The complete genome of the hyperthermophilic bacterium Aquifex aeolicus

Gerard Deckert*†, Patrick V. Warren*†, Terry Gaasterland‡, William G. Young*, Anna L. Lenox*, David E. Graham§, Ross Overbeek‡, Marjory A. Snead*, Martin Keller*, Monette Aujay*, Robert Huberl, Robert A. Feldman*, Jay M. Short*, Gary J. Olsen§ & Ronald V. Swanson*

* Diversa Corporation, 10665 Sorrento Valley Road, San Diego, California 92121, USA

‡ Mathematics and Computer Science Division, Argonne National Laboratory, Argonne, Illinois 60439, USA

§ Department of Microbiology, University of Illinois, Urbana, Illinois 61801, USA

Lehrstuhl für Mikrobiologie, Universität Regensburg W-8400, Regensburg W-8400, Germany

Aquifex aeolicus was one of the earliest diverging, and is one of the most thermophilic, bacteria known. It can grow on hydrogen, oxygen, carbon dioxide, and mineral salts. The complex metabolic machinery needed for *A. aeolicus* to function as a chemolithoautotroph (an organism which uses an inorganic carbon source for biosynthesis and an inorganic chemical energy source) is encoded within a genome that is only one-third the size of the *E. coli* genome. Metabolic flexibility seems to be reduced as a result of the limited genome size. The use of oxygen (albeit at very low concentrations) as an electron acceptor is allowed by the presence of a complex respiratory apparatus. Although this organism grows at 95 °C, the extreme thermal limit of the Bacteria, only a few specific indications of thermophily are apparent from the genome. Here we describe the complete genome sequence of 1,551,335 base pairs of this evolutionarily and physiologically interesting organism.

Complete genome sequences have been determined for a number of organisms, including Archaea¹, Bacteria²⁻⁷, and Eukarya⁸. Here we present and explore the genome sequence of *Aquifex aeolicus*. With growth-temperature maxima near 95 °C, *Aquifex pyrophilus* and *A. aeolicus* are the most thermophilic bacteria known. Although isolated and described only recently⁹, these species are related to filamentous bacteria first observed at the turn of the century, growing at 89 °C in the outflow of hot springs in Yellowstone National Park^{10,11}. The observation of these macroscopic assemblages would later be instrumental in the drive to culture hyperthermophilic organisms¹².

The Aquificaceae represent the most deeply branching family within the bacterial domain on the basis of phylogenetic analysis of 16S ribosomal RNA sequences^{13,14}, although analyses of individual protein sequences vary in their placement of Aquifex relative to other groups^{15–18}. The genera in this group, Aquifex and Hydrogenobacter, are thermophilic, hydrogen-oxidizing, microaer-ophilic, obligate chemolithoautotrophs^{9,19–21}. A. aeolicus (isolated by R.H. and K. O. Stetter) was cultured at 85 °C under an H₂/CO₂/O₂ (79.5:19.5:1.0) atmosphere in a medium containing only inorganic components. A. aeolicus does not grow on a number of organic substrates, including sugars, amino acids, yeast extract or meat extract. Unlike its close relative A. pyrophilus, A. aeolicus has not been shown to grow anaerobically with nitrate as an electron acceptor in the laboratory.

From study of the physiology of the organism, several predictions can be made. As an autotroph, *A. aeolicus* must have genes encoding proteins for one or more modes of carbon fixation and a complete set of biosynthetic genes. As autotrophy is a feature that is distributed throughout the Archaea and Bacteria, most of the associated genes are expected to be of ancient origin and clearly related to those characterized elsewhere. The obligate autotrophy suggests a biosynthetic rather than a degradative character. Oxygen respiration

implies the presence of corresponding utilization and tolerance genes. The early divergence of the *Aquificaceae* inferred from ribosomal RNA sequences leads to several questions. Are the machineries for oxygen usage and tolerance homologous to those found in mitochondria and well studied organisms such as *Escherichia coli*, or were they invented separately? If there was far less oxygen when the lineage originated, is there evidence for use of alternative oxidants?

Genome

General features of the A. aeolicus genome are listed in Box 1. We classified 1,512 open-reading frames (ORFs) into one of three categories, namely, identified (Table 1), hypothetical, or unknown. Identified ORFs were further classified into one of 57 cellular role categories adapted from Riley²² (Table 1). The relatively high G + C content of the two 16S-23S-5S rRNA operons (65%) is characteristic of thermophilic bacterial rRNAs²³. The genome is densely packed: most genes are apparently expressed in polycistronic operons and many convergently transcribed genes overlap slightly. Nonetheless, many genes that are functionally grouped within operons in other organisms, such as the tryptophan or histidine biosynthesis pathways, are found dispersed throughout the A. aeolicus genome or appear in novel operons. Even when they encode subunits of the same enzyme, the genes are often separated on the chromosome (for example, gltB and gltD, the genes encoding the large and small subunits of glutamate synthase). Operon organization of genes for the biosynthesis of amino acids is found in both Archaea and Bacteria but it is not universal in either group. A. aeolicus is extreme in that no two amino acid biosynthetic genes are found in the same operon. In contrast, genes required for electron transport, hydrogenase subunits, transport systems, ribosomal subunits, and flagella are often in functionally related operons in A. aeolicus (Fig. 1). No introns or inteins (protein splicing elements) were detected in the genome.

