	0.124		0.142	0.265		acetyltransferase, GNAT family, truncated
str0451	metG					0.436	0.377	methioninetRNA ligase
str0476	-	3.355	3.548					acetyltransferase, GNAT family
str0477	valS	4.339	4.178					valyl-tRNA synthetase
str0536	rpIJ	15.589	31.716	2.034		0.439	0.408	50Ś ribosomal protein L10
str0537	rplL	7.282	17.898	2,458			0.472	50S ribosomal protein L7/L12
str0572	thrS		3.543	2				threonyl-tRNA synthetase
str0592	rpsA		3.345			0.222	0.240	30S ribosomal protein S1
	ipsA	2.150				0.222	0.240	
str0653								tRNA methyltransferase, TrmA family
str0741	ileS	5.835	7.769		0.494	0.440		isoleucyl-tRNA synthetase
str0752	prfA					0.444	0.331	peptide chain release factor 1
str0753	hemK	3.406	2.810			0.441	0.281	protoporphyrinogen oxidase
str0754	-	3.017	2.856		2.036		0.304	hypothetical protein, Sua5/YciO/YrdC family protein
str0800						2,488	2.591	hypothetical protein
str0824			2.737	3.187				conserved hypothetical protein, translation initiation inhibitor protein
str0903	gid		2.101	0.485				glucose-inhibited division protein A
str1000	giù	3.276	3.846	0.405				rRNA methyltransferase, putative
	· .					0.407		
str1133	rpml	3.274	6.171			0.497	0.380	50S ribosomal protein L35
str1134	infC	3.565	8.713	2.444		0.447	0.365	translation initiation factor IF-3
str1146	prfB					0.449		peptide chain release factor 2
str1199	-				0.434	0.375		hypothetical protein
str1261	deaD					2.910	2.279	ATP-dependent RNA helicase
str1427	sunL	2.231						RNA-binding protein
str1456	-	6.029	9.337					ribosomal large subunit pseudouridine synthase, RluD subfamily
str1490	rpsU		3,489				0.484	30S ribosomal protein S21
str1559	1900		0.100				0.485	acetyltransferase, GNAT family
str1568	- rheA		2.286			0.446	0.485	ATP-dependent RNA helicase
			2.200					
str1574	prfC					0.236	0.195	peptide chain release factor 3
str1625	gatB	3.793	3.714					aspartyl/glutamyl-tRNA amidotransferase subunit B
str1627	gatC	2.580	2.288				0.462	aspartyl/glutamyl-tRNA amidotransferase subunit C
str1699	rheB					2.799	2.783	ATP-dependent RNA helicase
str1754	rpsF	5.748	11.649	2.027		0.396	0.278	30S ribosomal protein S6
str1790	rpsG	2.913	6.445			0.427	0.460	30S ribosomal protein S7
str1799	ksgA		0.469			2.220		dimethyladenosine transferase
str1806	tgt					0.196	0.235	queuine tRNA-ribosyltransferase
str1811	rnpA	5.903	5.051			0.289	0.226	ribonuclease P
str1814	gltX	3.281	3.236			0.200	0.448	glutamyl-tRNA synthetase
str1844	gin	5.201	0.293			0.473	0.448	cytidine/deoxycytidylate deaminase family protein, putative
str1870		7.394	5.926			0.473	0.399	tyrosyl-tRNA synthetase
str1907	tyrS	3.559	5.926			0.257	0.201	
	rplQ							50S ribosomal protein L17
str1909	rpsK	3.509	6.735			0.251	0.232	30S ribosomal protein S11
str1910	rpsM	3.323	5.709			0.261	0.250	30S ribosomal protein S13
str1911	rpmJ	4.027	5.309			0.333	0.265	50S ribosomal protein L36
str1912	infA	4.360	4.964			0.287	0.270	translation initiation factor IF-1
str1915	rplO	3.427	3.585			0.329	0.299	50S ribosomal protein L15
str1916	rpmD	3.227	5.594			0.418	0.378	50S ribosomal protein L30
str1917	rpsE	3.544	5.844			0.434	0.404	30S ribosomal protein S5
str1918	rpIR	4.123	7.612			0.436	0.349	50S ribosomal protein L18
str1919	rpIF	3.901	5.304			0.408	0.334	50S ribosomal protein L6
str1921	rpsN	4.034	4.218			0.364	0.292	30S ribosomal protein S14
str1921	rpsix	4.034	4.218			0.364	0.292	50S ribosomal protein L5
str1923	rpIX	3.702	5.194			0.393	0.342	50S ribosomal protein L24
str1925	rpsQ		4.542			0.384	0.332	30S ribosomal protein S17
str1927	rpIP	3.904	7.083			0.388	0.331	50S ribosomal protein L16
str1928	rpsC		6.751			0.385	0.319	30S ribosomal protein S3
str1930	rpsS	4.411	7.034			0.349	0.309	30S ribosomal protein S19
str1931	rplB	3.957	7.273			0.321	0.272	50S ribosomal protein L2
str1932	rplW	3.491	5.162			0.291	0.277	50S ribosomal protein L23
str1935	rpsJ		5.358			0.333	0.253	30S ribosomal protein S10
str1958	rpmB		0.000			0.333	0.255	50S ribosomal protein L28
str1969	aspS	2.227				0.468	0.429	aspartyl-tRNA synthetase
str1969	hisS	2.057				0.400	0.429	histidyl-tRNA synthetase
			=					
str1974	rpmF	4.122	7.130			0.490	0.417	50S ribosomal protein L32
str1975	rpmGB	4.469	7.761			0.434	0.354	50S ribosomal protein L33
	ipinioo					0.374	0.289	30S ribosomal protein S4
str1997	rpsD	2.668	5.930				0.203	
str1997 str2003	rpsD trmU	2.668				0.460	0.374	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
str1997	rpsD	2.668	5.930 0.309	0.470			0.374 0.219	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase tryptophanyl-tRNA synthetase
str1997 str2003	rpsD trmU	2.668		0.470		0.460	0.374	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase

Supplementary Table 4. Significant (FDR<0,05) differential expression of *L. bulgaricus* genes between parental mixed cultures and evolved mixed cultures, per functional category. Values represent ratios between the first and the second condition. Loci that showed a mutation in the comparative genome sequence analysis are in bold. P, parental culture; E_1 , evolved culture that is used in all analyses; E_2 , duplicate evolved culture.

	1ª e:	conential	phase	2 nd (exponential	phase	
Locus ID	E ₁ over	E ₂ over	E ₂ over	E ₁ over	E ₂ over	E ₂ over E1	Product
	P	Р	E1	Р	Р	E1	
Amino acid transpo	ort and metaboli	sm		=			
LBUL_0089 LBUL 0144			2.050	5.289 3.545		0.476 0.256	Homoserine trans-succinylase ABC-type polar amino acid transport system ATPase component
LBUL_0145				9.511		0.148	ABC-type polar amino acid transport system permease component
LBUL_0156		0.402					Phosphoribosylpyrophosphate synthetase
LBUL_0214	2.746	3.993		4.328		0.499	ABC-type amino acid transport system permease component
LBUL_0215 LBUL_0216				2.709	3,793	0.452	ABC-type amino acid transport system permease component
LBUL_0217	2,430	2.619		10.255	5.755	0.571	ABC-type polar amino acid transport system ATPase component ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0233	2.017	3.790		2.840		0.440	ABC-type oligopeptide transport system periplasmic component
LBUL_0236				5.774		0.308	ABC-type dipeptide/oligopeptide/nickel transport systems permease components
LBUL_0237 LBUL_0238	2.283			5.342 4.412		0.296 0.284	ABC-type dipeptide/oligopeptide/nickel transport systems permease components ABC-type dipeptide/oligopeptide/nickel transport system ATPase component
LBUL_0239	2.203			2.962		0.269	ABC-type oligopeptide/nicker transport system ATPase component
LBUL_0242						2.235	Aminopeptidase C
LBUL_0261 LBUL_0262		5.354	3.993			0.420	ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0262		5.354	3.993 4.330				ABC-type polar amino acid transport system ATPase component ABC-type amino acid transport system permease component
LBUL_0392		9.318	3.532				Aspartate/tyrosine/aromatic aminotransferase
LBUL_0431		6.584					Branched-chain amino acid permeases
LBUL_0452						2.369	Dipeptidase
LBUL_0458 LBUL_0459			2.931 2.764				ABC-type polar amino acid transport system ATPase component ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0462		2.856	2.704				ABC-type amino acid transport/signal transduction systems periplasmic component/domain
LBUL_0686	4.777	5.129					Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
LBUL_0737	0.098		5.181		0.393	0.293	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)
I BUL 0915	0.366	0.351					and their eukaryotic orthologs Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
LBUL_0931	0.335	0.551		2.196		0.319	Carbamoylphosphate synthase small subunit
LBUL_0932	0.363			2.327		0.259	Carbamov/phosphate synthase large subunit (split gene in MJ)
LBUL_0975				0.336	0.000		Carbamoylphosphate synthase small subunit
LBUL_1067 LBUL_1098		0.052			0.383		Phosphoglycerate dehydrogenase and related dehydrogenases ABC-type proline/glycine betaine transport systems ATPase components
LBUL_1098	2.311	0.002					Asparagine synthetase A
LBUL_1126	3.915						Di- and tripeptidases
LBUL_1180					2.189		Aspartate/tyrosine/aromatic aminotransferase
LBUL_1213 LBUL_1214				2.140		0.450	ABC-type polar amino acid transport system ATPase component ABC-type amino acid transport system permease component
LBUL_1219	2.143					0.450	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
LBUL_1231	3.430						5 10-methylenetetrahydrofolate reductase
LBUL_1232	2.168						Methionine synthase II (cobalamin-independent)
LBUL_1235 LBUL_1236	0.264 0.239	0.356		0.220 0.192	0.046	0.210 0.356	Cysteine synthase Cystathionine beta-lyases/cystathionine gamma-synthases
LBUL_1289	2.018	2.784		0.233	0.411	0.000	ABC-type dipeptide transport system periplasmic component
LBUL 1291	3.469	6.214		0.375	0.293		ABC-type dipentide/oligopeptide/nickel transport systems permease components
LBUL_1292	3.746 4.734	6.350	2.058	0.455	0.405		ABC-type oligopeptide transport system ATPase component
LBUL_1293 LBUL_1324	4.734	9.742	2.058		0.364 0.337		ABC-type dipeptide/oligopeptide/nickel transport system ATPase component Xaa-Pro aminopeptidase
LBUL_1353				6.616	2.465	0.373	Homoserine trans-succinylase
LBUL_1354				6.849		0.435	Cysteine synthase
LBUL_1368		0.373		0.364		2.597	Glutamine synthetase
LBUL_1474 LBUL_1575	0.065				2.003		Xaa-Pro aminopeptidase Xaa-Pro aminopeptidase
LBUL_1619	0.005	0.418					Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
LBUL_1622		0.148	0.132				Aspartate ammonia-lyase
LBUL_1646 LBUL_1691	3.652 5.731			2.930			Amino acid transporters Selenocysteine lyase
LBUL_1880	5.731			2.930		0.404	Oligoendopeptidase F
LBUL_2020				3.814		0.137	ABC-type polar amino acid transport system ATPase component
LBUL_2034	2.723		0.256				Thiamine pyrophosphate-requiring enzymes [acetolactate synthase pyruvate dehydrogenase (cytochrome)
							glyoxylate carboligase phosphonopyruvate decarboxylase]
Cell Division and C	Chromosome Pa	rtitioning					
LBUL_0590 LBUL_1900		0.450		10.982	10.262		Integral membrane protein possibly involved in chromosome condensation
LBUL_1900			0.105	2.685		0.40-	ATPases involved in chromosome partitioning
LBUL_2035 LBUL_0040	2.594	5.858	3.195	15.683	0.285	0.122	NAD/FAD-utilizing enzyme apparently involved in cell division Predicted nucleoside-diphosphate-sugar epimerases
LBUL_0108	2.084			3.929		0.349	Lipopolysaccharide biosynthesis proteins LPS:glycosyltransferases
LBUL_0140					2.550	3.483	Cell wall-associated hydrolases (invasion-associated proteins)
LBUL_0154	0.261	F				0.107	Glycosyltransferases involved in cell wall biogenesis
LBUL_0206 LBUL_0275	6.230 3.285	5.443				0.497	Phosphoglycerol transferase and related proteins alkaline phosphatase superfamily Large-conductance mechanosensitive channel
LBUL_0312	2.628	4.416					UDP-N-acetylmuramyl pentapeptide synthase
LBUL 0440	2.745	-	0.350				Glucosamine 6-phosphate synthetase contains amidotransferase and phosphosugar isomerase domains
LBUL_0498	2.682		0.400				UDP-glucose pyrophosphorylase
LBUL_0631 LBUL_0664	4.354 4.779	5.243					UDP-N-acetylmuramyl tripeptide synthase Cell shape-determining protein
LBUL_0671	3.101	0.243					Cell division protein Ftsl/penicillin-binding protein 2
LBUL_0672	5.761						UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase
LBUL_0673	2.264	0.000		0.010			UDP-N-acetylmuramoylalanine-D-glutamate ligase
LBUL_0929	0.206 16.556	0.296	0.226	2.249		0.243	Lipoprotein signal peptidase ABC-type transport system involved in lipoprotein release permease component
LBUL_0990 LBUL_1097	11.222		0.220				Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding
							protein)
LBUL_1356				2.215			Cyclopropane fatty acid synthase and related methyltransferases
LBUL_1600 LBUL_1664					2.111	2.181	Lipopolysaccharide biosynthesis proteins LPS:glycosyltransferases UDP-glucose 4-epimerase
LBUL_1707	2.226				2.111		Phosphoglycerol transferase and related proteins alkaline phosphatase superfamily
LBUL_1800	9.029	7.276				0.390	Cytidylyltransferase
LBUL_1801	5.476	3.678			0.329	0.320	LPS biosynthesis protein
LBUL_1807	3.792 2.562	4.022			0.383	0.347	Glycosyltransferase
LBUL_1810 LBUL_1843	2.562			2.071		0.379	UDP-galactopyranose mutase Glycosyltransferases probably involved in cell wall biogenesis
LBUL_1848	12.701		0.265	5.012		0.379	Glycosyltransferases involved in cell wall biogenesis
LBUL_1866	2.766	4.042					Cell wall-associated hydrolases (invasion-associated proteins)
LBUL_1982				2.078		0.454	Protein involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid (D-alanine transfer protein)
Cell Motility and Se	ecretion						
BUIL 0515	0 442						Negative regulator of genetic competence sporulation and motility