A single extrachromosomal element (ECE) was identified during sequencing. Sequence redundancy for the total project was calculated to be 4.83. The ECE, however, is significantly over-represented

[†] Present addresses: Codex Bioinformatics Services, PO Box 90273, San Diego, California 92169, USA (G.D.); Department of Bioinformatics, SmithKline Beecham Pharmaceuticals, Collegeville, Philadelphia 19426, USA (P.V.W.)

articles

relative to the chromosome; when calculated independently for the final assemblies, redundancies are 4.73 and 8.76 for the chromosome and for the ECE, respectively. The ECE therefore appears to be present at roughly twice the copy number of the chromosome. Although no ORFs on the ECE can be assigned a function with confidence, except for a transposase, two of the predicted proteins show similarity to hypothetical proteins in the *Methanococcus jannaschii* genome¹. One ORF on the ECE is also present in two identical copies on the *A. aeolicus* chromosome, providing evidence of genetic exchange between the chromosome and the ECE.

Reductive tricarboxylic acid cycle

As an autotroph, *A. aeolicus* obtains all necessary carbon by fixing CO₂ from the environment. An assay for activity of the reductive tricarboxylic acid (TCA) cycle in *A. pyrophilus* cell extracts showed *in vitro* activities for each proposed reaction²⁴. The reductive (reverse) TCA cycle fixes two molecules of CO₂ to form acetyl-coenzyme A (acetyl-CoA) and other biosynthetic intermediates²⁵. The *A. aeolicus* genome contains genes encoding malate dehydrogenase, fumarate hydratase, fumarate reductase, succinate-CoA ligase, ferredoxin oxidoreductase, isocitrate dehydrogenase, aconitase and citrate synthase, which together could constitute the TCA pathway. There is no biochemical evidence for alternative carbon-fixation pathways in *A. pyrophilus*^{24,25} nor is there sequence evidence for such pathways in *A. aeolicus*.

The TCA cycle is vital as it provides the substrates of many biosynthetic pathways. (It is beyond the scope of this report to detail these biosynthetic pathways, but they seem to be typically bacterial, and candidate genes for all or most of the enzymes have been identified in A. aeolicus.) The central role of the TCA cycle is emphasized by duplication of many of its constituent genes in A. aeolicus. Two genes encode proteins that are similar to malate dehydrogenase (in addition to a lactate dehydrogenase). The fumarate hydratase is split into amino- and carboxy-terminal subunits, as is the case in M. jannaschii¹. Unlinked genes encoding two ironsulphur proteins of fumarate reductase (alternatively succinate dehydrogenase) accompany a single flavoprotein subunit. Two sets of genes resembling succinate-CoA ligase (both the α - and β subunits) are present. A. aeolicus has two putative operons encoding four-subunit $(\alpha, \beta, \gamma, \delta)$ 2-acid ferredoxin oxidoreductases; members of this family catalyze reversible carboxylation/decarboxylation of pyruvate, 2-isoketovalerate, or 2-oxoglutarate with varying specificity²⁶. These duplicated genes may encode paralogous proteins with unique substrate specificity, as opposed to redundant functions. For example, a paralogue of succinate-CoA ligase may activate citrate with coenzyme A to form citryl-CoA, which citrate synthase can cleave to produce oxaloacetate and acetyl-CoA.

Gluconeogenesis through the Embden-Meyerhof-Parnas pathway

Growing autotrophically, *A. aeolicus* must synthesize pentose and hexose monosaccharides from products of the reductive TCA cycle. Pyruvate produced by pyruvate ferredoxin oxidoreductase or by pyruvate carboxylase (oxaloacetate decarboxylase)²⁴ may enter the Embden–Meyerhof–Parnas pathway of glycolysis and gluconeogenesis. Genes encoding fructose-1,6-bisphosphatase, an essential gluconeogenic enzyme in *E. coli*, have not been identified in the genomes of the autotrophs *A. aeolicus* or *M. jannaschii*¹, suggesting that an unidentified pathway may exist. The *A. aeolicus* genome also encodes enzymes of the pentose-phosphate pathway and enzymes for glycogen synthesis and catabolism. We found neither (phospho) gluconate dehydrase nor 2-keto-3-deoxy-(6-phospho)gluconate aldolase of the Entner–Doudoroff pathway.

Respiration

Aquifex species are able to grow by using oxygen concentrations as low as 7.5 p.p.m. (R.H. and K. O. Stetter, unpublished observations).

The enzymes for oxygen respiration are similar to those of other bacteria: ubiquinol cytochrome c oxidoreductase (bc_1 complex), cytochrome c (three different genes) and cytochrome c oxidase (with two different subunit I genes and two different subunit II genes). The alternative system, with cytochrome bd ubiquinol oxidase, is also present. Clearly, the Aquifex lineage did not independently invent oxygen respiration. This leaves at least three possibilities: consistent with the ability of Aquifex to use very low levels of oxygen, the oxygen-respiration system was highly developed when oxygen had only a small fraction of its present concentration before the advent of oxygenic photosynthesis; contrary to what is implied by the 16S phylogeny, the lineage including Aquifex originated after the rise in atmospheric oxygen; or oxygen respiration developed once, and was then laterally transferred among bacterial lineages and acquired by Aquifex.

Many other oxidoreductases are present in addition to those obviously involved in oxygen respiration. The physiological role of most of these oxidoreductases is unknown or ambiguous, but two deserve comment. There is a putative nitrate reductase in the genome, although *A. aeolicus* has not been observed to perform NO₃ respiration, unlike the closely related *A. pyrophilus*. The nitrate reductase gene is adjacent to a nitrate transporter, and may be involved in nitrogen assimilation rather than respiration. It is also possible that *A. aeolicus* has a latent ability to respire with nitrate but that the conditions required have not been found. Two gene sequences show strong similarities to Rieske proteins, even though the rest of the ubiquinol cytochrome *c* oxidoreductase subunits appear only once in the genome. One of these Rieske protein genes is adjacent to a sulphide dehydrogenase subunit, suggesting a role in sulphur respiration.

Oxidative stress

A. aeolicus grows optimally under microaerophilic conditions and consequently possesses various protective enzymes to counter reactive oxygen species, particularly superoxide and peroxide. The genome contains three genes encoding superoxide dismutases, two of the copper/zinc family and one of the iron/manganese family. The latter has also been noted in A. pyrophilus²⁷. One of the copper/zinc superoxide dismutase genes is located in a large gene cluster encoding formate dehydrogenase.

No catalase genes were identified. There are several genes in the genome that might encode proteins that catalyze the detoxification of H_2O_2 , including cytochrome c peroxidase, thiol peroxidase, and two alkyl hydroperoxide reductase genes. All of these enzymes require an exogenous reductant and therefore do not evolve O_2 . However, treatment of A. $pyrophilus^9$ or A. aeolicus biomass with H_2O_2 results in the rapid evolution of gas bubbles. This catalase activity may result from a novel enzyme that cannot yet be identified by sequence similarity.

Motility

Like A. pyrophilus⁹, A. aeolicus is motile and possesses monopolar polytrichous flagella. More than 25 genes encoding proteins involved in flagellar structure and biosynthesis have been identified in A. aeolicus (Box 1). However, no homologues of the bacterial chemotaxis system were identified. In enteric bacteria, membrane-bound receptors bind chemoattractants and repellents and mod-

Figure 1 Linear map of the *A. aeolicus* circular chromosome. Genes are shown as arrows which denote the direction of transcription and are coloured to denote functional categorization according to the key below the figure. The sequences of the two rRNA gene clusters are identical. Here, the first base of the coding sequence of *fusA* was arbitrarily assigned as base number 1 as no origin of replication has been identified. ORF numbers are discontinuous because some ORFs representing 100 amino acids or more are not predicted to be coding and are not shown.

ulate the activity of the histidine kinase CheA²⁸. Phosphoryl groups from CheA are transferred to CheY, which then binds to the flagellar switch, altering the direction of flagellar rotation. Homologous chemotaxis systems are present in the archaea Halobacterium salinarum²⁹ and Pyrococcus sp. OT3 (H. Sizuya, personal communication), although the bacterial and archaeal flagellar apparatuses are not homologous³⁰. The M. jannaschii genome also lacks homologues of known genes required for chemotaxis. Thus, either motility in A. aeolicus and M. jannaschii is undirected or input for controlling taxis is mediated through another, unidentified system. The most studied chemotaxis systems respond to sugars and amino acids, although responses to other inputs (for example, metals, redox potential, and light) may also occur. In contrast to all the organisms known to possess the classical chemotactic signaltransduction pathways, both A. aeolicus and M. jannaschii are obligate chemoautotrophs. Chemoautotrophs may respond to a different set of factors, such as concentrations of dissolved gas (CO₂, H₂ or O₂) or another critical parameter such as temperature.