Cell Motility and Secretion LBUL_0515 0.443

Negative regulator of genetic competence sporulation and motility

LBUL_0611		0.357			0.288		Type II secretory pathway component PuIF
Coenzyme metabolisr	n						
LBUL_0084	0.364	0.472			2.027		Lactate dehydrogenase and related dehydrogenases
LBUL_0208 LBUL_0209	2.797 5.203	2.985		2.489			Dihydroneopterin aldolase GTP cyclohydrolase I
LBUL_0210	5.445	2.572	0.472	2.045			Folylpolyglutamate synthase
LBUL_0211	3.694						Dihydropteroate synthase and related enzymes
LBUL_0276 LBUL 0405	0.444	0.480		3.645		0.298	Nicotinic acid phosphoribosyltransferase NAD synthase
LBUL_0829	0.444	0.400			2.410	4.522	Biotin-(acetyl-CoA carboxylase) ligase
LBUL_0917					2.596		Lactate dehydrogenase and related dehydrogenases
LBUL_1219	2.143			0.407			Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
LBUL_1455 LBUL_1532		2.839 0.029	2.577	2.497		0.294	S-adenosylmethionine synthetase 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
LBUL_1868		3.694	3.213	3.660		0.269	Lactate dehydrogenase and related dehydrogenases
LBUL_2034	2.723		0.256				Thiamine pyrophosphate-requiring enzymes [acetolactate synthase pyruvate dehydrogenase (cytochrome)
							glyoxylate carboligase phosphonopyruvate decarboxylase]
Defense mechanisms							
LBUL_0255 LBUL_0256	7.110	3.473 6.384					Lantibiotic modifying enzyme ABC-type multidrug transport system ATPase and permease components
LBUL_0624	7.110	0.304		4,795	3.935		Glycopeptide antibiotics resistance protein
LBUL_0978	4.043	4.967					Na+-driven multidrug efflux pump
LBUL_0989	7.506 51.057		0.219 0.081	5.936		0.063	ABC-type antimicrobial peptide transport system ATPase component ABC-type multidrug transport system ATPase and permease components
LBUL_1203 LBUL_1204	31.854	2.670	0.081	6.781		0.063	ABC-type multidrug transport system ATPase and permease components
LBUL_1300	7.319	7.140					ABC-type multidrug transport system ATPase and permease components
LBUL_1524	2.415		0.351			2.297	Beta-lactamase class C and other penicillin binding proteins
LBUL_1562 LBUL_1700			2.007				ABC-type multidrug transport system ATPase component ABC-type antimicrobial peptide transport system ATPase component
LBUL_1701				2.056	2.047		ABC-type antimicrobial peptide transport system permease component
DNA Replication Rea	ombination a	nd Penair					
DNA Replication, Rec LBUL_0001	ornomation a	nu repair		2.794		0.392	ATPase involved in DNA replication initiation
LBUL_0002				2.593		0.407	DNA polymerase sliding clamp subunit (PCNA homolog)
LBUL_0008	3.711	6.394		3 814		0.209	Single-stranded DNA-binding protein
LBUL_0075 LBUL_0212	5,489		0.461	3.814		0.209	Exonuclease III NTP pyrophosphohydrolases including oxidative damage repair enzymes
LBUL_0290		5.730					Serine/threonine protein kinase
LBUL_0313	5.686	4.458					Superfamily II DNA and RNA helicases
LBUL_0414 LBUL 0662	4.726 2.998	3.387					NAD-dependent DNA ligase (contains BRCT domain type II) DNA repair proteins
LBUL_0683	2.008	0.007					NTP pyrophosphohydrolases including oxidative damage repair enzymes
LBUL_0702	0.037	0.074			0.282		DNA uptake protein and related DNA-binding proteins
LBUL_0912 LBUL_0913	0.327 0.491	0.371 0.189					Putative primosome component and related proteins Predicted EndoIII-related endonuclease
LBUL_1132	3.674	0.103					Methylated DNA-protein cysteine methyltransferase
LBUL_1160		4.700					Transposase and inactivated derivatives
LBUL_1190 LBUL_1296	4.423	0.127					Topoisomerase IA RecG-like helicase
LBUL_1362		11.096			7.420		Transposase and inactivated derivatives
LBUL_1489						2.613	Nucleotidyltransferase/DNA polymerase involved in DNA repair
LBUL_1566 LBUL_1653	33.725	13.943		0.109			NTP pyrophosphohydrolases including oxidative damage repair enzymes Transposase and inactivated derivatives IS30 family
LBUL_1773	33.725	13.943		2.810			Transposase and inactivated derivatives IS30 family Transposase and inactivated derivatives IS30 family
LBUL_1842	3.264			3.094		0.349	Transposase and inactivated derivatives
	d conversion						
Energy production an LBUL_0084	0.364	0.472			2.027		Lactate dehydrogenase and related dehydrogenases
LBUL_0084 LBUL_0100	0.364 0.299	0.472 0.436					Lactate dehydrogenase and related dehydrogenases Malate/lactate dehydrogenases
LBUL_0084 LBUL_0100 LBUL_0618	0.364 0.299				2.027 3.071		Malate/lactate dehydrogenases Acetate kinase
LBUL_0084 LBUL_0100	0.364						Malate/lactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit)
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0692	0.364 0.299 2.075	0.436			3.071		Matatofactate dehydrogenases Acetate kinas F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Pyrtvate2-oxoglutarate dehydrogenase complex dihydrolipoarnide dehydrogenase (E3) component and related erzymes
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0692 LBUL_0716	0.364 0.299 2.075	0.436		5.560			Matate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privruste/2-xocugultarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitroreductase
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0692 LBUL_0716 LBUL_0726 LBUL_0917	0.364 0.299 2.075	0.436		5.560	3.071		Matate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Prvruste/2-xocugularate dehydrogenase compex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0692 LBUL_0716 LBUL_0726 LBUL_0917	0.364 0.299 2.075	0.436	0.178	5.560	3.071		Malate/lactate dehydrogenases Acetate kinas POFI-hype ATP synthase epsilon subunit (mitochondrial delta subunit) Pivruate/2-xocugultarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzyms Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases NAD-dependent aldehyd dehydrogenases
LBUL_0084 LBUL_0618 LBUL_0618 LBUL_0644 LBUL_0692 LBUL_0716 LBUL_0726 LBUL_0726 LBUL_0917 LBUL_1096 LBUL_1532	0.364 0.299 2.075 0.260	0.436 0.468 0.314 0.029	0.178		3.071	0 160	Matate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Prvruste/2-xosugularate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenasea/fumarate reductase flavoprotein subunit Lactate dehydrogenasea/fumarate reductase flavoprotein subunit Lactate dehydrogenasea/fumarate and related flavodoxin oxidoreductases NAD-dependent aldehydrogenasea
LBUL_0084 LBUL_0618 LBUL_0618 LBUL_0618 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0726 LBUL_0727 LBUL_0917 LBUL_1096 LBUL_1532 LBUL_1680	0.364 0.299 2.075 0.260	0.436	0.178	5.560 3.717 3.660	3.071	0.160 0.269	Matate/actate dehydrogenases Acetate kinas FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xosuglutarate dehydrogenase cimpex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenythpen oh ydroxylase and related flavodoxin oxidoreductases NaA-H+ antiporter Lactate dehydrogenases of related dehydrogenases
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0726 LBUL_0917 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1680 LBUL_1680 LBUL_1873	0.364 0.299 2.075 0.260 10.441 4.102	0.436 0.468 0.314 0.029 8.558 3.694		3.717 3.660	3.071	0.269	Malate/lactate dehydrogenases Acetate kinas PGPI-type ATP synthase epsilon subunit (mitochondrial delta subunit) PGPI-type ATP synthase epsilon subunit (mitochondrial delta subunit) Pivrate/2-xosultarate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit ADA-dependent dehydr dehydrogenases 2-polyprenytphenol hydroychogenases 2-polyprenytphenol hydroychase and related flavodoxin oxidoreductases Na+H+ antipoter Lactate dehydrogenase and related dehydrogenases Heme/cogner-type cychotromer/quinol oxidase subunit 1
LBUL_0084 LBUL_0618 LBUL_0618 LBUL_0618 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0726 LBUL_0727 LBUL_0917 LBUL_1096 LBUL_1532 LBUL_1680	0.364 0.299 2.075 0.260	0.436 0.468 0.314 0.029 8.558		3.717	3.071		Matate/actate dehydrogenases Acetate kinas FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xosuglutarate dehydrogenase cimpex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenythpen oh ydroxylase and related flavodoxin oxidoreductases NaA-H+ antiporter Lactate dehydrogenases of related dehydrogenases
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0684 LBUL_0682 LBUL_0716 LBUL_0717 LBUL_0917 LBUL_0917 LBUL_0917 LBUL_1682 LBUL_1682 LBUL_1823 LBUL_1823 LBUL_1823 LBUL_1820 Function unknown	0.364 0.299 2.075 0.260 10.441 4.102	0.436 0.468 0.314 0.029 8.558 3.694 0.364	3.213	3.717 3.660 4.485	3.071	0.269 0.148	Malatel/actate dehydrogenases Acetate kinas FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVT-type ATP synthase epsilon subunit dehydrogenase (E3) component and related Nitroreductase Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit NB-Dd-genedrati aldehyd dehydrogenases 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases Navi+tr antiporter Lactate dehydrogenase and related dehydrogenases Hemelcoper-type cytochromelquinol oxidases subunit 1 Fumarase
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0716 LBUL_0726 LBUL_0726 LBUL_0726 LBUL_1917 LBUL_1996 LBUL_1532 LBUL_1800 LBUL_1803 LBUL_1873 LBUL_1873 LBUL_1830 Function unknown LBUL_0663	0.364 0.299 2.075 0.260 10.441 4.102	0.436 0.468 0.314 0.029 8.558 3.694		3.717 3.660 4.485 6.389	3.071 10.851 2.596	0.269	Malate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xocyultarate dehydrogenase furmarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases NAD-dependent addehydo dehydrogenases Addependent addehydo dehydrogenases Addependent addehydrogenase and related thevdrogenases Addependent addehydrogenase and related dehydrogenases Hander dehydrogenase and related dehydrogenases Hanner copper-type cytochrome/quinol oxidases subunit 1 Furmarase
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_0717 LBUL_1096 LBUL_1532 LBUL_1686 LBUL_1686 LBUL_1680 LBUL_1693 LBUL_1693 LBUL_0063 LBUL_0082	0.364 0.299 2.075 0.260 10.441 4.102 0.316	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896	3.213	3.717 3.660 4.485	3.071	0.269 0.148	Malate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xosugularate dehydrogenase compex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenase and related dehydrogenases NAD-dependent addehydro dehydrogenases 2-polymenythynon hydroxytase and related dehydrogenases Lactate dehydrogenase and related dehydrogenases Haneicopper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Prediced membrane protein
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0682 LBUL_0726 LBUL_0726 LBUL_0727 LBUL_1080 LBUL_1080 LBUL_1080 LBUL_1888 LBUL_1873 LBUL_1873 LBUL_1873 LBUL_1873 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081	0.364 0.299 2.075 0.260 10.441 4.102 0.316	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961	3.071 10.851 2.596	0.269 0.148 0.300	Malate/lactate dehydrogenases Acetate kinase POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xosujutarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzymes Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumorates ADD-dependert aldehyd dehydrogenases 2-polyprenrylphenol hydroyenase and related flavodoxin oxidoreductases Na-H+ antijorter Lactate dehydrogenase and related dehydrogenases Heme/cogner-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized conserved protein
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0684 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_0917 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1686 LBUL_1873 LBUL_1868 LBUL_1873 LBUL_1806 LBUL_0063 LBUL_0082 LBUL_0082 LBUL_0205	0.364 0.299 2.075 0.260 10.441 4.102 0.316	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265	3.213 2.088	3.717 3.660 4.485 6.389 5.404	3.071 10.851 2.596	0.269 0.148	Malate/actate dehydrogenases Acetate kinase FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FOF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Privrate/2-xosugularate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzymes Nitoreductase Succinate dehydrogenase and related dehydrogenases NAD-dependent addehydro dehydrogenases AD-dependent addehydro dehydrogenases Succinate dehydrogenase and related dehydrogenases Located dehydropen hydroxylases and related dehydrogenases Hamit copper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized conserved in bacteria Predicated membrane protein Uncharacterized conserved protein
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0684 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_1076 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1688 LBUL_1873 LBUL_1808 LBUL_1830 Function unknown Function unknown LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0205 LBUL_0205 LBUL_0205	0.364 0.299 2.075 0.260 10.441 4.102 0.316	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961	3.071 10.851 2.596	0.269 0.148 0.300	Malate/lactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (Lactate dehydrogenase (E3) component and related enzymes Nutoreductase Succinate dehydrogenase and related dehydrogenases NAD-dependent addehydrogenases and related dehydrogenases Lactate dehydrogenase and related dehydrogenases Lactate dehydrogenase and related dehydrogenases Lactate dehydrogenase and related dehydrogenases Heme/copense-type cytochrome/quinol oxdases subunit 1 Fumarase Uncharacterized conserved in bacteria Predicied membrane protein Uncharacterized conserved protein Predicied oregin protein Uncharacterized protein comered in bacteria
LBUL_0084 LBUL_0100 LBUL_0613 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_0717 LBUL_1752 LBUL_1522 LBUL_1523 LBUL_1620 LBUL_1620 LBUL_1620 LBUL_0613 LBUL_0613 LBUL_0612 LBUL_0612 LBUL_0612 LBUL_0620 LBUL_0620	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961	3.071 10.851 2.596	0.269 0.148 0.300 0.364	Malateliactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase and related dehydrogenase (E3) component and related enzymes Nitroreductase Autochondrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit AD-dependent aldehyde dehydrogenases 2-polyprenytphenol hydroychoses and related flavodoxin oxidoreductases Na-Hr+ antipoter Lactate dehydrogenase and related flavodoxin oxidoreductases Na-Hr+ antipoter Lactate dehydrogenase and related dehydrogenases Heme/cogen-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0684 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_1076 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1688 LBUL_1873 LBUL_1808 LBUL_1830 Function unknown Function unknown LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0205 LBUL_0205 LBUL_0205	0.364 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596	0.269 0.148 0.300 0.364	Malatelisatate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitochondrial delta subunit) Evaluation dehydrogenasefumarate reductase flavoprotein subunit Lactate dehydrogenasefumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AND-dependent aldehydd dehydrogenases AwH+ antipoter Lactate dehydrogenase and related dehydrogenases Herneicogen-type cytochromelculuol oxdases subunit 1 Fumarase Uncharacterized conserved in bacteria Predicated membrane protein Uncharacterized conserved protein Dincharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0613 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0017 LBUL_0017 LBUL_1090 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1688 LBUL_1873 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961	3.071 10.851 2.596	0.269 0.148 0.300 0.364	Malatelisciate dehydrogenases Acetate kinase POF-1ype ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-1ype ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-1ype ATP synthase epsilon subunit (mitochondrial delta subunit) Evilope and the synthysis experiment of the subunit subunit Lactate dehydrogenase furmarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AND-dependent aldehyde dehydrogenases AvH-4 antipoter Lactate dehydrogenase and related dehydrogenases Herneicoper-type cytochromerkjunit oxidates subunit 1 Furmarase Uncharacterized protein conserved in bacteria Predicate onserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0612 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0917 LBUL_1096 LBUL_1532 LBUL_1680 LBUL_1680 LBUL_1680 LBUL_1680 LBUL_0801 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0091 LBUL_0519 LBUL_0519 LBUL_0519 LBUL_0519	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596	0.269 0.148 0.300 0.364	Malate/lactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Succinate dehydrogenase/fumarate reductase flavoprotein subunit Succinate dehydrogenases/fumarate reductase flavoprotein subunit ADA-dependent aldehyd dehydrogenases 2-polyprenytphenol hydrogenases AAH-4 antioproter Lactate dehydrogenase and related flavoprotein oxidoreductases Na+H+ antioproter Lactate dehydrogenase and related flavoprotein subunit Fum-cognet-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Prediced membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Prediced membrane protein Uncharacterized protein conserved in bacteria Prediced membrane protein
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_0017 LBUL_0017 LBUL_1090 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1688 LBUL_1873 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0073 LBUL_0201 LBUL_0	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596	0.269 0.148 0.300 0.364	Malatelizatate dehydrogenases Acetate kinase POFI-type ATP synthase epsilon subunit (mitochondrial delta subunit) POFI-type ATP synthase epsilon subunit (mitochondrial delta subunit) Pyrvatel2-oxegultarate dehydrogenase complex dihydrolipoamide dehydrogenase (E3) component and related enzymes Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenrylphenol hydroyales and related flavodoxin oxidoreductases NaH/H antipoter Lactate dehydrogenase and related dehydrogenases Heme/coper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Predicted membrane protein Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0100 LBUL_0100 LBUL_0642 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1096 LBUL_11530 LBUL_11530 LBUL_11530 LBUL_11530 LBUL_11530 LBUL_01031 LBUL_0031 LBUL_0031 LBUL_0032 LBUL_0032 LBUL_0032 LBUL_0032 LBUL_0032 LBUL_0032 LBUL_0032 LBUL_0031 LBUL_0032 LBUL_003 LBU	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499 34.489	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596	0.269 0.148 0.300 0.364 0.366	Malatelactate dehydrogenases Acetate kinase FOFI-type ATP synthase epsilon subunit (michondrial delta subunit) FOFI-type ATP synthase epsilon subunit (michondrial delta subunit) FOFI-type ATP synthase epsilon subunit (michondrial delta subunit) Euclated dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydroyenases and related flavodoxin oxidoreductases Na-HH- antipoter Lactate dehydrogenase and related flavodoxin oxidoreductases Na-HH- antipoter Lactate dehydrogenase and related flavodoxin oxidoreductases Na-HH- antipoter Lactate dehydrogenase and related flavoprogenases Henne/copper-type cytochrome(quinol oxidases subunit 1 Fumarase Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Hendrogene di bacteria Uncharacterized protein conserved in bacteria Hendrogene di bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0682 LBUL_0684 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_0176 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1868 LBUL_1873 LBUL_1868 LBUL_1873 LBUL_0816 LBUL_0816 LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_00781 LBUL_00781 LBUL_00781 LBUL_00781 LBUL_00781 LBUL_00782 LBUL_00781 LBUL_00782 LBU_00782 LBU_00772	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596 2.738	0.269 0.148 0.300 0.364 0.366	Malatelisatai dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (michondrial delta subunit) FVF1-type ATP synthase epsilon subunit (michondrial delta subunit) FVF1-type ATP synthase epsilon subunit (michondrial delta subunit) Succinate dehydrogenase/immarate reductase flavoprotein subunit Lactate dehydrogenase/immarate reductase flavoprotein subunit Lactate dehydrogenase/immarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AM-Hr antjoprent Lactate dehydrogenase and related dehydrogenases Hemelcoper-type cytochromelquinol oxdases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Predicted membrane protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Predicted membrane protein Uncharacterized protein conserved in bacteria Herdicated methrane protein Uncharacterized protein conserved in bacteria Predicted methrane protein Uncharacterized protein conserved in bacteria Predicted methrane protein Uncharacterized protein conserved in bacteria Predicted methrane protein Uncharacterized protein conserved in bacteria Herdicated methrane protein Uncharacterized conserved protein conserved in bacteria Herdicated methrane protein Uncharacterized conserved protein conserved in bacteria Herdicated conserved protein conserved in bacteria Herdicated conserved protein conserved in bacteria Herdicated conserved protein conserved in bacteria Herdicated conserved protein conserved in bacteria Uncharacterized conserved protein conserved in bacteria Uncharacterized conserved protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1753 LBUL_1532 LBUL_1532 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0750 LBUL_0750 LBUL_0750 LBUL_0750 LBUL_0750 LBUL_0750	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.053 2.763 4.499 34.489	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596 2.738	0.269 0.148 0.300 0.364 0.366	Malatelizatate dehydrogenases Acetate kinase FOFI-type ATP synthase epsilon subunit (michondriai delta subunit) FOFI-type ATP synthase epsilon subunit (michondriai delta subunit) Normadic aceguitarate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ anitopter Lactate dehydrogenase and related flavodoxin oxidoreductases Henne/coper-type cychothrome/quinol oxidases subunit 1 Fumarase Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicted membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conser
LBUL_0084 LBUL_0100 LBUL_0613 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1680 LBUL_1680 Function unknown LBUL_0063 LBUL_0081 LBUL_0084 LBUL_0084 LBUL_0084 LBUL_0096 LBUL_0096 LBUL_1138	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499 34.489	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596 2.738	0.269 0.148 0.300 0.364 0.366 2.612 0.170	Malatolactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenytphenol-hydroydnese and related flavodoxin oxidoreductases Na-H+ anitoret Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ anitoret Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ anitoret Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ anitoret Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ anitoret Lactate dehydrogenase Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0682 LBUL_0684 LBUL_0684 LBUL_0716 LBUL_0716 LBUL_0175 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1868 LBUL_1873 LBUL_0819 LBUL_0805 LBUL_0805 LBUL_0081 LBUL_0082 LBUL_0083 LBUL_0083 LBUL_0084 LBUL_0	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.053 2.763 4.499 34.489	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612	Malatelactate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitochondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitochondrial delta subunit) Evaluation (mitochondrial delta subunit) ADD-dependent aldehyd dehydrogenases 2-polyprenylphenol hydrogenases and related dehydrogenases ADD-dependent aldehyd dehydrogenases ANH-4 antiopreri Lactate dehydrogenase and related dehydrogenases AwH+4 antiopreri Lactate dehydrogenase and related dehydrogenases Predicate dehydrogenase and related dehydrogenases Hemelooper-type cytochonomelquinol oxdases subunit 1 Fumarse Uncharacterized conserved in bacteria Predicate domesi conserved in bacteria Predicate domesi nonserved in bacteria Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicate domesi no conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Predicate domesi no conserved in bacteria Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria
LBUL_0084 LBUL_0100 LBUL_0614 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1753 LBUL_1532 LBUL_1532 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_0817 LBUL_0081 LBUL_0081 LBUL_0082	0.384 0.299 2.075 0.260 10.441 4.102 0.316 0.423 4.296 2.053 2.763 4.499 34.489	0.436 0.468 0.314 0.029 8.558 3.694 0.364 2.896 0.411 5.265 0.142 2.326 0.315	3.213 2.088	3.717 3.660 4.485 6.389 5.404 2.961 2.710	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612 0.170	Malatelactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Nitroreductase Subunit dehydrogenase fumarate reductase flavoprotein subunit AD-dependent aldehyd dehydrogenases 2-polyprenytphenol hydrogenase and related flavodoxin oxidoreductases Na-H+ antipoter Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ antipoter Lactate dehydrogenase and related flavodoxin oxidoreductases Na-H+ antipoter Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Uncharacterized
LBUL_0084 LBUL_0100 LBUL_0614 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1753 LBUL_1532 LBUL_1532 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_0817 LBUL_0081 LBUL_0081 LBUL_0082	0.384 0.299 2.075 0.280 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 4.499 34.489 0.473 5.139	0.436 0.436 0.314 0.029 8.558 3.694 0.364 2.896 0.364 2.896 0.315 0.266 0.315	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612 0.170 2.216	Malatelactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Sactate dahydrogenase.fumarate reductase flavoprotein subunit AnD-dependent aldehyd dehydrogenases 2-polyprenylphenol hydrogenase and related flavodoxin oxidoreductases Na-Hr4 antipoter Lactate dehydrogenase Heme/cogen-type cytochrome/quinol oxidases subunit 1 Furmarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in b
LBUL_0084 LBUL_0100 LBUL_0100 LBUL_0613 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0726 LBUL_1753 LBUL_11532 LBUL_11532 LBUL_11533 LBUL_11633 LBUL_11633 LBUL_11673 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_1127 LBUL_1127 LBUL_1127 LBUL_1245 LBUL_1264	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612 0.170 2.216	Malatolaciate dehydrogenases POF1-type ATP synthase epsilon subunit (michondrial delta subunit) POF1-type ATP synthase epsilon subunit (michondrial delta subunit) POF1-type ATP synthase epsilon subunit (michondrial delta subunit) Excetate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AN-H- antipoter Lacate dehydrogenase and related flavodoxin oxidoreductases Na-H+ antipoter Lacate dehydrogenase and related dehydrogenases Henne/coper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Hended membrane protein Uncharacterized protein conserved in bacteria Hended membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Hended membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein cons
LBUL_0084 LBUL_0100 LBUL_0614 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1753 LBUL_1532 LBUL_1532 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_1683 LBUL_0817 LBUL_0081 LBUL_0081 LBUL_0082	0.384 0.299 2.075 0.280 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 4.499 34.489 0.473 5.139	0.436 0.436 0.314 0.029 8.558 3.694 0.364 2.896 0.364 2.896 0.315 0.266 0.315	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612 0.170 2.216 0.305	Malatelactate dehydrogenases Acetate kinase F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Sactate dahydrogenase.fumarate reductase flavoprotein subunit AnD-dependent aldehyd dehydrogenases 2-polyprenylphenol hydrogenase and related flavodoxin oxidoreductases Na-Hr4 antipoter Lactate dehydrogenase Heme/cogen-type cytochrome/quinol oxidases subunit 1 Furmarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Predicad membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in b
LBUL_0084 LBUL_0100 LBUL_0418 LBUL_0418 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0417 LBUL_1453 LBUL_1453 LBUL_1453 LBUL_1453 LBUL_1453 LBUL_0411 LBUL_0414 LBUL_144 LBUL_1	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938	0.269 0.148 0.300 0.364 0.366 2.612 0.170 2.216 0.305 2.368 3.464	Malatelactate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitchondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitchondrial delta subunit) PVI-type ATP synthase epsilon subunit (mitchondrial delta subunit) Executed dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AND-dependent aldehyd dehydrogenases ANH-4 antionptorer Lactate dehydrogenase and related dehydrogenases AnH-4 antioptorer Lactate dehydrogenase and related dehydrogenases Periodicate dehydrogenases Immeloogen-type cytochonomelquinol oxdases subunit Concarcetorized dehydrogenases Immeloogen-type cytochonomelquinol oxdases subunit Uncharacterized conserved in bacteria Predicate membrane protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bac
LBUL_0084 LBUL_0100 LBUL_0613 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1533 Function unknown LBUL_0063 LBUL_0081 LBUL_1176 LBUL_1176 LBUL_1176 LBUL_1243 LBUL_1442 LBUL_1442 LBUL_1442 LBUL_1442 LBUL_1442 LBUL_1442 LBUL_1442 LBUL_1440	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.170 2.216 0.305 2.368 3.464 2.450	Malatolaciate dehydrogenases POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Provinate/2-xougultarate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase/fumarate reductase flavoprotein subunit Lacate dehydrogenase and related flavodoxin oxidoreductases NaH-H antipoter Lacate dehydrogenase and related flavodoxin oxidoreductases Park-H antipoter Uncharacterized conserved in bacteria Predicide membrane protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacte
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1833 Function unknown LBUL_0081 LBUL_0137 LBUL_0137 LBUL_0205 LBUL_1205 LBUL_1205 LBUL_1225 LBUL_1426 LBUL_1426 LBUL_1426 LBUL_1428	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244	3.717 3.660 4.485 6.389 5.404 2.961 2.710 0.437	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.170 0.2216 0.305 2.2612 2.368 3.464 2.256	Malatelactate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitchondrial delta subunit) PVT-type ATP synthase epsilon subunit (mitchondrial delta subunit) PVT-type ATP synthase epsilon subunit (mitchondrial delta subunit) Executed dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AND-dependent aldehyd dehydrogenases AND-dependent aldehyd dehydrogenases ANH-4 antiopter Lactate dehydrogenase and related dehydrogenases Herneicoper-type cytochromeriquino xdases subunit Contracterized protein conserved in bacteria Predicate membrane protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in ba
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_175 LBUL_1753 LBUL_1823 LBUL_1823 LBUL_1873 LBUL_1873 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0084 LBUL_1124 LBUL_1245 LBUL_1264 LBUL_1264 LBUL_1264 LBUL_1463 LBUL_1655 LBUL_1555 LBUL_1555 LBUL_1555 LBUL_1555 LBUL_15	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244	3,717 3,660 4,485 6,389 5,604 2,961 2,710 0,437 3,027 2,842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.370 2.216 0.305 2.368 3.464 2.350 2.374 2.274	Malatolaciate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Euclate dehydrogenase/fumarate reductase flavoprotein subunit Lacitate dehydrogenase/fumarate reductase flavoprotein subunit Lacitate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydroyales and related flavodoxin oxidoreductases NaH/+ antipoter Lacitate dehydrogenase and related dehydrogenases Hemelcoper-type cytochromeriquinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserve
LBUL_0084 LBUL_0100 LBUL_0618 LBUL_0614 LBUL_0614 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1686 LBUL_1686 LBUL_1686 LBUL_1686 LBUL_1686 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_0082 LBUL_0082 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0638 LBUL_0772 LBUL_0583 LBUL_0772 LBUL_0583 LBUL_0772 LBUL_0583 LBUL_0772 LBUL_0583 LBUL_1776 LBUL_0894 LBUL_1776 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1786 LBUL_1283 LBUL_1786 LBUL_1283 LBUL_178 LBUL_1283 LBUL_178 LBUL_1283 LBUL_1284 LBUL_1284 LBUL_1284 LBUL_1284 LBUL_1284 LBUL_1284 LBUL_1485 LBUL_1599 LBUL_1485 LBUL_1485 LBUL_1485 LBUL_1599 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1599 LBUL_1599 LBUL_1485 LBUL_1485 LBUL_1599 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1799 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1799 LBUL_1799 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1799 LBUL_1799 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1599 LBUL_1799 LBUL_159 LBUL_1599 LBUL_159 LBUL_159 LBUL_159 LBUL_159 LBUL_159 LBUL	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244 2.882	3.717 3.660 4.485 6.389 5.404 2.710 0.437 3.027 2.842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.366 2.216 0.305 2.368 2.350 2.170 2.230 0.2174 0.305	Malatolactate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitchondrial delta subunit) FVF1-type ATP synthase epsilon subunit (mitchondrial delta subunit) FVF1-type ATP synthase epsilon subunit (mitchondrial delta subunit) Evaluation (market experiment) Succinate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases and related dehydrogenases AN-H- anjorden Idehydd edhydrogenases An-H- anjorder Lacate dehydrogenase and related dehydrogenases An-H- anjorder Homelcopen-type cytochromelquinol oxdases subunit Funares Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Homelcopen-type cytochromelquinol oxdases Homelcopen-type cytochromelquinol (Homelcopen-type) Homelcopen-type cytochromelquinol Homelcopen-type) Homelcopen-type cytochromelquinol Homelcopen-type cytochromelcopen-type Homel
LBUL_0084 LBUL_0618 LBUL_0619 LBUL_0619 LBUL_0614 LBUL_0644 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1752 LBUL_1532 LBUL_1532 BUL_1532 BUL_1532 BUL_1533 BUL_1533 LBUL_0737 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0270 LBUL_0307 LBUL_0307 LBUL_0307 LBUL_0307 LBUL_0307 LBUL_0307 LBUL_0519 LBUL_1127 LBUL_0521 LBUL_0521 LBUL_0521 LBUL_0521 LBUL_0521 LBUL_1128 LBUL_1264 LBUL_1264 LBUL_1264 LBUL_1264 LBUL_1465 LBUL_1465 LBUL_1465 LBUL_1465 LBUL_1476 LBUL_1465 LBUL_1476 LBUL_1465 LBUL_1476 LBUL_1476 LBUL_1476 LBUL_1465 LBUL_1465 LBUL_1465 LBUL_1465 LBUL_1476 LBUL_1476 LBUL_1465 LBUL_1476 LBUL_1786 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876 LBUL_1876	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 4.296 2.035 2.763 34.489 34.489 0.473 5.139 0.400 0.317	0.436 0.468 0.314 0.029 8.558 8.558 0.369 0.364 0.364 0.364 0.366 0.222	3.213 2.088 2.244 2.882	3,717 3,660 4,485 6,389 5,604 2,961 2,710 0,437 3,027 2,842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.370 2.216 0.305 2.368 3.464 2.350 2.374 2.274	Malatolaciate dehydrogenases Acetate kinase FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Euclate dehydrogenase/fumarate reductase flavoprotein subunit Lacitate dehydrogenase/fumarate reductase flavoprotein subunit Lacitate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases NaH/+ antipoter Lacitate dehydrogenase and related dehydrogenases Hemelcoper-type cytochromeriquinol oxidases subunit 1 Furarase Uncharacterized protein conserved in bacteria Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserv
LBUL_0084 LBUL_0010 LBUL_0613 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1697 LBUL_1697 LBUL_1697 LBUL_1697 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0396 LBUL_0494 LBUL_1476 LBUL_1428 LBUL_1	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 34.296 2.035 2.763 34.489 0.473 5.139 0.400 0.317 0.339	0.436 0.468 0.314 0.2314 0.2314 0.364 0.364 0.364 0.364 0.315 10.483 0.266 3.680 0.222 0.248	3.213 2.088 2.244 2.882	3.717 3.660 4.485 6.389 5.404 2.710 0.437 3.027 2.842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.366 2.216 0.305 2.368 2.350 2.170 2.230 0.2174 0.305	Malatolaciate dehydrogenases POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Provinate/2-oxoguitarate dehydrogenase (mitochondrial delta subunit) Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AnH-4 antipoter Lacate dehydrogenase and related dehydrogenases Henne/coper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria U
LBUL_0084 LBUL_0140 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0414 LBUL_0417 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1532 LBUL_1533 LBUL_1533 LBUL_0414 LBUL_04133 LBUL_0414 LBUL_04133 LBUL_0414 LBUL_144 LBU	0.384 0.299 2.075 0.280 10.441 4.102 0.316 0.423 4.296 2.035 2.763 4.499 34.489 0.473 5.139 0.473 5.139 0.400 0.317 0.339	0.436 0.468 0.314 0.2314 0.2314 0.364 0.364 0.364 0.364 0.315 10.483 0.266 3.680 0.222 0.248	3.213 2.088 2.244 2.882	3.717 3.660 4.465 6.389 5.404 2.961 0.437 0.437 3.027 2.842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.366 2.216 0.305 2.368 2.350 2.170 2.230 0.2174 0.305	Malatelactate dehydrogenases FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) FQF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Succinate dehydrogenase/fumarate reductase flavoprotein subunit Lactate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AND-dependent aldehyd dehydrogenases AND-dependent aldehyd dehydrogenases ANH-4 anjoter Lactate dehydrogenase and related dehydrogenases AnH-4 anjoter Harnietzgen-type cytochonome(quint) oxdases subunit 1 Eurarase Uncharacterized donydrogenases Predicate membrane protein Uncharacterized conserved in bacteria Predicate donserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Predicate membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria U
LBUL_0084 LBUL_0010 LBUL_0613 LBUL_0614 LBUL_0614 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_0716 LBUL_1096 LBUL_1532 LBUL_1532 LBUL_1697 LBUL_1697 LBUL_1697 LBUL_1697 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0081 LBUL_0082 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0370 LBUL_0396 LBUL_0494 LBUL_1476 LBUL_1428 LBUL_1	0.384 0.299 2.075 0.260 10.441 4.102 0.316 2.035 2.763 34.296 2.035 2.763 34.489 0.473 5.139 0.400 0.317 0.339	0.436 0.468 0.314 0.2314 0.2314 0.364 0.364 0.364 0.364 0.315 10.483 0.266 3.680 0.222 0.248	3.213 2.088 2.244 2.882	3.717 3.660 4.485 6.389 5.404 2.710 0.437 3.027 2.842	3.071 10.851 2.596 2.738 2.081 2.938 0.095	0.269 0.148 0.300 0.364 0.366 2.612 0.366 2.216 0.305 2.368 2.350 2.170 2.230 0.2174 0.305	Malatolaciate dehydrogenases POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) POF1-type ATP synthase epsilon subunit (mitochondrial delta subunit) Provinate/2-oxoguitarate dehydrogenase (mitochondrial delta subunit) Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase/umarate reductase flavoprotein subunit Lacate dehydrogenase and related dehydrogenases 2-polyprenylphenol hydrogenases AnH+ antipoter Lacate dehydrogenase and related dehydrogenases Henne/coper-type cytochrome/quinol oxidases subunit 1 Fumarase Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized conserved protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Predicated membrane protein Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conserved in bacteria Uncharacterized protein conser