In *E. coli*, the flagellar switch is essential for flagellar structure and function and coupling of chemotaxis signals. But the *A. aeolicus* genome encodes homologues of only two of the three *E. coli* proteins that make up the switch, FliG and FliN. Biochemical³¹ and genetic³² studies implicate the missing FliM protein as the receptor for phosphorylated CheY, the switch signal. The absence of both FliM and CheY in *A. aeolicus* supports the identification of FliM as the receptor for phosphorylated CheY in *E. coli*. This result also argues against a direct role for FliM in torque generation.

DNA replication and repair

The A. aeolicus primary replicative DNA polymerase, corresponding to the DNA polymerase III holoenzyme in E. coli, probably consists

Figure 2 Histogram representation of the similarity of selected classes of predicted proteins to predicted proteins from the E. coli (EC) and M. jannaschii (MJ) genomes. Predicted A. aeolicus proteins representing each category were independently compared to sets of all potential polypeptides (≥100 amino acids) from the two genomes using FASTA⁴⁴. If the top scoring alignment covered ≥80% of the length of the A. aeolicus protein, the score was plotted. There were more positives found in the E. coli genome in nearly every category. Hypothetical proteins (those identified by database match but of unknown function) are very similarly represented by M. jannaschii and E. coli. There are a small number of very highly conserved hypotheticals that are shared between A. aeolicus and M. jannaschii. Generally, biosynthetic categories show less discrimination than information-processing categories, which are clearly more E. coli-like. The variation in the apparent rates of evolution in different categories suggests that different phylogenies may be inferred depending on the sequence analysed. Within each graph, correspondence to E. coli is shown in white and M. jannaschii is shown in black. Avg id, average identity; count, number of proteins analysed.

Box 1 Aquifex aeolicus genome features

General

Length 1,551, 335 bp G + C content 43.4% Protein-coding regions 93%

Stable RNA 0.8%

Non-coding repeats (none significant)

Intergenic sequences 6.2%

RNA

Ribosomal RNA Chromosome coordinates

16S-23S-5S 572785-567770 16S-23S-5S 1192069-1197084

Transfer RNA

44 species (7 clusters, 28 single genes)
Other RNAs Chromosome coordinates

tmRNA 1153844-1153498

Chromosomal coding sequences

849 similar to protein of known function (average length 1,066 bp) 256 similar to protein of unknown function (average length 898 bp)

407 unknown coding regions (average length 762 bp)

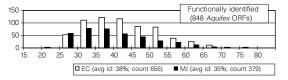
1,512 total (average length 956)

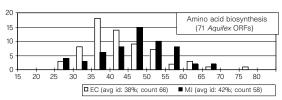
Extrachromosmal element (ECE)

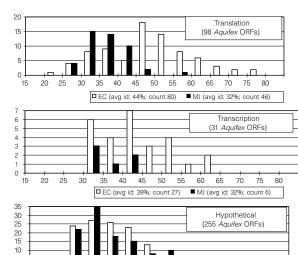
Length 39,456 bp G+C content 36.4% Protein-coding regions 53.5%

ECE-coding sequences

1 similar to proteins of known function (length 948 bp) 4 similar to proteins of unknown function (average length 667 bp) 27 unknown coding regions (average length 648 bp)







Per cent identity

50 55

□ EC (avg id: 32%; count 121) ■ MJ (avg id: 33%; count 115)

60 65

40 45

15 20 25

Number of proteins displaying similarity

articles

of a core structure containing α - and ϵ -subunits, a γ - τ -subunit and an additional member of the γ - τ / δ' -family. A gene encoding a protein homologous to the β -sliding clamp was also found. This minimalistic complex lacks homologous θ -, δ -, χ - and ψ -subunits, as does the *Mycoplasma genitalium* holoenzyme³. Translation of the 54K (relative molecular mass) γ - τ -ATPase subunit may proceed without a programmed frameshift to produce a protein similar to the N-terminal region of the *E. coli* γ -subunit. DNA polymerase I is present as separate Klenow fragment and $5' \rightarrow 3'$ exonuclease subunits, encoded by two non-adjacent ORFs. Although the repair polymerase, DNA polymerase II, has not been found in *A. aeolicus*, one ORF (Aq1422) encodes a protein similar to the eukaryotic DNA repair polymerase- β . A member of the same family has been identified in *Thermus aquaticus*³³ and *Bacillus subtilis*.

Transcriptional and translational apparatuses

The transcriptional apparatus of A. aeolicus is similar to that of E. coli and lacks any components specific to the Eukarya or Archaea (Fig. 2). In addition to the core RNA polymerase α -, β -, and β' subunits, four σ -factors which determine promoter specificity are present (Table 1). Several different families of bacterial transcriptional regulators were also identified, including two-component systems. All of the ribosomal proteins and elongation factors common to other bacteria are present, indicating that all bacteriaspecific ribosomal proteins were present in the common ancestor of Aquifex and other bacteria. Also present are the four sel genes required for the cotranslational incorporation of selenocysteine. These latter genes are clustered in a 15-kilobase-pair segment that also encodes the biosynthetic and structural proteins for formate dehydrogenase, the only selenocysteine-containing protein identified. The gene that encodes selenocysteine transfer RNA, selC, is apparently cotranscribed with the genes encoding the formate dehydrogenase structural proteins.

A. aeolicus lacks glutaminyl-tRNA and asparaginyl-tRNA synthetases. The genes required for transamidation of glutamyl-tRNA Gln are present³⁴. Charging of asparaginyl-tRNA is likely to proceed through the analogous reaction, as shown in halobacteria³⁵, although the genes(s) for that transamidase are unknown. The canonical methionyl- and leucyl-tRNA synthetases have only been seen previously as single polypeptide enzymes; however, in A.

aeolicus the homologues appear fragmented into two subunits. In both cases, the genes that encode the N- and C-terminal portions are widely separated on the chromosome. No complete three-dimensional structural data are available for either methionyl- or leucyl-aminoacyl tRNA synthetases, but the subunit organization in the A. aeolicus aminoacyl-tRNA synthetases may reflect domain organization in the homologous proteins.

Thermophily

The *A. aeolicus* genome is the second completely sequenced genome of a hyperthermophile. By comparing the *A. aeolicus* and *M. jannaschii* genomes and contrasting them with the complete genomes of mesophiles, we can discover whether there are aspects of the genome or the encoded information that are diagnostic of hyperthermophiles. The G+C content of the stable RNAs is clearly indicative of the high growth temperature of the organism. This property can be used to identify stable RNAs against the relatively low G+C background of the *A. aeolicus* genome. The gene encoding tmRNA (or 10Sa RNA)³⁶, an RNA involved in tagging polypeptides translated from incomplete messenger RNAs for degradation, was located in this way.

Two genes for reverse gyrase are present in the genome. This is the only protein known to be present only in thermophiles. Other proteins, currently described as hypotheticals, may be diagnostic of hyperthermophiles but the data sets are not yet large enough to decide this with confidence.

Although features of stabilization may not be apparent in any given protein³⁷, a large enough data set may reveal general trends in amino-acid usage that are informative. Particularly important in this regard is inclusion of multiple genomes of hyperthermophiles so as not to allow the idiosyncracies of a single organism to bias the conclusions. As shown in Table 2, comparison of the amino-acid composition encoded by six genomes shows that use of individual amino acids can vary significantly from genome to genome. The data suggest trends that may be correlated with the thermostability of the encoded proteins. One apparent trend is that the hyperthemophile genomes encode higher levels of charged amino acids on average than mesophile genomes³⁸, primarily at the expense of uncharged polar residues. Glutamine in particular seems to be significantly discriminated against in the hyperthermophiles. Although this observation might be rationalized on the basis of

		Thermophiles					
Amino acid	H. influenzae	H. pylori	E. coli	Synechosystis	A. aeolicus	M. jannaschii	
A	8.21	6.83	9.55	9.07	5.90	5.54	
С	1.03	1.09	1.11	1.01	0.79	1.27	
D	4.98	4.77	5.20	5.07	4.32	5.52	
E	6.48	6.88	5.91	6.20	9.63	8.67	
F	4.46	5.41	3.87	3.75	5.13	4.20	
G	6.65	5.76	7.42	7.77	6.75	6.41	
Н	2.05	2.12	2.26	1.93	1.54	1.43	
I	7.10	7.20	5.95	6.31	7.32	10.45	
K	6.32	8.94	4.48	4.26	9.40	10.36	
L M N	10.50 2.44 4.89	11.18	10.56	10.93	10.57 1.92 3.60	9.38 2.33 5.24	
		2.28	2.86	2.12			
		5.83	3.88	3.76			
P	3.72	3.28	4.41	5.09	4.07	3.38	
Q	4.64	3.70	4.42	5.26	2.04	1.44	
R	4.47	3.46	5.58	5.18	4.91	3.85	
S	5.84	6.81	5.67	5.46	4.79	4.46	
Т	5.20	4.37	5.35	5.53	4.21	4.06	
V	6.68	5.59	7.11	7.10	7.93	6.85	
W	1.12	0.70	1.48	1.30	0.93	0.71	
Υ	3.12	3.68	2.83	2.78	4.13	4.33	
		Mesop	philes		Thermophiles		
Charged residues (DEKRH)		24.1	11	=	29.84	4	
Polar/uncharged resid		31.1			26.79		
Hydrophobic residues (LMIVWPAF)		44.			43.36		

an increased rate of deamidation of this residue at higher temperatures, aspargine does not appear subject to similar discrimination.