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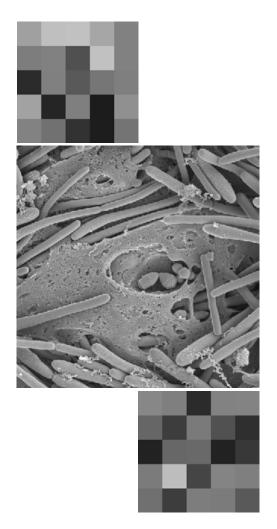
		0.470			0.007		
LBUL_0084 LBUL_0123	0.364 0.432	0.472 0.173	0.401	4.022	2.027 6.914		Lactate dehydrogenase and related dehydrogenases Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase
LBUL_0212	5.489	0.170	0.461	1.011	0.014		NTP pyrophosphohydrolases including oxidative damage repair enzymes
LBUL_0223		0.333				2.729	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase
LBUL_0225	5.504	16.478	2.994	4.440		0.412	Metal-dependent amidase/aminoacylase/carboxypeptidase Predicted HD superfamily hydrolase
LBUL_0230 LBUL_0290	3.621	4.662 5.730		4.446		0.412	Serine/threonine protein kinase
LBUL_0393		4.651					Predicted membrane protein putative toxin regulator
LBUL_0445				2.201		0.463	ATPase components of ABC transporters with duplicated ATPase domains
LBUL_0450	4.000			2.314	3.756	3.829	Integral membrane protein interacts with FtsH
LBUL_0500 LBUL_0516	4.069			0.489		3.829	Hydrolases of the alpha/beta superfamily Competence protein
LBUL_0536				0.100		0.310	Predicted HD superfamily hydrolase
LBUL_0572	3.002						Predicted hydrolases of the HAD superfamily
LBUL_0661	2.008	2.667					Predicted phosphatase/phosphohexomutase
LBUL_0683 LBUL_0703	2.008	0.284			0.495	0.343	NTP pyrophosphohydrolases including oxidative damage repair enzymes Predicted hydrolase (metallo-beta-lactamase superfamily)
LBUL_0707	2.226	0.201			0.400	0.010	Predicted hydrolase of the metallo-beta-lactamase superfamily
LBUL_0749	3.646						Metal-dependent hydrolases of the beta-lactamase superfamily III
LBUL_0776	2.330	2.720					Predicted GTPases
LBUL_0814 LBUL_0816	3.102		0.134				Predicted solute binding protein Predicted permease
LBUL_0818			0.154	0.439	4.045	9.218	3-oxoacyl-(acyl-carrier-protein)
LBUL_0821				0.397	3.656	9.216	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
LBUL_0828				0.451	2.156	4.782	Enoyl-(acyl-carrier-protein)
LBUL_0917 LBUL_0938	4.170	4.648			2.596		Lactate dehydrogenase and related dehydrogenases Predicted permease DMT superfamily
LBUL_0961	3.647	4.040		2.603			Metal-dependent amidase/aminoacvlase/carboxypeptidase
LBUL_1122	0.011			2.000	0.385	0.289	Uncharacterized protein with an alpha/beta hydrolase fold
LBUL_1128	10.645	4.844					Predicted SAM-dependent methyltransferase
LBUL_1193	3.713						Predicted GTPases
LBUL_1255	0.371	0.252		0.135			Predicted O-methyltransferase Predicted kinase related to dihudrovyacetone kinase
LBUL_1297 LBUL_1351	3.660	0.202					Predicted kinase related to dihydroxyacetone kinase Predicted acyl esterases
LBUL_1500				0.437			ATPase components of ABC transporters with duplicated ATPase domains
LBUL_1566				0.109			NTP pyrophosphohydrolases including oxidative damage repair enzymes
LBUL_1606	2.334	2.352		2.077	2.428	2 007	Predicted kinase
LBUL_1624 LBUL_1768				0.467	2.276	2.997	Predicted solute binding protein Aldo/keto reductases related to diketogulonate reductase
LBUL_1784				2.348	2.210	0.475	Superfamily I DNA and RNA helicases
LBUL_1802	11.995						Membrane protein involved in the export of O-antigen and teichoic acid
LBUL_1808	3.513	3.177					Predicted glycosyltransferases
LBUL_1834		5.979	4.151			0.407	Plasmid maintenance system antidote protein
LBUL_1841 LBUL_1861	6.380	0.246				0.197	Membrane protein involved in the export of O-antigen and teichoic acid GTPases
LBUL_1868		3.694	3.213	3.660		0.269	Lactate dehydrogenase and related dehydrogenases
LBUL_1906	2.660	2.563		3.392			Predicted flavoprotein
LBUL_1907	2.648	2.774					Predicted flavoprotein
LBUL_1924		0.405			2.048	2.049	Uncharacterized C-terminal domain of topoisomerase IA
LBUL_1959 LBUL_1996		2.105 15.733	8.504	6.236		0.187	Predicted permeases Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein
LBUL_2001		5.362	0.004	6.031	2.702	0.448	Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein
LBUL_2002				2.301			Uncharacterized ABC-type transport system periplasmic component/surface lipoprotein
LBUL_2003		2.396	2.538	2.429		0.483	ABC-type uncharacterized transport systems ATPase components
LBUL_2004 LBUL_2005	2.775	6.195 3.824	2.232 2.349				ABC-type uncharacterized transport system permease component Uncharacterized ABC-type transport system permease component
LBUL_2021		3.024	2.040	2.784		0.294	Permeases
LBUL_2036		4.110	2.288	8.992		0.158	Predicted GTPase
Inorganic ion transport LBUL_0087	and metabo	lism		3.686		0.476	ABC-type metal ion transport system periplasmic component/surface antigen
LBUL_0138				0.397	2,469	6.221	Na+/H+ antiporter NhaD and related arsenite permeases
LBUL_0176				2.926			ABC-type phosphate/phosphonate transport system periplasmic component
LBUL_0177	2.688	3.211		2.336		0.309	ABC-type phosphate/phosphonate transport system ATPase component
LBUL_0178	2.734	4.220		2.144		0.325	ABC-type phosphate/phosphonate transport system permease component
LBUL_0179 LBUL_0236	2.757	3.285		5.774		0.308	ABC-type phosphate/phosphonate transport system permease component ABC-type dipeptide/oligopeptide/nickel transport systems permease components
LBUL_0237				5.342		0.296	ABC-type dipeptide/oligopeptide/nickel transport systems permease components
LBUL_0238	2.283			4.412		0.284	ABC-type dipeptide/oligopeptide/nickel transport system ATPase component
LBUL_0296	4.847	9.201					Cation transport ATPase
LBUL_0406	0.450	0.407			2.201		Cation transport ATPase
LBUL_0423 LBUL_0607	0.450	0.487		5.841		0.174	Carbonic anhydrase ABC-type metal ion transport system periplasmic component/surface adhesin
LBUL_0763		0.480		3.041			
LBUL_0867					0.222		
LBUL_0882				0.306	0.222 0.266	-	ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component ABC-type phosphate transport system periplasmic component
	2.673	2.441		10.530		0.138	ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component ABC-type phosphate transport system periplasmic component ABC-type cobalt transport system ATPase component
LBUL_0883	3.908	5.111		10.530 9.960		0.151	ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component ABC-type phosphate transport system partpasmic component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component
LBUL_0884	3.908 3.386			10.530 9.960 14.394	0.266	0.151 0.153	ABC-type nitrale/sulfonate/bicatonate transport system ATPase component ABC-type phosphate transport system pariplasmic component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system Per a component CbiQ and related transporters
LBUL_0884 LBUL_1157 LBUL_1291	3.908 3.386 2.600 3.469	5.111 3.956 6.214		10.530 9.960	0.266 3.842 0.293	0.151	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type pobaphate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component CbiQ and related transporters Cation transport ATPase
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293	3.908 3.386 2.600 3.469 4.734	5.111 3.956 6.214 9.742	2.058	10.530 9.960 14.394 0.110	0.266	0.151 0.153	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type pobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component Cation transport system permease component CbIQ and related transporters Cation transport ATPase ABC-type dipeptide/biopopetide/nickel transport system ATPase component ABC-type dipeptide/biopopetide/nickel transport system ATPase component
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327	3.908 3.386 2.600 3.469 4.734 0.273	5.111 3.956 6.214		10.530 9.960 14.394 0.110	0.266 3.842 0.293	0.151 0.153	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type probabilet transport system pariplasmic component ABC-type cobait transport system ATPase component ABC-type cobait transport system ATPase component ABC-type cobait transport system Parimeses component ABC-type cobait ATPaper system permease component ABC-type dispetitie/collopopetide/collopopeti
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1327 LBUL_1541	3.908 3.386 2.600 3.469 4.734	5.111 3.956 6.214 9.742	2.058 0.202	10.530 9.960 14.394 0.110 0.375	0.266 3.842 0.293 0.364	0.151 0.153 34.985	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPases component Cation transport system permease component CbIQ and related transporters Cation transport ATPase ABC-type dipeptide/oilogopetide/nickle transport systems permease components ABC-type dipeptide/oilogopetide/nickle transport system ATPase component Arsenate reductase and related proteins glutaredoxin family
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1293 LBUL_1327 LBUL_1541 LBUL_1652 LBUL_1658	3.908 3.386 2.600 3.469 4.734 0.273 2.637	5.111 3.956 6.214 9.742		10.530 9.960 14.394 0.110	0.266 3.842 0.293	0.151 0.153 34.985 0.315	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type posphate transport system pariplasmic component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component Cb/Q and related transporters Cation transport system permease component Cb/Q and related transporters Cation transport system permease component Cb/Q and related transporters ABC-type dipatified/clipopetide/nickel transport system ATPase component ABC-type dipatified/clipopetide/clipopetide/nickel transport system ATPase component ABC-type dipatified/clipopetide/clipopetide/nickel transport system ATPase component ABC-type dipatified/clipopetide/
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1327 LBUL_1541	3.908 3.386 2.600 3.469 4.734 0.273	5.111 3.956 6.214 9.742		10.530 9.960 14.394 0.110 0.375 0.490	0.266 3.842 0.293 0.364	0.151 0.153 34.985	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPases component Cation transport system permease component CbIQ and related transporters Cation transport ATPase ABC-type dipeptide/oilogopetide/nickle transport systems permease components ABC-type dipeptide/oilogopetide/nickle transport system ATPase component Arsenate reductase and related proteins glutaredoxin family
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1327 LBUL_1541 LBUL_1652 LBUL_1658 LBUL_1929	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364	5.111 3.956 6.214 9.742 0.141	0.202	10.530 9.960 14.394 0.110 0.375 0.490 4.258	0.266 3.842 0.293 0.364	0.151 0.153 34.985 0.315 0.266	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component Cb/Q and related transporters Cation transport system permease component SABC-type dipeptide/oilogopetide/nickel transport system ATPase component ABC-type dipeptide/oilogopetide/nickel transport systems Parses component ABC-type dipeptide/oilogopetide/nickel transport system ATPase component Arsenate reductase and related proteins glutaredoxin family Armmonia permease Cyanate permease
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1541 LBUL_1652 LBUL_1658 LBUL_1929 Intracellular trafficking,	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a	5.111 3.956 6.214 9.742 0.141	0.202	10.530 9.960 14.394 0.110 0.375 0.490 4.258	0.266 3.842 0.293 0.364	0.151 0.153 34.985 0.315 0.266 0.158	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component Cation transport system permease component Cb/D and related transporters Cation transport system permease component SABC-type dispetide/illogopetide/inckel transport systems permease components ABC-type dispetide/illogopetide/inckel transport systems Parea component ABC-type dispetide/illogopet
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1327 LBUL_1541 LBUL_1652 LBUL_1658 LBUL_1929	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364	5.111 3.956 6.214 9.742 0.141	0.202	10.530 9.960 14.394 0.110 0.375 0.490 4.258	0.266 3.842 0.293 0.364	0.151 0.153 34.985 0.315 0.266	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type pochate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component ABC-type cobalt/doilogopetid/divickel transport system ATPase component ABC-type dipetid/doilogopetid/divickel transport system ATPase Asenate reductase and related proteins gluaredoxin family Ammonia permease D- and transboxilae transporters Preprotein translocase subunit SecY
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1327 LBUL_1541 LBUL_1652 LBUL_1658 LBUL_1658 LBUL_1929 Intracellular trafficking, LBUL_0370	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795	5.111 3.956 6.214 9.742 0.141	0.202 Ir transport	10.530 9.960 14.394 0.110 0.375 0.490 4.258	0.266 3.842 0.293 0.364	0.151 0.153 34.985 0.315 0.266 0.158 0.431	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component Cation transport system permease component Cb/Q and related transporters Cation transport system permease component SABC-type dipeptide/cligopeptide/nickel transport system Partese components ABC-type dipeptide/cligopeptide/nickel transport systems Partese components ABC-type dipeptide/cligopeptide/nickel transport systems Partese component Arsenate reductase and related proteins glutaredoxin family Ammonia permease Quantication/intic transporter Di- and tricarboxylate transporters Preprotein translocase subunit SecY Proteases Ubunit 6 ATP-dependent Clp proteases
LBUL_0884 LBUL_1157 LBUL_1291 LBUL_1293 LBUL_1329 LBUL_1329 LBUL_1541 LBUL_1659 LBUL_1659 LBUL_059 Intracellular trafficking, LBUL_0559 LBUL_0559 LBUL_0519	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795	5.111 3.956 6.214 9.742 0.141 und vesicula 4.528	0.202 Ir transport	10.530 9.960 14.394 0.110 0.375 0.490 4.258	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565 0.243	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type dispetide/silopopetide/nickel transport system Parease component ABC-type dispetide/silopopetide/nickel transport systems permease components ABC-type dispetide/silopopetide/nickel transport systems permease components ABC-type dispetide/silopopetide/nickel transport systems Parease components ABC-type dispetide/silopopetide/nickel transport systems Parease components ABC-type dispetide/silopopetide/nickel transport systems Parease components Arsenate reductase and related proteins glutaredoxin family Armonia permease Quantovinitie transporter Di- and tricarboxylate transporters Di- and tricarboxylate transporters Preprotein translocase subunit SecY Proteases ubunit d ATP-dependent Clp proteases Type II secretory pathway component PulF
LBU_U_0884 LBU_1157 LBU_1291 LBU_1293 LBU_1327 LBU_1541 LBU_1658 LBU_1658 LBU_1658 LBU_1929 Intracellular trafficking, LBU_0559 LBU_0611 LBU_0611	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751 0.206	5.111 3.956 6.214 9.742 0.141 ind vesicula 4.528 0.357	0.202 Ir transport	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type poolshate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system Partmase component CAC-type cobalt transport system permease component CbN and related transporters ABC-type dispetide/clipopetide/inickel transport system ATPase component ABC-type dispetide/clipopetide/inickel transport system ATPase ABC-type dispetide/clipope
LBUL_0884 LBUL_1157 LBUL_1293 LBUL_1293 LBUL_1293 LBUL_1542 LBUL_1654 LBUL_1654 LBUL_1658 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0559	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751	5.111 3.956 6.214 9.742 0.141 und vesicula 4.528 0.357 0.296	0.202 Ir transport	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.249	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565 0.243 2.428	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component Cation transport system permease component Cb/Q and related transporters Cation transport aTPase ABC-type dipeptide/cligopeptide/nickel transport system ATPase components ABC-type dipeptide/cligopeptide/nickel transport system ATPase component Asc-type dipeptide/cligopeptide/nickel transport system ATPase component Assenter reductase and related proteins glutaredoxin family Ammonia permease Cyanate reductase transporter Di- and trcachoxylate transporter Di- and trcachoxylate transporters Preprotein translocase subunt SecY Protease subunt 6 ATP-dependent Cip proteases Type II secretory pathway component PulF Lipoprotein signal peptidase Signal recognition particle GTPase
LBUL_0884 LBUL_1157 LBUL_1237 LBUL_1237 LBUL_1237 LBUL_1237 LBUL_1527 LBUL_1652 LBUL_1652 LBUL_1652 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_0551 LBUL_1546	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751 0.206	5.111 3.956 6.214 9.742 0.141 4.528 0.357 0.296 6.078	0.202 ar transport 0.388	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.2249 2.528	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565 0.243 2.428 0.379	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type posphate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component Cb/Q and related transporters Cation transport system permease component Cb/Q and related transporters Cation transport system permease component Cb/Q and related transporters ABC-type clopatific/cild/transport system ATPase component ABC-type clopatific/cild/transport system ATPase component ABC-type clopatific/cild/transport system ATPase component ABC-type dipatific/cild/transport system ATPase component ABC-type dipatific/cild/transporter Di- and tricarboxylate transporters Di- and tricarboxylate transporters Preprotein translocase suburit & cY Preprotein signal peptidae Upportein signal peptidae Signal perticael Signal perticael Signal perticael
LBUL_0884 LBUL_1157 LBUL_1231 LBUL_1232 LBUL_1232 LBUL_1232 LBUL_1652 LBUL_1652 LBUL_1652 LBUL_1659 LBUL_0559 LBUL_0559 LBUL_0559 LBUL_0611 LBUL_0559 LBUL_0612 LBUL_1232 LBUL_1546 LBUL_1246 LBUL_1246	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751 0.206	5.111 3.956 6.214 9.742 0.141 und vesicula 4.528 0.357 0.296	0.202 Ir transport	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.249	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565 0.243 2.428	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type nobabite transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component Cation transport system permease component Cb/Q and related transporters Cation transport aTPase ABC-type dipeptide/cligopeptide/nickel transport system ATPase components ABC-type dipeptide/cligopeptide/nickel transport system ATPase component Asc-type dipeptide/cligopeptide/nickel transport system ATPase component Assenter reductase and related proteins glutaredoxin family Ammonia permease Cyanate reductase transporter Di- and trcachoxylate transporter Di- and trcachoxylate transporters Preprotein translocase subunt SecY Protease subunt 6 ATP-dependent Cip proteases Type II secretory pathway component PulF Lipoprotein signal peptidase Signal recognition particle GTPase
LBU_U_0884 LBU_1157 LBU_1293 LBU_1223 LBU_1327 LBU_1541 LBU_1652 LBU_1652 LBU_1652 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_0559 LBU_21282 LBU_11282 LBU_1282 LBU_1546 LBU_2037 LIPId metabolism	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751 0.206	5.111 3.956 6.214 9.742 0.141 4.528 0.357 0.296 6.078	0.202 ar transport 0.388	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.249 2.528 3.895	0.266 3.842 0.293 0.364 0.154	0.151 0.153 34.985 0.266 0.158 0.431 2.565 0.243 2.428 0.379 0.330	ABC-type nitrate/sulfonate/bicathonate transport system ATPase component ABC-type pochate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component ABC-type dispetitie/collopopetide/incikel transport system ATPase component ABC-type dispetitie/collopopetide/incikel transport system ATPase component ABC-type dispetitie/collopopetide/incikel transport system ATPase component ABC-type dispetitie/collopopetide/incikel transport system ATPase component ABC-type dispetitie/collopopetide/incikel transport system ATPase Asenate reductase and related proteins glutaredoxin family Armonia permease D- and transporters D- and transporters Preprotein translocase subunit SecY Proteins signal petidase Signal petidase I Signal petidase Signal petidase I Signa
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LBU_U_0884 LBU_1157 LBU_1293 LBU_1293 LBU_1327 LBU_1652 LBU_1655 LBU_1658 LBU_1658 LBU_1658 LBU_0679 LBU_0679 LBU_0679 LBU_0679 LBU_0679 LBU_0679 LBU_0759 L	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.397 0.364 secretion, a 4.795 2.751 0.206	5.111 3.956 6.214 9.742 0.141 4.528 0.357 0.296 6.078	0.202 ar transport 0.388	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.249 2.528 3.895	0.266 3.842 0.293 0.364 0.154 0.288	0.151 0.153 34.985 0.266 0.158 0.431 2.565 0.243 2.428 0.379 0.330	ABC-type nitrate/suffontate/bicathonate transport system ATPase component ABC-type poolate transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system ATPase component ABC-type cobalt transport system permease component CbU and related transporters ABC-type dispetitive/super-transport system permease component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase component ABC-type dispetitive/super-transport system ATPase Asenate reductase and related proteins gluaredoxin family Ammonia permease Di- and transporter Di- and transporter Di- and transporters Preprotein translocase subunt SecY Preprotein signal peptidase Signal petidase I Signal recognition particle GTPase Preprotein translocase subunt SecE Preprotein translocase subunt SecE Preprotein translocase subunt SecE Preprotein translocase subunt SecE
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LBU_ 0884 LBU_ 1157 LBU_ 129 LBU_ 1232 LBU_ 1232 LBU_ 1232 LBU_ 1241 LBU_ 1652 LBU_ 1652 LBU_ 1652 LBU_ 1652 LBU_ 0551 LBU_ 0551 LBU_ 0551 LBU_ 0551 LBU_ 0551 LBU_ 1246 LBU_ 1246 LBU_ 1246 LBU_ 1066 LBU_ 0106 LBU_ 0106	3.908 3.386 2.600 3.469 4.734 0.273 2.637 0.364 3.654 3.654 3.654 0.206 2.641 5.616	5.111 3.956 6.214 9.742 0.141 advesicula 4.528 0.357 0.296 6.078 6.673 6.605	0.202 ar transport 0.388	10.530 9.960 14.394 0.110 0.375 0.490 4.258 5.814 2.2249 2.528 3.895 3.005 5.480 3.675 2.2504	0.266 3.842 0.293 0.364 0.154 0.288 2.330	0.151 0.153 34.985 0.315 0.266 0.158 0.431 2.565 0.243 2.428 0.379 0.330 0.278 0.240 0.251 0.331 0.303	ABC-type nitrate/sufficient/bioteries/ ABC-type nitrate/sufficient/bioteries/ ABC-type cobalit transport system ArPase component ABC-type cobalit transport system ArPase component ABC-type cobalit transport system ArPase component ABC-type cobalit transport system permease component CbD and related transport system permease component CbD and related transport system permease component ABC-type diopetide/clipopetide/in/ckel transport system ArPase component ABC-type diopetide/clipop
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LBUL_1955 2.441 0.228 Dihydroorotate dehydrogenase	
LBUL 2017 3.881 0.34 Deoxynucleoside kinases	
LBUL_2018 3.529 0.30 Deoxynucleoside kinases	
Posttranslational modification, protein turnover, chaperones	
LBUL_0191 0.454 Predicted metalloendopeptidase	
LBUL_0243 4.685 Molecular chapterone (small heat shock protein) LBUL_0339 0.416 ATPases with chaptorone activity ATP-binding subunit	
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LBUL 0515 0.443 Negative regulator of genetic competence sporulation and motility	
LBUL_0559 2.751 0.388 2.565 Protease subunit of ATP-dependent Clp proteases	
LBUL_0605 2.964 Peptide-methionine suffoxide reductase LBUL_1004 3.536 Peptidy-protyl cist-strama is ionerase (or curanase) - cyclophilin family	
LBUL_1101 0.382 Zn-dependent protease with chaperone function	
LBUL_1105 8.220 7.754 0.221 0.138 Subtilisin-like serine proteases	
LBUL_1186 2.720 ATP-dependent protease HsIVU (ClpYQ) ATPase subunit LBUL_122 4.349 0.248 5.327 DnaJ-class molecular chaperone with I-derminal Zn linger domain	
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LBUL_1466 2.848 Thioredoxin reductase LBUL_1496 0.490 0.333 4.713 Chaperonin GroEL (HSP60 family)	
LBUL 1497 0.249 7.597 Co-chaperonin GroES (HSP10)	
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Mixed culture experimental evolution