Phylogeny

The placement of the Aquifex lineage as one of the earliest divergences in the eubacterial tree^{13,14} is interesting because of the insights it could provide into the ancestral eubacterial phenotype, including the hypothesized thermophilic nature of the first bacteria. Proteinbased phylogenies often do not support the original rRNA-based placement^{15,16,18}. Thus, the availability of some 1,500 genes from an Aquifex species would seem to offer a definitive resolution of the phylogeny. However, our analyses of ribosomal proteins, aminoacyl-tRNA synthetases, and other proteins do not do so, showing no consistent picture of the organism's phylogeny. We cannot make a more complete analysis and discussion here, but some observations can be made. These proteins do not yield a statistically significant placement of the Aquifex lineage or of other major eubacterial lineages. This situation partially reflects the inadequacy of some protein sequences as indicators of distant molecular genealogy because of their particular evolutionary dynamic, including the patterns and rates of amino-acid replacements. In some cases (such as the aminoacyl-tRNA synthetases for arginine, cysteine, histidine, proline and tyrosine), the analyses are further complicated by the presence of paralogous genes and/or apparent lateral gene transfers. It seems that a more extensive survey of genes and a better sampling of major eubacterial taxa will be required to confidently confirm or refute an early divergence of the Aquifex lineage.

Conclusions

Advances in sequencing techniques have allowed us to move beyond studies of single genes to studies of complete genomes only recently². This rapid advance has created the opportunity to begin to characterize an organism with the full knowledge of the genome in hand. The complete genome summarized in this report represents our first view of *A. aeolicus*. The challenge now is to ask specific questions in ways which take advantage of the whole-genome data.

Beyond studies of any single organism in isolation, complete genomes allow comprehensive comparisons between organisms. For instance, comparisons of the similarity of genes can be made that reveal that genes in different categories vary in their relative conservation (Fig. 2). In addition, genome-wide trends are apparent. For example, why is there not more of a tendency to group functionally related genes (for example, biosynthetic pathways) into operons in A. aeolicus? This was also seen in the genome sequence of the autotroph M. jannaschii¹. Is this because the autotrophic lifestyle decreases the need for selective regulation? There also seem to be a few multifunctional, fused proteins in A. aeolicus and M. jannaschii. Although this seems unlikely to be related to autotrophy, it might be associated with extreme thermophily. The large number of diverse genome sequences that will become available in the coming years will allow more detailed correlation of global genomic properties with particular physiologies.

Methods

Sequencing strategy. The sequencing strategy used to assemble the complete genome was based on the whole genome random (or 'shotgun') approach, which has been successfully used for other genomes of similar size¹⁻⁴. Shotgun sequencing projects are characterized by two phases: an initial completely random phase in which the bulk of the data is collected, followed by a closure phase where directed techniques are used to close gaps and complete the assembly. By pursuing a strategy where only 97% coverage was initially achieved, we were able to limit the number of sequences needed for the random phase to only 10,500 (ref. 39).

Sequences were generated from a small insert library constructed in λ ZAP II vectors^{40,41} (average insert length 2.9 kilobase pairs). Two different methods were used for sequencing: first, dye-primer M13-21 and M13 reverse primer ABI Prism CS⁺ ready reaction kits, analysed on 48-cm 4% polyacrylamide

gels; and second, dye-terminator (ABI Prism FS+) reactions using two pBluescript-specific primers. These reactions were analysed on 36-cm 5% Long-Ranger gels.

The sequence fragments were assembled on an Apple Power Macintosh computer using Sequencher (Gene Codes, Ann Arbor, MI), an assembly and editing program. Assembly was typically performed in batches of roughly 200–400 sequences, and was followed by inspection and editing of the assemblies. All sequences in the set were compared with all others through this process. After assembly, the sequences comprised \sim 750 contigs at the end of the random phase. Sequences were obtained from both ends of \sim 200 randomly chosen clones from a fosmid library^{42,43}. These sequences were then assembled with consensus sequences derived from the contigs of random-phase sequences using Sequencher. Gaps between contigs were closed by direct sequencing on fosmids not wholly contained within a contig. The fosmid library thus served a purpose analogous to that of the λ -scaffold in other projects¹⁻⁴. The final eight gaps were closed by direct sequencing of polymerase chain reaction (PCR) products generated with the TaqPlus Long PCR System (Stratagene Cloning Systems, La Jolla, CA).

Consequences of reducing the number of sequences in the random phase are the large number of gaps that remain to be closed in the directed phase, and the reduction in overall coverage. To ensure that reduced coverage did not compromise accuracy, $\sim\!200$ oligonucleotide primers were synthesized to resequence regions of ambiguity identified by visual inspection of the entire assembly. 13,785 sequences, with an average edited read length of 557 base pairs, constitute the final assembly. On the basis of a relatively small number of errors identified during the annotation process, we estimate the error frequency to be $<\!0.01\%$, comparable to other published genomic sequence estimates.