LBUL_0313 LBUL 0343	5.686	4.458 2.282					Superfamily II DNA and RNA helicases
LBUL_0376	2.123	2.329					DNA-directed RNA polymerase beta' subunit/160 kD subunit DNA-directed RNA polymerase alpha subunit/40 kD subunit
LBUL_0399	0.287	0.272					Transcriptional regulators
LBUL_0566 LBUL_0587					2.142	6.759	Transcriptional regulator contains sigma factor-related N-terminal domain Predicted transcriptional regulator
LBUL_0737	0.098		5.181		0.393	0.293	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)
LBUL_0780	3.660		0.488	3.624		0.261	and their eukaryotic orthologs Transcriptional regulator
LBUL_1099	0.199	0.057					Predicted transcriptional regulator
LBUL_1229 LBUL 1243	4.041	2.637	0.347	0.216		5.126	Transcriptional regulator of heat shock gene Predicted nucleic-acid-binding protein implicated in transcription termination
I BI II 1244		2.804	2.433	2.501		0.377	Transcription elongation factor
LBUL_1287 LBUL_1296	0.026	0.127	7.986			6.466	dsRNA-specific ribonuclease RecG-like helicase
LBUL_1381	2.408	0.127					Transcription elongation factor
LBUL_1535				2.277	2.267		Putative transcription activator
LBUL_1545 LBUL_1563		2.464	0.333				Transcription antiterminator Predicted transcriptional regulators
LBUL_1705						0.466	Exoribonuclease R
LBUL_1758 LBUL_1781				0.239	0.222	0.273	Transcriptional regulator Response regulator of the LytR/AlgR family
LBUL_1822	7.823	11.042		0.200	U.LLL		Predicted transcriptional regulators
LBUL_1901 LBUL_1914	4.881	0.020				0.376	Predicted transcriptional regulators Transcriptional regulator
LBUL_1957		3.962	2.138	3.727		0.153	Cold shock proteins
Translation Diberra		nd Discourse					
Translation, Ribosom LBUL_0007	4.632	nd Biogene 7.086	esis				Ribosomal protein S6
LBUL_0009	3.093	6.782	2.193	2.196		0.317	Ribosomal protein S18
LBUL_0219				2.812		0.455	Tyrosyl-tRNA synthetase Ribosomal protein L31
LBUL_0311 LBUL_0313	5.686	4.458					Superfamily II DNA and RNA helicases
LBUL_0327 LBUL_0328		3.860 2.129				0.373	tRNA-dihydrouridine synthase Lysyl-tRNA synthetase (class II)
I BUI 0346	2.331	3.063					Ribosomal protein S12
LBUL_0347 LBUL_0348	2.115 2.934	2.411 2.778					Ribosomal protein S7 Translation elongation factors (GTPases)
LBUL_0349		7.554	2.183				Ribosomal protein S10
LBUL_0350	3.828	6.602 5.900					Ribosomal protein L3
LBUL_0351 LBUL_0352	3.621 4.279	5.900					Ribosomal protein L4 Ribosomal protein L23
LBUL_0353 LBUL_0354	3.841	6.753					Ribosomal protein L2
LBUL_0354 LBUL_0355	3.614 3.478	6.839 5.455					Ribosomal protein S19 Ribosomal protein L22
LBUL_0356	3.611	5.516					Ribosomal protein S3
LBUL_0357 LBUL_0358	3.156 4.060	4.851 5.199					Ribosomal protein L16/L10E Ribosomal protein L29
LBUL_0359	3.464	4.917					Ribosomal protein S17
LBUL_0360	3.500	4.955					Ribosomal protein L14
LBUL_0361 LBUL_0362	3.250 3.741	4.117 4.938					Ribosomal protein L24 Ribosomal protein L5
LBUL_0363	3.741 3.541	4.259					Ribosomal protein S14
LBUL_0364 LBUL_0365	3.480 3.859	4.219 4.661					Ribosomal protein S8 Ribosomal protein L6P/L9E
LBUL 0366	2.927	3.894					Ribosomal protein L18
LBUL_0367 LBUL_0368	4.469 4.277	4.699 4.831				0.455	Ribosomal protein S5 Ribosomal protein L30/L7E
LBUL_0369	3.215	4.831				0.455	Ribosomal protein L30/L/E Ribosomal protein L15
LBUL_0372	2.280	2.401 2.868					Translation initiation factor 1 (IF-1)
LBUL_0373 LBUL_0374		2.868					Ribosomal protein L36 Ribosomal protein S13
LBUL_0375 LBUL_0377		2.929					Ribosomal protein S11
LBUL_0377	2.235	2.971				0.458	Ribosomal protein L17 Ribosomal protein L13
LBUL_0382 LBUL_0383	2.962	4.013					Ribosomal protein S9
LBUL_0501 LBUL_0654	4.237 2.200	6.788 2.166					SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase Ribosomal protein S4 and related proteins
LBUL_0706	3.627	6.032		2.087		0.486	Ribosomal protein S15P/S13E
LBUL_0751	2.812	2.116 3.094					Ribosomal protein L32
LBUL_0812 LBUL_0813	2.812 3.603	3.094 4.390					Histidyl-tRNA synthetase Aspartyl-tRNA synthetase
LBUL 0930	0.192	0.330		2.305		0.290	Pseudouridylate synthases 23S RNA-specific
LBUL_1166 LBUL_1167	2.353	2.414 2.127					Glycyl-tRNA synthetase beta subunit Glycyl-tRNA synthetase alpha subunit
LBUL_1173	2.232						Ribosomal protein S21
LBUL_1242 LBUL_1247		2.333		2.023		0.449	Ribosomal protein HS6-type (S12/L30/L7a) Prolyl-tRNA synthetase
LBUL_1253	2.346	2.948				0.408	Translation elongation factor Ts
LBUL_1254 LBUL_1273	4.643 4.054	6.418 5.065				0.426	Ribosomal protein S2 Ribosomal protein L19
LBUL_1273 LBUL_1281	4.054 5.445	5.065		2.014		0.473	Ribosomal protein S16
LBUL_1299		2.446					Ribosomal protein L28
LBUL_1325 LBUL_1326	4.116 3.144	5.567 4.415					Ribosomal protein L27 Ribosomal protein L21
LBUL_1396	3.887	10.574	2.720				Ribosomal protein L20
LBUL_1397 LBUL_1398	3.519 3.489	7.483 7.312	2.127 2.096				Ribosomal protein L35 Translation initiation factor 3 (IF-3)
LBUL_1401	3.403	7.512	2.030		2.164		Threonyl-tRNA synthetase
LBUL_1451					2.157 2.114	2.011	Leucyl-tRNA synthetase
LBUL_1486 LBUL_1536	2.470	2.146			2.114	2.011 0.318	AlanyI-tRNA synthetase Ribosomal protein L7/L12
LBUL_1537 LBUL_1547	3.271	2.836					Ribosomal protein L10
LBUL_1547 LBUL_1552	3.308	5.421 0.342				0.463	Ribosomal protein L33 rRNA methylases
LBUL_1560	2.489	3.441					Glutamyl- and glutaminyl-tRNA synthetases
LBUL_1748 LBUL_1749		0.445		2.334			Seryl-IRNA synthetase Acetyltransferases including N-acetylases of ribosomal proteins
LBUL_1778	3.483						Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
LBUL_2038		5.717	3.172	4.106		0.324	RNase P protein component

A genome-scale metabolic model of mixed culture growth of S. *thermophilus* and *L. bulgaricus*



Sander Sieuwerts, Willem M. de Vos, Johan E.T. van Hylckama Vlieg and Bas Teusink

ABSTRACT

The interactions between microorganisms are of key importance for the performance of mixed culture fermentations such as the yoghurt fermentation, which is carried out by a consortium of Streptococcus thermophilus and Lactobacillus bulgaricus. These two species stimulate each other's growth by the exchange of growth factors associated with purine and amino acid metabolism (5, 7, 9). However, a detailed view on the regulatory responses and metabolic basis of these stimulatory interactions remains to be established. To advance this insight, mapping the metabolism of the two separate species can be instrumental. We used genome-scale metabolic modeling to identify the reactions occurring in both bacteria. Moreover, carbon and amino acid fluxes in both bacteria were calculated and included in the models. Finally, we demonstrate the possibility to couple such models in order to identify reactions associated with interactions between consortium members. In this case nutritional exchange was indeed predicted to be based on formic acid, folic acid and proteolysis. In addition, the experimental observation of an increased biomass yield on lactose was confirmed in the model. It is anticipated that such models will aid the development or improvement of other mixed culture fermentations in the near future.

INTRODUCTION

Microorganisms are almost uniquely found in ecosystems consisting of multiple species. The interplay with other microorganisms is of key importance for their behavior and performance (13, 17). A well-known example in the field of food fermentations is the yoghurt fermentation. In this process (bovine) milk is transformed into yoghurt, through the combined action of the two lactic acid bacteria (LAB) *Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus*. These two species stimulate each other's growth by the exchange of growth factors associated with purine and amino acid (AA) metabolism (5, 7, 9, 23), in a process also referred to as protocooperation. A number of recent post-genomic studies identified several genetic and physiological responses associated with co-cultivation (11, 12, 26).

Previously, kinetic models of the yoghurt fermentation were constructed to quantify interactions between *S. thermophilus* and *L. bulgaricus* in yoghurt (6, 27). Although these models proved to be very useful for the quantification of interactions in mixed cultures, they are highly specific to the conditions used for the assessment of the kinetic parameters and they have little predictive value for other

conditions. These black-box models also do not allow the identification of the underlying mechanisms behind the mutualistic interactions between *S. thermophilus* and *L. bulgaricus*. Genome-scale metabolic models, on the other hand, may provide an attractive alternative as they enable the prediction of the behavior of a microorganism in a complex and changing environment, especially when fed with experimental fermentation data used to calculate fluxes (30, 32). However, the construction of metabolic models that take into account the effects of competition and the exchange of metabolites between members of a microbial community is still challenging (2, 35).

Here we report the construction of genome-scale metabolic models of *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365 and their validation using experimental fermentation data. Furthermore, we comment on the possibility to couple both models in order to identify the nature of the interactions between both bacteria in yoghurt. Preliminary results suggest interactions based on the exchange of formic acid, folic acid (provided by *S. thermophilus*) and proteolysis (executed by *L. bulgaricus*), which is in accordance with literature findings and the data reported in chapter 4. Although determining the metabolite fluxes in the mixed culture model presented is not finalized yet and the model needs to be validated with additional experimental data, it is anticipated that such genome-scale metabolic models are valuable for the prediction of mixed culture growth in dynamic environments

MATERIALS AND METHODS

Strains and culture conditions

S. thermophilus CNRZ1066 (3), *L. bulgaricus* ATCC BAA-365 (16) and two coadapted strains by an experimental evolution study, *S. thermophilus* NIZO3938 and *L. bulgaricus* NIZO3939 (24), were maintained as frozen M17 broth (Difco) and MRS broth (Difco) cultures with 22% glycerol (Scharlau) at -80 °C. Pre-cultures and 275 mL final cultures were prepared as described in (26). Colony-forming units (CFUs) were determined by selective plating (M17 agar supplemented with 1% (w/v) glucose, aerobic at 42°C for *S. thermophilus* and MRS agar, anaerobic at 42°C for *L. bulgaricus*) using the faster plating method developed before (25).

Optical density, dry weight and metabolite measurements

The optical density at 600 nm (OD_{600}) of yoghurt cultures was determined in duplicate by mixing one volume of culture was mixed with 9 volumes of a 0.2%

(w/v) NaEDTA / 0.2% (w/v) NaOH solution. The cell dry weight of cultures was derived from OD_{600} values after calibration as described in (21).

Sugar (lactose, glucose, galactose), acid (lactic acid, acetic acid, formic acid, citric acid and succinic acid) and ethanol content of the medium were determined using HPLC as described before (24). The AA content was determined as described in (26).

Calculation of fluxes

Fluxes of metabolites (mmol gDW⁻¹) were calculated as follows. The average increase in biomass (g h⁻¹) was calculated by linear regression of the growth curve. The average production (or consumption) of substrates and metabolites (mmol h⁻¹) was calculated in the same way. The specific production of metabolites per g dry weight was calculated by dividing the metabolite production by the biomass production.

Exopolysaccharide isolation

Exopolysaccharides (EPS) were extracted from 275 mL cultures grown for 24 h at 42°C as described before (26). The composition of EPS was determined as in (15).

Model development

Two genome-scale metabolic models were constructed on the basis of the genomes of *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365 (see Table 1). First drafts of the models were generated using the AUTOGRAPH method (18). In short, the genome of each organism was compared with the genomes for which a curated genome-scale metabolic model was already available, i.e. for *Lactobacillus plantarum* WCFS1 (30), *Bacillus subtilis* ATCC 23857 (19), *S. thermophilus* LMG18311 (20) and *Lactococcus lactis* MG1363 (Teusink and Notebaart, unpublished results). For orthologous genes, the corresponding gene-protein-reaction associations were copied to the draft models. For the *S. thermophilus* model, the model of strain LMG13811 was used with priority; for *L. bulgaricus*, *L. plantarum* was used as primary source. The other models were used as supplements for reactions that were not present in the *S. thermophilus* LMG18311 and *L. plantarum* models.

The draft models were manually curated as described before (30, 32). All gene-protein-reaction associations were checked manually for consistency and by comparing with other annotation resources such as the ERGO bioinformatics suite and KEGG pathways. In case a gene encoded an enzyme with a specific metabolic function, it was included in the model. Here after, the models were analyzed for

potential gaps in the network by testing their ability to produce biomass components *in silico*. Corresponding gaps in the models of *S. thermophilus* LMG18311 and *L. plantarum* were used for insertion of non-gene associated reactions. Such non-gene associated reactions are inferred to be present based on physiological or biochemical data without having identified the gene that codes for the corresponding enzyme (note that also non-enzymatic reactions fall into this category). The genomes of the organisms studied have gone through a process of extensive reductive evolution (16, 34) leading to potential of cross-feeding between the two species. Therefore, it is difficult to determine *a priori* whether a postulated metabolic gap is genuine. We therefore only allowed non-gene associated reactions if they were present in at least one of the already curated models. Other gaps were considered real and potentially filled by cross-feeding (see below).

Table 1. Numbers of genes, reactions and metabolites included in the curated models of *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365.

	S. thermophilus	L. bulgaricus
Genes	1968	1933
Included in model	464 (23%)	500 (26%)
Reactions	511	423
Non-gene associated	65 (13%)	61 (14%)
Metabolites	549	492
Extracellular	76	70

For growth in milk, new reactions that had not previously been included in any genome-scale metabolic model of LAB had to be included in the models. These involved proteolysis of casein and uptake and degradation of the resulting peptides. Casein was defined in terms of the average AA composition as published in (29). It was assumed that all AA of casein were accessible as peptides or free AA through proteolysis. For ATP-driven peptide uptake, an average peptide length of 9 AA was assumed, based on the finding that the substrate-binding subunit of OppA has the highest affinity for peptides consisting of 9 AA (8). In addition, it was assumed that peptides taken up by the cell were completely hydrolyzed into the free AA by peptidolysis. Reversible AA transporters were defined to accommodate efflux of excess AA where needed.

Modeling the consortium

Once the models of the individual strains allowed growth *in silico* using casein (*L. bulgaricus*) or casein-derived peptides (*S. thermophilus*) as a nitrogen source, the two models were combined into one model. In the combined model all extracellular metabolites were assumed to be available to both organisms provided that the required transport activity was defined (see Figure 1). Extracellular metabolites were allowed to be exchanged with the environment through so-called exchange reactions in order to prevent accumulation. For example, lactose was allowed to go into the system, whereas galactose could leave the system. In this way, appropriate sources and sinks for substrates and products were created, allowing e.g. steady state growth. If no such exchange reactions were defined for external metabolites, they had to be balanced by the organisms themselves (e.g. compounds Y and Z in Figure 1).

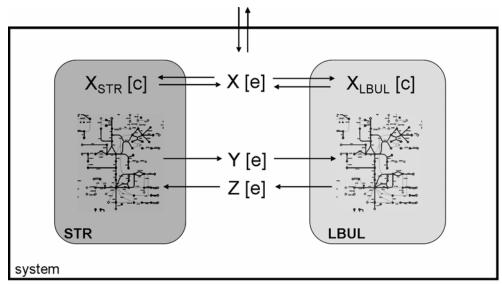


Figure 1. Principle of multi-species modeling of the yoghurt consortium. All external metabolites (denoted by [e]) are shared by both organisms (but only if the appropriate transporters are present). Exchange reactions, represented by the arrows at the top of the figure, define which compounds can enter or leave the system, and hence, can net be consumed or taken up by the consortium (in the figure, only X can be net produced or consumed: Y and Z can only be exchanged between the two organisms). Once internalized, conversion of X[c] ([c] for cytosol) becomes organism specific. STR, *S. thermophilus*; LBUL, *L. bulgaricus*.

In such a combined multi-species model, essential interactions between the organisms can be predicted by deletion analysis. For that both species are grown *in silico* in a medium containing the minimal set of compounds that both require for growth. Subsequently, reactions in one organism are deleted one by one and growth in the other organism is maximized using Flux Balance Analysis (FBA). If the growth rate is zero, the reaction in the one organism apparently provides a necessary compound for the other organism. When doing this for the yoghurt consortium (in a medium containing lactose, milk protein and a minimal set of vitamins), *S. thermophilus* genes essential for growth of *L. bulgaricus* are all involved in folic acid or formic acid production. Proteolysis by *L. bulgaricus* was the only essential reaction for *S. thermophilus* growth.

Genome-scale metabolic models are used for interpretation of fermentation data (32) and even prediction of yields and fluxes (30), using constraint-based modeling approaches. This is not trivial in a multi-species model. The most important complication is the fact that a single objective function that is optimized with FBA in mono-cultures is biologically not meaningful in a mixed culture. For instance, optimizing growth rate cannot be used. The rate of which of the two (or more) should be chosen? In order to circumvent this, it is possible to assume a fixed ratio for growth of both species (28). There is no principle argument for this constraint in general, and also in our case growth rates were not equal (see Figure 2). In fact, growth in yoghurt cultures is often partly sequential (6). Therefore alternative ways were explored to use constraint-based modeling for mixed cultures: (i) fixing the growth rate ratio to 1 (as done before (22)) and (ii) by calculating the maximal growth of one species as a function of the other, and vice versa. In both cases, it is important to realize that the fluxes within the organisms are usually expressed as specific rates (mmol h⁻¹ gDW⁻¹). A major complication is the normalization with respect to the biomass of the two organisms. In this study we have solved this issue by constraining essential input (or output) fluxes through linkage to the growth rate. That means, uptake rate and growth rate are coupled through the yield. Experimentally, it was found that lactose consumption for the evolved S. thermophilus (STR) mono-culture was 170 mmol/gDW, and for the evolved L. bulgaricus (LBUL) mono-culture it was 140 mmol/gDW (see Table 2). Therefore, we used the constraints:

$$10^{-4} \leq \frac{r_{\text{lactose,STR}}}{\mu_{\text{STR}}} \leq 170 \tag{Eq 1}$$

$$10^{-4} \leq \frac{r_{\text{lactose,LBUL}}}{\mu_{\text{LBUL}}} \leq 140$$

Where $r_{lactose}$ is the uptake rate of lactose in mmol gDW⁻¹. Note that because in the biomass equation we define components in terms of mmol gDW⁻¹ as well (e.g. biomass of STR contains x mmol protein gDW⁻¹), the growth rate μ is dimensionless. One could multiply the uptake rate by the actual growth rate (in h⁻¹) to get an uptake rate in the usual units mmol h⁻¹ gDW⁻¹, but the current notation emphasizes the fact that this unit refers to yields (see (31) for more details). The constraints of Eq 1 ensure that lactose can only be taken up if there is also growth. Without this constraint, fluxes could run through the network of these organisms without there being any biomass to catalyze it. In this way we can also model interactions between the two organisms. For *L. bulgaricus* to grow better, it requires formate produced by *S. thermophilus*, but for this, it has to allow S. *thermophilus* to grow as well (and utilize lactose). This constraint needs to be applied to all inputs or outputs in the network relevant for the interaction:

$$10^{-4} \leq \frac{r_{\text{proteolysis,LBUL}}}{\mu_{\text{LBUL}}} \leq 40$$

$$10^{-4} \leq \frac{r_{\text{formate,STR}}}{\mu_{\text{STR}}} \leq 6$$
(Eq2)

The constraint on formate production comes from the formate yield in the mono-culture of *S. thermophilus* (see Table 2). The constraint on proteolysis in *L. bulgaricus* is based on the assumptions that (i) all casein-derived peptides are taken up completely, (ii) excess AA that cannot be incorporated into biomass or metabolized by the network, are exported into the medium (see Figure 3), and (iii) the uptake of peptides is in excess of what is needed for growth (growth is assumed to be limited by formate availability), and the extent of excess is estimated by fitting proteolysis to the average rate of export of AA.

		Avera	ge produ	ction per	h			Averag	mass			
	S. thermo	philus	L. bulg	aricus	Mi	xed	S. therm	ophilus	L. bulgaricus		Mix	ed
	Par	Ev	Par	Ev	Par	Ev	Par	Ev	Par	Ev	Par	Ev
Biomass (mg/L)	8.19	11.79	11.64	11.85	45.81	73.26						
EPS (mg/L)	33.26	49.22	60.94	56.27	63.46	163.08	4061.10	4174.73	5235.54	4748.90	1385.35	2226.09
lactose	-2.13	-2.01	-1.75	-1.67	-2.81	-4.16	-259.77	-170.59	-150.39	-140.66	-61.44	-56.73
glucose	0.75	0.00	0.10	0.30	0.00	0.00	92.17	0.00	8.30	25.51	0.00	0.00
galactose	1.44	1.51	0.97	1.21	2.39	3.17	175.43	127.81	83.08	101.81	52.13	43.27
citric acid	-0.07	-0.03	-0.06	-0.03	-0.10	-0.12	-8.24	-2.86	-4.99	-2.17	-2.27	-1.59
lactic acid	1.97	3.53	1.69	1.87	5.02	6.78	241.09	299.58	145.15	158.13	109.67	92.54
formic acid	0.06	0.07	0.05	0.06	0.11	0.13	7.23	6.01	4.20	5.30	2.46	1.79
succinate	0.00	0.00	0.07	0.09	0.02	0.05	0.00	0.00	5.95	7.29	0.50	0.70
ethanol	-0.01	-0.02	-0.01	-0.01	-0.01	-0.03	-1.81	-1.43	-0.43	-0.89	-0.22	-0.34
acetic acid	0.02	0.01	0.05	0.07	0.03	0.07	2 22	1 25	4 04	5 77	0.73	0.94

Table 2. Overview of formed biomass and primary metabolism metabolites in 24 h. The values of the metabolites are in mM. Par, parental strains CNRZ1066 and ATCC BAA-365; Ev, evolved strains NIZO3938 and NIZO3939. Note that negative values represent consumption.