Gene (ORF + RNA) identification and functional assignment approaches.

Coding regions of the *A. aeolicus* genome were analysed and assigned using primarily the programs BLASTP⁴⁴ and FASTA⁴⁵ to search against a non-redundant protein database. Many analyses were carried out within the context of MAGPIE^{46,47}, an integrated computing environment for genome analysis. The results of these analyses are available for user interpretation, validation, and categorization. Additional ORFs were identified and start sites refined using the program CRITICA (J. H. Badger and G.J.O., unpublished program). Finally, all presumed 'intergenic regions' were examined with BLASTX for similarities to known protein sequences⁴⁸. Transfer RNA genes were identified with the program tRNAscan-SE⁴⁹.

Received 26 August 1997; accepted 3 February 1998.

- Bult, C. et al. Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. Science 273, 1058–1073 (1996).
- Fleischmann, R. D. et al. Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. Science 269, 496–511 (1995).
- Fraser, C. M. et al. The minimal gene complement of Mycoplasma genitalium. Science 270, 397–403 (1995).
- Tomb, J.-F. et al. The complete genome sequence of the gastric pathogen Helicobacter pylori. Nature 388, 539–547 (1997).
 Himmelreich, R. et al. Complete sequence analysis of the genome of the bacterium Mycoplasma
- pneumoniae. Nucleic Acids Res. 24, 4420–4449 (1996).

 6. Kaneko, T. et al. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
- Kaneko, I. et al. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC7803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions. DNA Res. 3, 109–136 (1996).
- Blattner, F. R. et al. The complete genome sequence of Escherichia coli K-12. Science 277, 1453–1462 (1997).
- 8. Goffeau, A. et al. Life with 6000 genes. Science 274, 546 (1996).
- Huber, R. et al. Aquifex pyrophilus gen. nov. sp. nov. represents a novel group of marine hyperthermophilic hydrogen oxidizing bacteria. Arch. Microbiol. 15, 340–351 (1992).
- Reysenbach, L., Wickham, G. S. & Pace, N. R. Phylogenetic analysis of the hyperthermophilic pink filament community in Octopus Spring, Yellowstone National Park. Appl. Environ. Microbiol. 60, 2113–2119 (1994).
- 11. Setchell, W. A. The upper temperature limits of life. Science 17, 934–937 (1903).
- 12. Brock, T. D. The road to Yellowstone—and beyond. Annu. Rev. Microbiol. 49, 1-28 (1995).
- 13. Burggraf, S., Olsen, G. J., Stetter, K. O. & Woese, C. R. A phylogenetic analysis of *Aquifex pyrophilus*. Syst. Appl. Microbiol. 15, 353–356 (1992).
- Pitulle, C. et al. Phylogenetic position of the genus Hydrogenobacter. Int. J. Syst. Bacteriol. 44, 620–626 (1994).
- Baldauf, S. L., Palmer, J. D. & Doolittle, W. F. The root of the universal tree and the origin of eukaryotes based on elongation factor phylogeny. Proc. Natl Acad. Sci. USA 93, 7749–7754 (1996).
- Klenk, H.-P., Palm, P. & Zillig, W. in Molecular Biology of the Archaea (eds Pfeifer, F., Palm, P. & Scleeifer, K. H.) 139–147 (Vch Pub, 1994).
- 17. Bocchetta, M. et al. Arrangement and nucleotide sequence of the gene (fus) encoding elongation factor G (EF-G) from the hyperthermophilic bacterium Aquifex pyrophilus: phylogenetic depth of hyperthermophilic bacteria inferred from analysis of the EF-G/fus sequences. J. Mol. Evol. 41, 803–812 (1995).
- Wetmur, J. G. et al. Cloning, sequencing, and expression of RecA proteins from three distantly related thermophilic eubacteria. J. Biol. Chem. 269, 25928–25935 (1994).
- 19. Kawasumi, T., Igarashi, Y., Kodama, T. & Minoda, Y. Hydrogenobacter thermophilus gen. nov., sp. nov.