RESULTS

Fermentations

Mono and mixed cultures were sampled every 1.5 h for 12 h and at the end of fermentation, after 24 h, for measurement of optical density, CFUs and metabolite profiling (see Table 2 and Figures 2 and 3). The OD_{600} was recalculated to dry weight. Growth of the mixed culture was similar to what was described before (14, 26). After the lag phase, there were two exponential phases separated by a transition phase. The mono-cultures, however, showed only one exponential phase. The *L. bulgaricus* mono-culture showed improved growth compared to previous studies (24, 26), which may be caused by mixing the culture every time prior to sampling (1) or the fact that another milk batch was used.

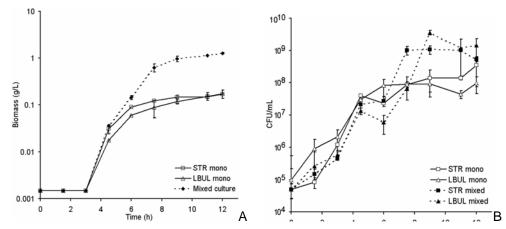


Figure 2. Growth of the evolved strains *S. thermophilus* NIZO3938 and *L. bulgaricus* NIZO3939 in mono and mixed culture in milk. A, Biomass production per culture in g L⁻¹. B, CFU mL⁻¹ per strain per culture. STR, *S. thermophilus*; LBUL, *L. bulgaricus*. Error bars indicate standard deviations of triplicate measurements.

In accordance with previous results, the amount of produced biomass and EPS and the quantity of consumed lactose consumed per h was higher in the mixed cultures compared to the mono-cultures (24). Moreover, the evolved strains – which were used because they showed an improved protocooperation in mixed culture compared to a mixed culture of both parental strains in a previous study (24) – displayed a higher production/consumption rate than the parental strains. The yield of biomass on lactose increased from 3.8 g to 5.9 g per mol of lactose for the parental and the evolved *S. thermophilus*, respectively. For *L. bulgaricus* this was an increase from 6.6 g to 7.1 g per mol lactose and for the mixed culture from

16.3 g to 17.6 g per mol of lactose for the parental and the evolved cultures, respectively. That means that the yield of biomass produced per lactose increased significantly in both mixed cultures compared to their corresponding mono-cultures. Moreover, the yield of the evolved strains was higher than that of the parental strains. For the flux calculations during modeling, the measurements of the evolved strains were used.

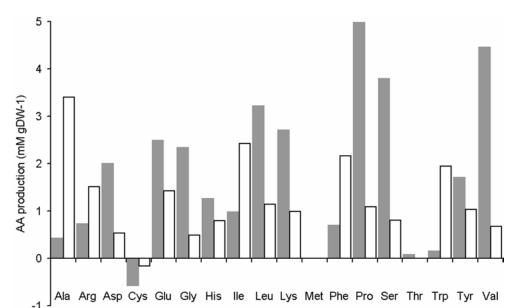


Figure 3. Measured amino acid production per g DW (grey) versus model prediction (white) of the evolved *L. bulgaricus* mono-culture. The production per g DW was calculated by dividing linear regression values of biomass and AA production. Model prediction was based on a presumed limitation of the growth rate by proteolysis of casein. The model prediction suggests that actual proteolysis is in 3-fold excess over biomass requirement.

Modeling the mono-cultures

When comparing the models of *S. thermophilus* and *L. bulgaricus*, the most obvious differences are in AA metabolism. Whereas *S. thermophilus* is almost completely prototrophic except for histidine and cysteine (20), *L. bulgaricus* requires all AA for growth (34) which is in agreement with the absence of complete pathways of many AA biosynthetic pathways. As a consequence all AA (except the one that limits protein synthesis and, hence, growth) are taken up in excess in the form of peptides by *L. bulgaricus* and excreted into the medium. Indeed, we found significant AA accumulation in the *L. bulgaricus* cultures, especially in that containing the evolved strain (see Figure 3).

The modeling of growth of L. bulgaricus in milk was complicated by the fact that the carbon balance was significantly off. Despite the fact the balances were based on samples at 10 different time-points throughout the fermentation, the carbon input to output ratio was in the order of 0.6-0.7. This may be due to the low rate of galactose export compared to lactose import. Of the 40.3 mM consumed lactose (i.e. 40.3 mM galactose) in the evolved L. bulgaricus, 26.2 mM was secreted as galactose and 3.7 mM ended up in EPS (the ratio of glucose to galactose in L. bulgaricus EPS is 1), leaving 10.3 mM of untraceable galactose. The carbon balance problem was circumvented by constraining only the input and leaving the output unconstraint, unless we had good evidence that a specific product was not formed (such as ethanol and acetate, see Table 2). Another unexpected finding is the formation of small amounts of formic acid by L. bulgaricus. According to the model and current insights, L. bulgaricus either is strictly dependent on S thermophilus for formic acid (6, 23) or at least there is a strong stimulation of formic acid supplementation (26). Apparently, there are alternative routes in L. bulgaricus for formic acid production that remain to be identified.

Initial modeling and experiments suggested that proteolysis is not limiting growth of L. bulgaricus. When formic acid and folic acid were supplied in excess and proteolysis was tuned to match a growth rate of 1 (thereby simulation a proteolysis-limited condition), most predicted AA production yields were lower than what was measured experimentally (on average the model yields were only 30% of the experimental yields, see figure 3). However, the relative distribution of measured and predicted amino acid production profiles are similar with few exceptions (there was more ala, arg, ile, phe and trp produced in silico than experimentally). The higher amino acid production than what is needed for growth strongly suggests that growth is not limited by amino acid acquisition but by other factors, notably products of S. thermophilus, such as formate and folic acid. The experimentally found production of formate by L. bulgaricus was ignored based on previous results (26), and for modeling purposes. In silico, formate was used as a proxy for any positive interaction that S. thermophilus has on L. bulgaricus. Formate consumption was set to limit growth of L. bulgaricus in mono-culture, the uptake limit of which was 0.06 mmol gDW⁻¹ to reach a growth rate of 1. Under this constraint, we adjusted the proteolysis rate such that the average AA production rate matched the measured one. This rate was 40 mmol gDW⁻¹ in the AA composition of casein. Under these conditions (formate 0.06; proteolysis 40; lactose 140 mmol gDW⁻¹) we subsequently performed a Flux Variability Analysis (FVA) to determine the flexibility in the network to reach the growth yield of 1. Since

growth was not energy limited, lactose consumption could be uncoupled from growth as discussed in (32). The minimum lactose uptake rate needed to support growth under these conditions was 78 mmol gDW⁻¹. Without EPS production as a constraint, minimal lactose uptake was only 24 mmol gDW⁻¹. This observation will be relevant in future efforts for extended modeling of the consortium.

S. thermophilus is mostly prototrophic for AA. Nevertheless, AA analysis revealed that the essential AA histidine and cysteine were not consumed to appreciable extent to support the observed growth. This observation points to (short) peptides as additional source of AA in the milk medium used. The carbon balance for S thermophilus did not show major gaps as 90-95% of the lactose could be accounted for in terms of metabolic end products (galactose and lactic acid being the major products, see Table 2). Using the measured data as constraints (lactose uptake 170 mmol gDW⁻¹, no limitation in his and cys), growth yields were up to 9 times higher than expected: clearly, lactose is not limiting growth. The flux distributions pointed at very high rates of urea assimilation as a nitrogen source for AA production. We therefore assumed that nitrogen (in the form of either ammonia or urea) is limiting growth in the evolved S. thermophilus. An uptake rate of 3 mmol gDW⁻¹ urea was fitted to obtain the reference growth yield of 1. Using FVA, the minimal lactose uptake rate needed to support growth and EPS production was 96 mmol gDW⁻¹. This was only 26 mmol gDW⁻¹ without EPS, showing the degree of uncoupling of growth and lactose consumption under these conditions.

Modeling the mixed culture

We constrained growth in the models of the mono-cultures of *L. bulgaricus* and *S. thermophilus* by formate and urea, respectively. Improved growth was therefore expected in the consortium as *L. bulgaricus* would provide additional nitrogen to *S. thermophilus* in the form of amino acids. In turn, *S. thermophilus* would provide formate to *L. bulgaricus*. Indeed, when we constrained growth of both species to be equal, we found a substantial increase in growth of both species (maximal yield of 1.23) giving a 2.5 fold increase in total biomass production. This increase is reaching the limit of fully coupled growth and energy limitation. The experimentally found lactose uptake yield was only 57 mmol gDW⁻¹ lactose, which is close to 2.5 times 25 mmol gDW⁻¹ lactose that would be expected to be the minimum lactose uptake needed for a growth yield of 2.5). That is, if EPS production is neglected. When EPS production is taken into account, biomass production is actually higher than the theoretical limit suggested by the model. That may be caused by

energetically beneficial interactions that are not yet included in the model such as uptake of fatty acids by *L. bulgaricus* upon lipolytic action by *S. thermophilus*. *S. thermophilus* could economize on lactose consumption by consuming amino acids secreted by *L. bulgaricus*. We found that in the optimal flux distribution, all peptides released by proteolysis by *L. bulgaricus* were also taken up by *L. bulgaricus*. In this scenario, *S. thermophilus* profits from proteolysis exclusively via the AA excreted by *L. bulgaricus*. These AA were, however, partly still accumulating in the medium. *In silico*, *L. bulgaricus* profits from proteolysis and amino acid secretion, as AA export results in proton extrusion which corresponds to the generation of 1/3 ATP per exported AA. Since uptake of 1 amino acid via the Opp transport system costs on average 1/9 ATP (8), the model predicts that the operation of this pathway results in energy generation.

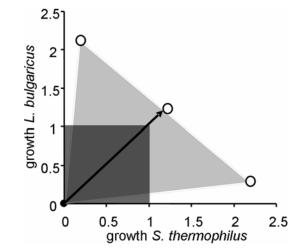


Figure 4: Expansion of growth rate potential in mixed culture compared to mono-culture. Dark grey square area is the growth rate range in mono-culture, light grey triangle area the range in the mixed culture. The arrow points to the result obtained if the growth ratio is fixed at 1.

When we used the second modeling technique, i.e. maximizing one species as a function of the other, we found that the maximal yield of *S. thermophilus* was 2.2, with the yield for *L. bulgaricus* being 0.7. Alternatively, the maximal yield of *L. bulgaricus* was 2.1, with the yield for *S. thermophilus* maximally being 0.3. This is a substantial increase in biomass yield which is in close agreement with the total biomass produced when growth rates were fixed to equal rates (see Figure 4). The increase in yield was confirmed experimentally (see Table 2) and in literature (6, 11, 26). However, in the current optimization scenario's, peptide uptake was

equally divided between *S. thermophilus* and *L. bulgaricus* when growth for *S. thermophilus* was maximized. Moreover, since growth of *L bulgaricus* was relatively low (0.3), not all casein could be proteolysed (see constraints Eq. 2) suggesting - much to our surprise - that already at very low growth rates of *L. bulgaricus*, the competition for lactose outweighs the benefit of peptide or amino acid provision to *S. thermophilus*. As expected, *S. thermophilus* peptide uptake was zero when growth of *L. bulgaricus* was maximized.

DISCUSSION AND FUTURE PROSPECTS

We have developed two functional genome-scale metabolic models of S. thermophilus and L. bulgaricus. Based on an in silico simulation of knock-outs and in silico growth, we were able to confirm metabolites that are exchanged between the two bacteria in milk. These were formic acid, folic acid (provided by S. thermophilus) and AA (released by proteolysis by L. bulgaricus). These interactions resulted in a total yield of the mixed culture that was increased 2.3-2.5 fold compared to the mono-cultures. That means that the interaction between the two organisms, despite lower uptake of lactose per g DW (57 mmol gDW⁻¹ instead of 140 and 170 for L. bulgaricus and S. thermophilus, respectively), resulted in a much larger possible range of growth rates (see Figure 4). Indeed, the amount of lactose consumed per g of biomass was 2.5-3.0 fold lower in our experimental data. The lower uptake of lactose can partly be explained by lower EPS production compared to the biomass production (2.2 g per g biomass in the evolved mixed culture versus 4.2 g and 4.7 g for the S. thermophilus and L. bulgaricus monocultures, respectively, see Table 2). That is striking, because genes coding for EPS biosynthesis were shown to be higher expressed in mixed culture in a previous study (26). The lower uptake of lactose per g produced biomass can also partly be explained by less spilling of AA into the medium. The AA secreted by L. bulgaricus were utilized by S. thermophilus, reducing the need for lactose for de novo AA production. The modeling exercise also showed the extent of uncoupling that is possible in milk between ATP production through glycolysis and growth. Although some improvement is seen in the evolved mono-cultures compared to the parental ones (see Table 2), the real improvement in lactose yield is caused by the provision of essential growth components by the other species in mixed cultures. The nature of the limitation is still speculative at the moment due to lack of required data sets, but the explanation provided by the model seems insensitive to the exact molecules being exchanged, and formate appears a reasonable proxy for that purpose.

By calculating fluxes using fermentation data, we were able to nearly close the carbon balance of the S. thermophilus model, but were not successful in closing that of L. bulgaricus. The consumed galactose moiety from lactose was much higher (25%) than the secreted galactose, either as galactose monomers or as EPS. With few exceptions (4), L. bulgaricus was reported to be unable to utilize galactose due to the absence of a galT gene (10, 33). Indeed, blasting the galT gene of L. plantarum WCFS1 against the L. bulgaricus ATCC BAA-365 genome showed that this gene is not present. We have not been able to find an explanation for the galactose gap so far. The measured AA secretion by L. bulgaricus did not correspond to that predicted by the model, i.e. on average it was 3 fold higher. Moreover, the ratio between the experimentally measured and the predicted AA secretion differed for a number of AA (i.e. ala, arg, ile, phe and trp). This may have two explanations: (i) L. bulgaricus also grows on free peptides in milk that have a different composition than casein or (ii) the AA content of L. bulgaricus biomass is significantly different from that of *L. plantarum*, of which the AA content was taken as that of L. bulgaricus (30). Explanation (i) is also supported by the growth of S. thermophilus in mono-culture. As this organism is non-proteolytic, auxotroph for histidine, which is present as free AA in a negligible quantity in milk (24 µM), S. thermophilus probably has another source of histidine, such as small peptides present in milk.

The current mixed culture model is not finished yet, but it allows the yoghurt consortium to grown in silico and predicts the type of mutualistic interactions of which we know that they do occur (11, 23, 26). This model fulfills the requirements for a novel class of predictive microbial growth models (35): because it is wholegenome based, it takes into account the interactions between both consortium members and has therefore a much higher molecular resolution than previous models (6, 27). Furthermore, the model can be updated with new information of reactions catalyzed by enzymes in both species and with experimental data, improving the accuracy of the model. At this moment, we propose the inclusion of other fermentation data such as the production of volatile components (the quantity of produced acetaldehyde, diacetyl and acetone by these bacteria is significant (24)) and the quantity of folic acid, produced by S. thermophilus and consumed by L. bulgaricus (7), that is available in the medium. Further improvements may deal with the discrepancies between (i) measured and predicted AA secretion by L. bulgaricus and (ii) the content of casein and the free AA in milk after fermentation. Therefore, the precise AA content of L. bulgaricus and S. thermophilus should be

experimentally determined. Moreover, the presence and AA content of peptides initially present in milk should be studied. Finally, the gap in the carbon balance of *L. bulgaricus* should be fixed, possibly by the identification of other means of galactose metabolism (i.e. a currently unknown galactose utilization pathway) or by measuring more potential end products of primary metabolism. Once these improvements of the mono-culture models and the mixed culture model provide a reliable representation of the fermentation, it should be possible to model the different growth phases of the fermentations, providing predictions of the extent and the nature of the interactions between *S. thermophilus* and *L. bulgaricus*.

It is expected that these models, when elaborated as described above, will be suitable also to predict the performance of this culture in other dairy or non dairy substrates. Furthermore, as sequencing and genome-scale modeling rapidly develop, we anticipate that multi-strain and community genome-scale models will find wider application in research on microbial ecosystems.

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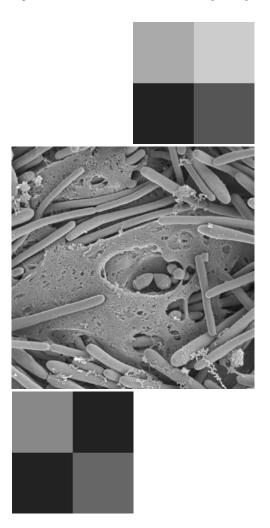
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Chapter 7

Summary, discussion and future perspectives



INTRODUCTION AND SUMMARY

Most microbial ecosystems consist of multiple species. The interactions between consortium members in these systems are at the base of the performances of the individual bacteria. Consequently, in fermentations the interactions between microbes are very important for the culture's performance and the quality of the fermented foods. There is a strong need in industry to improve the efficiency of existing industrial fermentations or to develop more sustainable processes. In addition, the current market trends demand a wider range of healthy fermented foods (20) and the application of strains marketed as probiotics. These trends importance of characterizing the interactions underpin the between microorganisms, not only quantitatively, but also qualitatively by unraveling the underlying molecular mechanisms. This also includes a higher predictability of (the interactions involved in) the final microbial composition of fermentations (42). Moreover, there is considerable interest in the interactions that structure microbial communities from an ecological (29, 36) and evolutionary (36, 37) perspective. Therefore, unraveling the interactions between the microbes in a fermentation is highly relevant from an industrial and a scientific point of view.

A well-studied fermentation is the one carried out by the lactic acid bacteria (LAB) Streptococcus thermophilus and Lactobacillus delbrueckii subsp. bulgaricus. The combined action of these two bacteria turns milk into yoghurt. It has been recognized in the first half of the 20th century that these two LAB stimulate each other in growth and acid production when co-cultivated (49). This mutual stimulation is also referred to as protocooperation. The basis behind this protocooperation has partly been unraveled in the last six decades. It was shown that S. thermophilus stimulates L. bulgaricus by supplying formic acid (16), folic acid (9, 59) and CO₂ (18), all involved in purine metabolism. L. bulgaricus, in turn, provides S. thermophilus with peptides and amino acids (AA) released from milk casein with its exoprotease PrtB (8). With the classical microbiological methods that were available until the 1980's, it was not possible to further unravel the molecular basis behind these interactions. However, the availability of genome sequences of these bacteria and of ~omics tools the last decade meant a breakthrough in interaction research (26, 38). A number of post-genomic studies of the yoghurt fermentation revealed the involvement of sulfur AA, branched-chain AA (BCAA) specifically in the protocooperation between S. thermophilus and L. bulgaricus (33, 34). The research described in this thesis aimed at further unraveling the interactions between these two species using an integrated approach of classical and novel techniques and methodologies. As these novel techniques are based on ~omics approaches, two sequenced strains, namely S. thermophilus CNRZ1066 and L. bulgaricus ATCC BAA-365, were used in all studies. Chapter 1 gave a general introduction to the subject and briefly discussed the novel techniques that were used in this thesis research, i.e. transcription profiling, high-throughput screening and next-generation sequencing. Also experimental evolution and genome-scale metabolic modeling were briefly introduced. Chapter 2 summarized the status of mixed culture research in general and of the yoghurt consortium in more detail. In addition, it described the current trends in the use of ~omics in mixed culture research. Chapter 3 described a tool for rapid assessment of viable counts of microorganisms in (mixed) cultures. This method was used in the research of Chapters 4, 5 and 6. In Chapter 4, a combination of transcriptomics and screening was used to identify the genetic and physiological basis behind the interactions between the two yoghurt bacteria grown in milk (see also the section below). It confirmed that interactions between the yoghurt bacteria are based on the exchange of formic acid, folic acid and AA. Supply of sulfur AA and BCAA through proteolysis was not sufficient to sustain the increased growth in mixed culture, leading to a higher expression of sulfur AA and BCAA production genes in both species. Moreover, it was shown that exopolysaccharide (EPS) synthesis genes were higher expressed in both species in mixed culture and that L. bulgaricus lowered the expression of long-chain fatty acids (LCFA) biosynthesis upon co-culture, possibly due to lipolytic action of S. thermophilus. In Chapter 5, the two sequenced strains of S. thermophilus and L. bulgaricus that that had no history of co-cultivation were co-evolved for ~1000 generations in milk. A detailed analysis of fermentation profiles (e.g. acidification rate), gene expression, and mutations further elucidated the molecular basis behind their protocooperation. Moreover, it was shown that as little as ~1000 generations of co-evolution is sufficient to adapt a relatively slow growing and acidifying mixed culture into one that is comparable to a commercial starter in terms of acidification rate and EPS production. The development of a genomebased mixed culture model of the yoghurt fermentation was discussed in Chapter 6. Although the model is currently still in development, various predictions could be made about the interactions based on the genome content of the two species. Indeed, the predicted interactions included AA metabolism (i.e. proteolysis) and purine metabolism (i.e. formic acid and folic acid), which was already experimentally confirmed in Chapter 4. Using flux balance analysis (FBA), it was possible to determine the effects of the protocooperation on biomass yields on lactose. The biomass yields were found to be significantly improved in the mixed culture compared to the mono-cultures. The general discussion below will elaborate on the findings in this thesis, place these in a wider context and discuss the future perspectives of this thesis research.

IMPROVED UNDERSTANDING OF THE YOGHURT CONSORTIUM USING ~OMICS TECHNOLOGIES AND MODELING

We have successfully applied mixed culture gene expression studies and genomebased metabolic modeling on the yoghurt consortium in order to identify genes and pathways that play a role in the interactions during, or are affected by, co-culture growth. In Chapter 4, the effect of adding specific components, expected to influence the interactions, on the growth and acidification of mono-cultures and mixed cultures were studied. The results were combined with results of transcription profiling studies of both bacteria during the fermentation. By using this combined approach we were able to identify (i) the effects of the single compounds on the performance of both species in milk, and (ii) which pathways were differently expressed in both species in mixed cultures compared to the mono-cultures. This confirmed the involvement of purine and AA in the interactions as was also found in a recent transcriptome study on S. thermophilus by Hervé-Jimenez et al. (33). Moreover, a role for LCFA metabolism and peptidolysis was found in the interactions, and the genes for iron metabolism in S. thermophilus and EPS biosynthesis in both species were shown to be affected by the interactions (see Figure 1 and below).

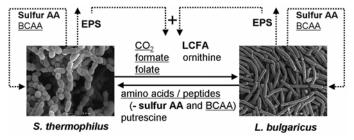


Figure 1. Schematic representation of the mutualistic interactions between *S. thermophilus* and *L. bulgaricus* in yoghurt. Solid arrows indicate interactions; dotted arrows indicate pathways that are affected by the interactions. Pathways that were for the first time shown to be regulated at the transcriptome level upon co-culture are indicated in bold. Pathways that were confirmed in our study to be regulated at the transcriptome level upon co-culture are underlined. EPS is hypothesized to promote the exchange of both bacteria. There was no evidence at the transcriptome level for the exchange of putrescine and ornithine. AA, amino acids; BCAA, branched-chain AA; EPS, exopolysaccharides; LCFA, long-chain fatty acids.

Long-chain fatty acids acquisition by L. bulgaricus. It was shown that L. bulgaricus lowered the expression of LCFA biosynthesis genes (i.e. those coding for decarboxylases, hydrolases, oxidoreductases and acyltransferases) in mixed culture. The last step in the phosphatidic acid synthesis from acyl-carrier proteins containing the fatty acid chains was higher expressed in mixed than in monoculture. Although LCFA such as lauric acid and oleic acid had previously been reported to stimulate the growth of L. bulgaricus (47), no attempts have been made to link this to the protocooperation between the yoghurt bacteria. In an earlier study, several genes involved in fatty acid production (fabH, accC and fabl) were higher expressed in L. bulgaricus as an adaptation to an acidic (pH 4.2) environment (23). However, these genes (LBUL_0822, LBUL_0829 and LBUL_0828 in L. bulgaricus ATCC BAA-365, respectively) were 3-10-fold lower expressed in mixed culture compared to mono-culture despite the lower pH. This suggests that the acyl-carrier proteins were loaded with fatty acid chains from another source, for instance fatty acids liberated from milk fat by the lipolytic action of S. thermophilus (53). It is not clear how these fatty acids are taken up by L. bulgaricus, but evidently this species is capable of utilizing fatty acids from the medium (47). Possibly, this role is executed by the so far uncharacterized LBUL_0063 identified in Chapter 5. The S. thermophilus genome encodes multiple lipolytic enzymes (3, 25, 39) that also play a role in the flavor formation (48).

Branched-chain and sulfur amino acids. It was stated in Chapter 4 that the proteolytic activity of L. bulgaricus does not supply a sufficient amount of BCAA leading to a higher expression of *de novo* synthesis of this pathway in both species. This is notably the case for the BCAA transaminase (LBUL_1219 and str0590) responsible for the formation of valine, leucine and isoleucine from 3-4-methyl-2-oxopentanoate and methyl-2oxobutanoate, (S)-3-methyl-2oxopentanoate, respectively. This is most likely due to the high abundance of valine, leucine and isoleucine in the total proteomes of S. thermophilus (33) and L. bulgaricus (GenomeAtlas database (30)). Moreover, the pathways for sulfur AA biosynthesis were upregulated in both species when grown in a mixed culture. This may be due to the low amount of sulfur AA in casein (cysteine 0.35% and methionine 2.9%) (58) that becomes available during proteolysis of milk compared to that of the proteome of S. thermophilus and L. bulgaricus (cysteine ~1% and methionine ~2%). Indeed, the measured levels of free cysteine and methionine were very low. In addition, it was previously reported based on a transcription profiling approach with a S. thermophilus mono-culture that sulfur AA limitation is likely to occur, particularly in the later stages of fermentation, and that this also occurs in mixed culture (34).

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Exopolysaccharide biosynthesis. EPS is mainly synthesized in the later phases of fermentation (4). Although there has not been assigned an evident function for EPS in yoghurt, it is possible that EPS plays a role in acid resistance (45) or in facilitating exchange of metabolites by allowing stable close proximities or even physical contact between the two species, which is likely also the function of EPS in kefir (6, 7). In addition, the combination of different EPS-producing strains of S. thermophilus was shown to stimulate total EPS production in mixed culture (14, 24). However, these observations had not yet been linked to gene expression. Interestingly, in Chapter 4 it was shown that the expression of EPS biosynthesis genes in both species was increased during growth in mixed culture. Furthermore, this was confirmed in a transcription profiling study of mixed culture biofilms, suggesting that this effect is generic. Basically, there were two reasons to choose for biofilm growth to confirm this effect: (i) when grown in biofilms, there is a forced physical contact between S. thermophilus and L. bulgaricus strengthening potential interactions; (ii) biofilms are relatively well accessible for analytical techniques such as staining and microscopy compared to liquid cultures (see also Chapter 4). Indeed, the mixed culture biofilm showed a stronger staining by Wheat-Germ Agglutin, a lectin that is commonly used for staining polysaccharides, than the mono-culture biofilm (31). In fact, the EPS concentrations after 24 h culturing at 42°C increased from 0.80±0.02 g/L in a S. thermophilus mono-culture and 1.18±0.12 g/L in a L. bulgaricus mono-culture to 1.46±0.04 g/L in the mixed culture. In the cultures with the evolved strains from Chapter 5 this was 1.35±0.26 g/L, 1.52±0.03 g/L and 3.91±0.48 g/L, respectively. This all underpins the importance of EPS for the bacteria, especially in mixed culture.

Mixed culture metabolic modeling. In Chapter 6, the development of a mixed culture metabolic model, which was based on the genome content of both species, was presented. It confirmed that the interactions were based on the exchange of formic acid, folic acid and on AA metabolism. By measuring the biomass and EPS production and by determining the fluxes of lactose and fermentation products, it was possible to calculate the yield of biomass on lactose. This was substantially higher (2.3-2.9 fold) in the mixed culture than in the corresponding mono-cultures, which can be explained by a lower EPS production per g of total biomass and by the benefits of the interactions. In the model, these benefits included less spilling of AA. That means that *S. thermophilus* consumed a part of the AA that were released by proteolysis and peptidolysis by *L. bulgaricus*, i.e. *L. bulgaricus* consumed all the released peptides and secreted all AA, except the one that was limiting growth. Subsequently, *S. thermophilus* could consume these AA in stead of synthesizing them itself, saving energy and thus lactose.

However, in the mixed culture transcriptome study (Chapter 4), it was shown that *S. thermophilus* in mixed culture mainly upregulates peptide transporters and peptidases in stead of AA transporters. In addition, the carbon balance of *L. bulgaricus* was not closed: around 25% of the consumed galactose moiety in lactose could not be found as secreted galactose monomers or in EPS. Due to the absence of a *galT* gene (10, 32).*L. bulgaricus* can not utilize galactose (27, 60). These two discrepancies should still be dealt with in order to make the mixed culture model sufficiently predictive.

In conclusion, there is strong evidence from various studies (physiological, transcription profiling, experimental evolution and genome-scale metabolic modeling) that the interactions between *S. thermophilus* and *L. bulgaricus* are based on the exchange of various growth factors provided by *S. thermophilus*, proteolysis (executed by *L. bulgaricus*) and lipolysis (executed by *S. thermophilus*). The growth factors provided by *S. thermophilus* are related to purine and AA biosynthesis: formic acid, folic acid and CO_2 (the latter is not discussed here, see Chapter 4). In addition, there is a potential role for EPS in facilitating these nutritional exchanges (see Figure 1). There was no evidence for the exchange of ornithine and putrescine as suggested by Van de Guchte *et al.* (62), but it can not be excluded if any benefits resulting from their exchange do not lead to evident differential gene expression or increased growth.

EXPERIMENTAL EVOLUTION IMPROVES KEY CHARACTERISTICS OF YOGHURT PRODUCTION REPRODUCIBLY

In Chapter 5, experimental evolution has proven to be a useful methodology for the optimization of mixed culture fermentations. For the development of novel industrial starters, or for the improvement of existing ones, it is definitely worthwhile to investigate the possibilities of experimental evolution. In this thesis research, a relatively slow growing and acidifying mixed culture (i.e. *S. thermophilus* CNRZ1066 and *L. bulgaricus* ATCC BAA-365) was turned into one that can meet with commercial starters in the course of ~1000 generations of co-culture. The acidification rate increased step-wise (see Figure 1 in Chapter 5) caused by the accumulation of rare beneficial mutations (21, 35). The acidification rate of the evolved mixed culture was closer to that of the commercial starter yoghurt culture I-St than to its own parental mixed culture. Moreover, the efficiency of biomass production increased from 0.12 g/mol consumed lactose in the parental culture to 0.22 g/mol in the evolved culture (this is 0.30 g/mol for the commercial culture I-St)

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during exponential growth. That indicates that either the metabolism of the evolved organisms compared to their parental strains had become more efficient, or that the interactions between the two species improved making the evolved mixed culture more efficient than the original mixed culture. The flux balance analysis in Chapter 6 and the improved stimulation of parental strains by evolved strains suggest that both instances occurred.

The amount of produced EPS in 24 h more than doubled from 1.46 g/L by the parental mixed culture to 3.91 g/L by the evolved mixed culture (see also above). This was also reflected in the culture's viscosity, which also increased by a factor of 2.6-2.8. The viscosity of the evolved culture was comparable to – or even higher than – that of the commercial starter composed of *S. thermophilus* Sts and *L. bulgaricus* lb. This higher production of EPS was related to the higher expression of EPS biosynthesis genes, notably in *S. thermophilus*. Interestingly, the increase in EPS production, visualized in biofilms, also occurred step-wise (see Figure 2), indicating that the higher production is not solely due to the higher quantity of cells in the evolved culture. Unfortunately, no mutation was found that clearly indicates the cause of this higher EPS production in evolved strains compared to their parental strains.

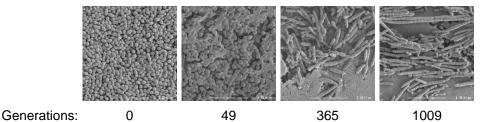


Figure 2. SEM images of *S. thermophilus* cells grown as mono-culture biofilms in the course of evolution. Single colony isolates were selected from the evolving culture and grown on anopore as mono-culture before imaging. The increasing extracellular matrix is assumed to be EPS (see Chapter 4).

It appears to be not a coincidence that specifically these improvements (faster acidification, more growth and more EPS production) occur during experimental evolution with the strict growth regime discussed in Chapter 5. A second culture of *S. thermophilus* and *L. bulgaricus* that had undergone the same process also showed a higher acidification rate and a higher viscosity. It was shown that this second evolved *S. thermophilus* had mutations compared to the parental strains in three of the same sites. Gene expression studies showed upregulation of the same pathways as the strains from the other evolved culture. This is by itself not very

surprising as the optimization strategies of comparable cultures in the same ecological conditions are likely to be similar (55, 63). Interestingly, the gene expression study showed that in particular pathways involved in folic acid (*L. bulgaricus*), sulfur AA, BCAA, LCFA (*L. bulgaricus*) and EPS were differentially expressed between the evolved and parental strains. This indicates the fine-tuning of interactions in order to maximize growth in both species.

Novel types of mixed cultures show similar improvements. The experimental evolution procedures (Chapter 5) were also applied to uncommon species combinations containing the probiotic *Lactobacillus plantarum*. Previously, it had been shown that growth of some *L. plantarum* strains was stimulated by *L. bulgaricus*, but there was no stimulation of yoghurt bacteria by *L. plantarum* (12). All possible two-species and three-species combinations of *S. thermophilus, L. bulgaricus* and five different *L. plantarum* strains were prepared (see Table 1). The two strains that probably have a higher number of IS elements (61) were assumed to have a potentially higher mutation rate and a correspondingly faster adaptation.

The step-wise increase in acidification rate reported for the two evolved yoghurt cultures was also evident in all five evolved cultures consisting of *S. thermophilus* and *L. plantarum* and the five three-species cultures (see Figure 3). It did not occur in any of the evolved cultures consisting of *L. bulgaricus* and *L. plantarum*. This implies that the step-wise increases in acidification rates were caused by mutations in *S. thermophilus* (13).

Table 1. The five L. plantarum strains that were co-evolved for ~1000 generations in milk with S.
thermophilus CNRZ1066, L. bulgaricus ATCC BAA-365, or both. The rationale behind their use is stated
at the right. The strains were obtained from NIZO food research, the Netherlands.

L. plantarum strain	Rationale
WCFS1	Reference strain with sequenced genome
LMG9208 (NIZO 2806)	Relative good growth in milk
BLL(EI31) (NIZO 2830)	Relative good growth in milk
SECT4645 (NIZO 2776)	High number of IS elements (61)
NCTH19-1 (NIZO 2484)	High number of IS elements (61)

As expected, all five *L. plantarum* strains remained stable in co-cultures with *L. bulgaricus*. In the cultures containing *S. thermophilus* and *L. plantarum*, only the strains SECT4645 and NCTH19-1 were outcompeted within five transfers. That was due to their slow growth rate compared to the other three *L. plantarum* strains. When serial transfers were applied every other day, *L. plantarum* SECT4645 and NCTH19-1 stayed at a constant level in combination with *S. thermophilus*. In all three-species cultures, *L. plantarum* was present for at least 800 generations.

However, in the course of evolution, the amount of viable *L. plantarum* cells decreased in all five cultures. Strains WCFS1, LMG9208 and NCTH19-1 were below the detection limit ($\sim 10^3$ /mL) after ~800 generations. This was associated with the step-wise increase in acidification rate, indicating that the rapid (lactic) acid production by *S. thermophilus* and *L. bulgaricus* inhibited growth of *L. plantarum*. Indeed, a pH below 6 and the presence of lactic acid impede optimal growth of *L. plantarum* (28), leading to fewer cells at each transfer despite any stimulatory effects of the yoghurt bacteria.

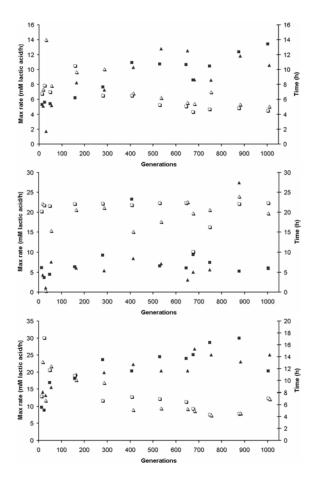


Figure 3. Maximal acidification rate $(\Delta \text{lactic acid}/\Delta t)$ ($\blacksquare, \blacktriangle$) and the time necessary to reach this maximal rate (\Box, Δ) of three different cultures in duplicate in the course of evolution. Squares and rectangles represent two duplicate evolving cultures. Acidification was measured in 10 mL milk at 37°C as described before (56). Top, a mixed culture of S. thermophilus and L. plantarum; middle, a mixed culture of L. bulgaricus and L. plantarum; bottom, a three-species mixed culture.

Above-mentioned results signify two main conclusions. (i) The high reproducibility of experimental evolution of these mixed cultures indicates that experimental evolution procedures can very well be applied to adapt other unfamiliar strain combinations to each other and to their environment. The highly reproducible outcome of experimental evolution had also been found for monocultures of *Escherichia coli* cells grown under a strict regime (63), supporting this conclusion. (ii) Although interactions between yoghurt bacteria also promote growth of other (probiotic) species, the interactions within new species combinations do not necessarily strengthen to form a well-performing stable mixed culture. That means that it may be necessary to rationally introduce nutritional dependencies in advance in order to stably include probiotics at a reasonable level $(10^5-10^8 \text{ per}$ gram of product (44)) in existing relatively optimal fermentations such as the yoghurt fermentation (10, 32) (see below). However, this is the case for *L. plantarum* and may not necessarily apply to other newly included species that already display mutually synergistic interactions. Moreover, the addition of probiotic species or strains in suboptimal systems, such as a combination with either *S. thermophilus* or *L. bulgaricus*, is more likely to succeed as there is much more room for improvement and the development of interdependencies (22, 51).

As discussed, in order to include probiotics in existing optimized mixed culture fermentations, rationally engineering of interactions may be necessary. Therefore, it is not only from a scientific but also from an industrial point of view relevant to identify the exact modes of interaction and their underlying molecular mechanisms in the current mixed cultures. Once the engineering of interactions between an endogenous species and the probiotic species has been performed, experimental evolution can be applied to optimize these new interactions and stabilize the new mixed culture. The high reproducibility of experimental evolution indicates that the outcome can – at least in part – be predicted based on the new (environmental) conditions the microorganisms find themselves in (15). The structure of the environment and the conditions used for the fermentations are therefore important considerations when applying experimental evolution (22, 51, 54).

EVALUATION OF THE USED MODERN TECHNOLOGIES

Transcription analysis with mixed culture microarrays.

The face of transcription analysis has changed rapidly the past decade with the use of whole-genome analysis tools such as microarrays. Currently, there are many studies where microarrays containing probes targeting different species are used. Examples include the use of metatranscriptomics in the field of metagenomics such as in environmental microbial communities and fermented food products (46). Microarrays have also been used before to differentiate between different *Bifidobacterium* species in the intestine (2) and to study gene

expression of one species in a mixed culture (33, 43). The use of microarrays targeting the whole genomes of both species in a food fermentation is novel. It is not trivial as the probes in the microarrays should be selective (see Chapter 4): the target gene in one of the species may be very similar to its orthologue in the other species, especially when closely related species are used. Moreover, the efficacy of the applied extraction method is essential for the quality of the extracted RNA (52). That is, one has to ensure that the method works equally efficient for both bacteria in order to circumvent a bias in the normalization of gene expression data if the hybridized cDNA of one species is overrepresented compared to that of the other species. This problem can be avoided by using next-generation sequencing of cDNA in stead of microarrays as discussed in (40), but this method is still in development.

Next-generation sequencing.

In Chapter 5, Illumina Solexa sequencing was used to identify mutations in the evolved strains of *S. thermophilus* and *L. bulgaricus* compared to their parental strains. The alignment of data is not trivial. Issues regarding local low coverage and repeatedly occurring sequences have been discussed in Chapter 1. Moreover, the choice of cut-offs is and the alignment method(s) applied are important factors in the reliability of the results (17, 57). We applied different alignment methods and filtered their results with a stringent cut-off for the quality score (see Chapter 5), providing the possibility to find substitutions as well as (one base and larger) insertions or deletions. Solexa sequencing has indeed proven to be a good method for the detection of mutations.

Mixed culture metabolic modeling.

Considering the rapid increase in papers discussing genome-scale metabolic modeling (no Pubmed hits before 2002, 25 in 2008 and 25 until July 1, 2009), there is a great and growing interest in this topic. That is not an odd development as such models provide a solid interpretative framework for experimental data related to gene content and metabolic state of the microorganism (19). Coupling two of these models in order to identify possible modes of interaction and their effects on both bacteria is a novel application. It is expected that the inadequacies of the current mixed culture model discussed above and in Chapter 6 can be settled in the near future.

CONCLUDING REMARKS AND FUTURE PERSPECTIVES

This thesis research has provided novel insights in the protocooperation between *S. thermophilus* and *L. bulgaricus*, in particular in the molecular base behind these interactions (see Figure 1). It has not been shown before that EPS biosynthesis genes were induced in mixed culture in both species and that EPS production increased in the course of mixed culture experimental evolution. This strongly suggests that EPS has a function in the interactions, but the details of this function remain to be elucidated. Similarly, a novel finding is that genes coding for LCFA production in *L. bulgaricus* were lower expressed in mixed culture despite the higher use of LCFA to sustain a higher growth rate. It was suggested that lipolysis executed by *S. thermophilus* provides here a novel mode of interaction, but hard experimental evidence to confirm that still has to come. The gene *LBUL_0063* is a good target to start with.

The extensive list of interactions based on nutritional exchanges indicates the complexity that can occur in a relatively simple (in terms of members involved) microbial community such as the yoghurt consortium. However, the interactions in this system are indicative for the types of interaction that can be expected in other mixed culture ecosystems. Experimental evolution (Chapter 5) and mixed culture modeling (Chapter 6) showed the extent of the benefits that microorganisms can achieve by cross-feeding in terms of increased growth rate and efficiency of metabolism. Indeed, there are numerous examples of cross-feeding interactions in the microbial world (5). In conclusion, nutritional interdependencies like in the yoghurt consortium are ubiquitous and likely structure and stabilize many different ecosystems (1, 11, 50). The post genomic approaches applied in this thesis have increased our understanding of this classic mixed culture fermentation process. Suggested further research might start with improving the annotation of the genomes, i.e. 32% of the COGs in S. thermophilus CNRZ1066 are not or poorly annotated (3); in L. bulgaricus ATCC BAA-365 this is 38% (41). The galactose sink and the production of formic acid by L. bulgaricus discussed in Chapter 6 clearly indicate that there are metabolic pathways operational for which the corresponding genes and proteins remain to be identified. Therefore, the mixed culture model will be elaborated in the near future as discussed.

How can we apply the used methods in future research? The rapid plating method discussed in Chapter 3 can be implemented easily for any type of microbiological work that requires the assessment of large numbers of colonies. For this, there is no need for special equipment. Furthermore, it reduces the use of consumables and the concomitant production of waste by a factor 100 compared to conventional

Chapter 7

plating, which is becoming increasingly important in this era of environmental problems. The mixed culture microarrays can be used to evaluate the molecular responses of both yoghurt consortium members to various environmental factors. For example, the responses to supplementation of fatty acids to a yoghurt culture growing in fat-free milk may confirm the suggestion of lipolysis playing a role in the interactions. Moreover, by using transcription profiling of other strains, it will be possible to identify whether responses associated with co-culture are similar in other strain combinations.

Currently, most industrial mixed culture starters are selected by screening combinations of strains for desired properties. Given the results in this thesis, it is anticipated that directed experimental evolution of mixed cultures containing interesting strains or species, such as probiotics, can allow the production of industrially relevant starters that would not be selected otherwise. In addition, the new insights in the yoghurt consortium interactions provide targets for the rational development or optimization of stable mixed cultures, e.g. by introducing similar mutual dependencies in other mixed cultures. In the near future, the work described in this thesis will (i) improve research techniques in other mixed culture studies such as in kefir or cheese, (ii) lead a further increase in knowledge on the yoghurt consortium by providing novel targets for additional research, and (iii) facilitate (food) industry to develop new or improved fermented products with desired properties.

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Nederlandse samenvatting

Melkzuurbacteriën zijn een groep Grampositieve bacteriën die suikers zoals lactose fermenteren en daarbij hoofdzakelijk melkzuur produceren. Het is een groep van industrieel belangrijke micro-organismen, die worden toegepast voor de productie van veel gefermenteerd voedsel. Dit omvat zowel voedingsmiddelen van plantaardige origine (b.v. zuurkool en wijn) als van dierlijke origine (b.v. worst en zuivelproducten zoals yoghurt). De huidige tendensen in de voedselmarkt, zoals de toename van duurzame en gezondheidsbevorderende producten, vragen efficiëntere en meer verschillende fermentaties. De meeste fermentaties worden uitgevoerd door combinaties van verschillende soorten micro-organismen. De interactie tussen consortiumleden zijn belangrijk voor de prestaties van de individuele micro-organismen binnen een microbieel ecosysteem, en daarmee ook van de gehele fermentatie. Deze microbiële interacties zijn vaak slecht begrepen. Streptococcus thermophilus en Lactobacillus delbrueckii subsp. bulgaricus zijn twee melkzuurbacteriesoorten die middels fermentatie (koeien-) melk in yoghurt omzetten. Deze twee bacteriën stimuleren elkaars groei en zuurproductie. Zij produceren exopolysacchariden, belangrijk voor de textuur van yoghurt, en kenmerkende aromaverbindingen zoals acetaldehyde en diacetyl. De moleculaire basis van de mutualistische interactie tussen deze twee bacteriën was nog niet goed bekend.

In dit promotieonderzoek werd een combinatie gebruikt van screening, mengcultuur transcriptoomanalyse, genoomwijde metabolische modellering, experimentele evolutie en next-generation sequencen. Dit werd gedaan om de moleculaire basis van de interactie tussen S. thermophilus en L. bulgaricus in melk te ontrafelen. De resultaten toonden aan dat de interactie hoofdzakelijk was gebaseerd op de uitwisseling van metabolieten. Bovendien werd getoond welke genen/pathways werden beïnvloed door de interacties. Er was bewijs gevonden dat S. thermophilus L. bulgaricus mierenzuur, foliumzuur (allebei betrokken bij met purinemetabolisme), lange-keten vetzuren (door de actie van lipolytische enzymen om melkvet af te breken) en CO₂ verschafte. De proteolyse door de exoprotease van L. bulgaricus verschafte beide soorten peptiden, die door de cel kunnen worden opgenomen en vervolgens tot aminozuren worden afgebroken door intracellulaire peptidases. Dit zorgde echter niet voor voldoende beschikbaarheid van valine, leucine, isoleucine en zwavelhoudende aminozuren, wat bleek uit een hogere expressie van biosynthese genen voor deze aminozuren in beide soorten in mengcultuur. Daarnaast waren ook de biosynthesegenen voor exopolysacchariden hoger tot expressie gebracht in gemengde cultuur, wat tot meer productie van exopolysacchariden en een hogere viscositeit van de yoghurt leidde.

Een genoomwijd metabolisch model van de mengcultuur bevestigde dat de interacties tussen de yoghurtbacteriën waren gebaseerd op het purine en het aminozuur metabolisme. Daarnaast werd dit model gebruikt om aan te tonen dat de interactie een significant voordeel aan beide bacteriën opleverde, d.w.z. hun opbrengst van biomassa op lactose was ongeveer 50% hoger in mengcultuur.

Experimentele evolutie onthulde dat het mogelijk is om een nieuwe combinatie van *S. thermophilus* en *L. bulgaricus* stammen aan elkaar aan te passen. Het bleek dat hun wederzijdse stimulatie versterkte door hun interactie te optimaliseren middels het fine-tunen van pathways die betrokken zijn bij de interactie. Slechts ~1000 generaties samen kweken volstond om de relatief slecht groeiende mengcultuur te veranderen in één die vergelijkbaar was met een commerciële cultuur in zeer belangrijke kenmerken zoals verzuringsnelheid en viscositeit.

Het betere begrip van de interacties die ten grondslag liggen aan de yoghurtfermentatie geven ons doelwitten voor de rationele optimalisering van bestaande mengcultuurfermentaties en de rationele ontwikkeling van nieuwe industrieel relevante mengculturen, zoals die met probiotica. Bovendien zijn de resultaten in het bijzonder interessant voor het onderzoeksgebied van microbiële ecologie aangezien zij tonen hoe de wederzijdse interacties evolueren en de microbiële samenstelling van dit ecosysteem structureren.

List of publications

Genomics and high-throughput screening approaches for optimal flavour production in dairy fermentation. 2008. Margreet I. Pastink[#], <u>Sander Sieuwerts</u>[#], Frank A.M. de Bok, Patrick W.M. Janssen, Bas Teusink, Johan E.T. van Hylckama Vlieg, Jeroen Hugenholtz. *International Dairy Journal* 18:781-789. [#]These authors contributed equally to this work

A simple and fast method for determining colony forming units. 2008. <u>Sander Sieuwerts</u>, Frank A.M. de Bok, Erik Mols, Willem M. de Vos and Johan E.T. van Hylckama Vlieg. *Letters in applied Microbiology* 47(4):275-278

Unraveling microbial interactions in food fermentations; from classical to genomics approaches. 2008. <u>Sander Sieuwerts</u>, Frank A.M. de Bok, Douwe Molenaar, Jeroen Hugenholtz and Johan E.T. van Hylckama Vlieg. *Applied and Environmental Microbiology* 74(16):4997-5007

Effect of amino acid availability on Vitamin B12 production in *Lactobacillus reuteri*. 2009. Filipe B. Santos, Douwe Molenaar, Bas Teusink, Maurice van Heck, <u>Sander Sieuwerts</u>, Willem M. de Vos and Jeroen Hugenholtz. *Applied and Environmental Microbiology* 75(12):3930-3936

Mixed culture transcriptome analysis reveals the molecular basis of co-culture growth and its consequences in *Streptococcus thermophilus* and *Lactobacillus bulgaricus*. <u>Sander</u> <u>Sieuwerts</u>, Douwe Molenaar, Sacha A.F.T. van Hijum, Colin J. Ingham, Marke Beerthuyzen, Marc J.A. Stevens, Patrick W.M. Janssen, Frank A.M. de Bok, Willem M. de Vos and Johan E.T. van Hylckama Vlieg. *Manuscript submitted for publication.*

Experimental evolution of yoghurt cultures improves co-culture growth and interactions. <u>Sander Sieuwerts</u>, Frank A.M. de Bok, Colin J. Ingham, Marke Beerthuyzen, Sacha A.F.T. van Hijum, Douwe Molenaar, P.M. (Ellen) Slegers, Elisabeth H. Tolls, Willem M. de Vos and Johan E.T. van Hylckama Vlieg. *Manuscript in preparation.*

A genome-scale metabolic model of mixed culture growth of *S. thermophilus* and *L. bulgaricus*. <u>Sander Sieuwerts</u>, Johan E.T. van Hylckama Vlieg, Willem M. de Vos and Bas Teusink. *Manuscript in preparation*.

Volatile compound fingerprinting of mixed culture fermentations. Frank A.M. de Bok, Patrick W.M. Janssen, Juma Bayjanov, <u>Sander Sieuwerts</u>, Arjen Lommen, Johan E.T. van Hylckama Vlieg and Douwe Molenaar. *Manuscript in preparation.*

Combinatorial screening of mixed cultures of lactic acid bacteria in milk and soymilk. Frank A.M. de Bok, Patrick W.M. Janssen, <u>Sander Sieuwerts</u>, Douwe Molenaar, Johan E.T. van Hylckama Vlieg. *Manuscript in preparation.*

Hoe yoghurtbacteriën samenwerken aan een gezonde en lekkere voeding. 2009. <u>Sander</u> <u>Sieuwerts</u>, Eddy J. Smid, Jeroen A. Wouters and Frank A.M. de Bok. *VMT* 20.

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There are many other people that I worked with or at least enjoyed their presence at work and/or outside work hours. It would simply double the size of my thesis if I was to write a short note of them all separately. I will therefore only briefly mention some highlights; the people involved will know it is about them. I really enjoyed the C-015 team and in particular the collaborations I had with some of them. I think the thesis research would not be so complete without your contributions. That also counts for the 'computer guys' BT, DM, MW and SvH that helped me with the more advanced bioinformatics. Moreover, I think that working wouldn't have been so pleasant without the people in the Kluyver lab (not to be confused with Kluyver Centre) and the office. We have had some good laughs, especially at the Friday afternoons. Similarly, I enjoyed the great discussions we sometimes started when I actually came for one small question. Though I saw the basement-people

on a less regular basis, I definitely feel that they've been an enrichment to my stay at Nizo as well.

As a PhD student sometimes you get a bit (well... a bit) fed-up with all the practical work and you want to do something else. Fortunately, I had three excellent students KZ, ES and ET coming to the rescue. They continued the practical work giving me time to write and attend conferences and courses. Thank you! Similarly, it was good to spend some time with other people during teaching, for instance (KH, SP, JS, LB and MG). And I am sure that I would have thrown my computer, a centrifuge or something else expensive through the window if I did not cool down talking to BvdB or MP. As I sill have to work at Nizo for two more years, I am very grateful for their excellent listening skills.

Not so much involved in my work and currently far away, there were some people important in my personal life. AC, GF and MdV, you were worthwhile to spend the scarce free time with these last four years. I must say that *I still miss you; Ancora lo manco; ik mis je nog.*

Last but definitely not least, I want to give special thanks to my two paranymphs PJ and FdB. I think you are two of the few people that know me quite well and I am delighted that you are willing to put on your suits for the special occasion of my thesis defense.

Well, that's it for so far. If you still would like to be mentioned in particular, please fill in the following line: Dear , you are the best and therefore I want to thank you for

Sander

Curriculum Vitae

Sander Sieuwerts was born at March 8, 1982 in Zoetermeer, the same city as he lived the first 23 years of his life. There he followed primary and secondary school as most other kids. At secondary school Sander followed preparatory scientific education (VWO) with mainly science subjects. Although he had always been a person that likes nature very much, it was there that he decided to study biology and focus on molecular biology. In 2000, Sander started his MSc (doctoraal) studies at Leiden University, which he managed to finish in March 2005. During these studies he performed three internships in plant physiology (TNO-TPW, Leiden), fungal genetics (DSM-DFS-GEN, Delft) and plant genetics (Leiden University). Although plants stayed important in his personal life, Sander considered microorganisms more fun to work with. He was excited when he was offered the position of PhD student in project C-015 (Biodiversity and mixed cultures) at WCFS (the former TI Food and Nutrition). In March 2005, he started working for four years at NIZO food research under supervision of Johan van Hylckama Vlieg as primary supervisor and Willem de Vos as promotor. The results of this fundamental yet applied research are described in this thesis. After a short but very welcome holiday, Sander started working as a postdoc for the Kluyver Centre for Industrial fermentation on a research topic closely related to his thesis research: interactions between (lactic acid) bacteria and yeasts.



Overview of completed training activities

Discipline specific activities

- Principles of ~omics data analysis, EPS/NBIC, 2005
- Food fermentation, VLAG, 2008
- Stralingshygiëne, VLAG/Larenstein, 2005
- SRS/BLAST/ClustalW, CMBI, 2006
- Protein sequence analysis, CMBI, 2006
- Applied genomics of industrial microorganisms (incl. poster presentation), BODL/Kluyver, 2006
- Genetics and physiology of food associated microorganisms, VLAG, 2007
- NIZO dairy conference (incl. poster presentation and oral presentation), Arnhem, 2007
- Kluyver centre symposium 08 (incl. poster presentation), Egmond aan Zee, 2008
- 9th International symposium on lactic acid bacteria (incl. poster presentation), Egmond aan Zee, 2008
- Kluyver centre symposium fall 08 (incl. oral presentation), Wageningen, 2008
- Kluyver centre symposium 09 (incl. poster presentation), Egmond aan Zee, 2009
- International dairy federation Science and technology week (incl. oral presentation), Rennes, France, 2009

General courses

- PhD scientific writing, CENTA, 2005
- PhD presentation skills, CENTA, 2006
- Assisting in undergraduate microbial physiology practical, 2007/8
- MSc course Didactiek en communicatie (ECS-20806), ECS, 2008

Other activities

- Preparation of PhD thesis research proposal, 2005
- PhD VLAG week, VLAG, 2006
- WE-days WCFS/TIFN (Programme 3 Microbial functionality and safety), 2005-8
- Organisation of Programme 3 WCFS Fall WE-days, Koudum, 2007
- Project meetings Biodiversity and mixed cultures, 2005-9
- Bio-IT meetings WCFS/TIFN, 2005-8
- Schoolpracticum (ECS-31306), ECS, 2008