- an extremely thermophilic, aerobic, hydrogen-oxidizing bacterium. Int. J. Syst. Bacteriol. 34, 5-10 (1984).
- Kristjannson, J., Ingason, A. & Alfredsson, G. A. Isolation of thermophilic obligately autotrophic hydrogen-oxidizing bacteria, similar to Hydrogenobacter thermophilus, from Icelandic hotsprings. Arch. Microbiol. 140, 321–325 (1985).
- Kryukov, V. R., Savel'eva, N. D. & Pusheva, M. A. Calderobacterium hydrogenophilum gen. nov., sp. nov. an extreme thermophilic bacterium and its hydrogenase activity. Microbiology (Engl. Trans. Mikrobiologiya) 52, 611–618 (1983).
- 22. Riley, M. Functions of the gene products of Escherichia coli. Microbiol. Rev. 57, 862-952 (1993).
- Weisburg, W. G., Giovannoni, S. J. & Woese, C. R. The Deinococcus-Thermus phylum and the effect of rRNA composition on phylogenetic tree construction. Syst. Appl. Microbiol. 11, 128–134 (1989).
- Beh, M., Strauss, G., Huber, R., Stetter, K. O. & Fuchs, G. Enzymes of the reductive citric acid cycle in the autotrophic eubacterium Aquifex pyrophilus and in the archaebacterium Thermoproteus neutrobilus. Arch. Microbiol. 160, 306–311 (1993).
- 25. Fuchs, G. in Autotrophic Bacteria (eds Schegel, H. G & Bowein, B.) 365-382 (Springer, New York, 1987)
- Mai, X. & Adams, M. W. Characterization of a fourth type of 2-keto acid-oxidizing enzyme from a hyperthermophilic archaeon: 2-ketoglutarate ferredoxin oxidoreductase from *Thermococcus litoralis*. J. Bacteriol. 178, 5890–5896 (1996).
- Lim, J. H. et al. Cloning and expression of superoxide dismutase from Aquifex pyrophilus, a hyperthermophilic bacterium. FEBS Lett. 406, 142–146 (1997).
- Bourret, R. B., Borkovich, K. A. & Simon, M. I. Signal transduction pathways involving protein phosphorylation in prokaryotes. *Annu. Rev. Biochem.* 60, 401–441 (1991).
- Rudolph, J., Tolliday, N., Schmitt, C., Schuster, S. C. & Oesterhelt, D. Phosphorylation in halobacterial signal transduction. EMBO J. 14, 4249–4257 (1995).
- Jarrell, K. F., Bayley, D. P. & Kostyukova, A. S. The archaeal flagellum: a unique motility structure. J. Bacteriol. 178, 5057–5064 (1996).
- 31. Welch, M., Oosawa, K., Aizawa, S. I. & Eisenbach, M. Effects of phosphorylation, Mg²⁺, and conformation of the chemotaxis protein CheY on its binding to the flagellar switch protein FliM. *Biochemistry* 33, 10470–10467 (1994).
- Sockett, H., Yamaguchi, S., Kihara, M., Irikura, V. M. & Macnab, R. M. Molecular analysis of the flagellar switch protein FliM of Salmonella typhimurium. J. Bacteriol. 174, 793–806 (1992).
- Motoshima, H. et al. Molecular cloning and nucleotide sequence of the aminopeptidase T gene of Thermus aquaticus YT-1 and its high-level expression in Escherichia coli. Agric. Biol. Chem. 54, 2385

 – 3297 (1990)
- Curnow, A. W. et al. Glu-tRNAGIn amidotransferase: a novel heterotrimeric enzyme required for correct decoding of glutamine codons during translation. Proc. Natl Acad. Sci. USA 94, 11819–11826 (1997).
- 35. Curnow, A. W., Ibba, M. & Söll, D. tRNA-dependent asparagine formation. Nature 382, 589–590 (1996).

- Tu, G. F., Reid, G. E., Zhang, J. G., Moritz, R. L. & Simpson, R. J. C-terminal extension of truncated proteins in *Escherichia coli* with a 10Sa decapeptide. *J. Biol. Chem.* 270, 9322–9326 (1995).
- Böhm, G. & Jaenicke, R. Relevance of sequence statistics for the properties of extremophilic proteins. Int. J. Pept. Protein Res. 43, 97–106 (1994).
- Choi, I.-G. et al. Random sequence analysis of genomic DNA of a hyperthermophile: Aquifex pyrophilus. Extremophiles 1, 125–134 (1997).
- Lander, E. S. & Waterman, M. S. Genomic mapping by fingerprinting random clones: a mathematical analysis. Genomics 2, 231–239 (1988).
- Short, J. M., Fernandez, J. M., Sorge, J. A. & Huse, W. D. Lambda ZAP: a bacteriophage lambda expression vector with in vivo excision properties. Nucleic Acids Res. 16, 7583–7600 (1988).
- 41. Alting-Mees, M. A. & Short, J. M. pBluescript II: gene mapping vectors. *Nucleic Acids Res.* 17, 9494
- Shizuya, H. et al. Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in Escherichia coli using an F-factor-based vector. Proc. Natl Acad. Sci. USA 89. 8794–8797 (1992).
- Kim, U.-J., Shizuya, H., de Jong, P. J., Birren, B. & Simon, M. I. Stable propagation of cosmid sized human DNA inserts in an F factor based vector. *Nucleic Acids Res.* 20, 1083–1085 (1992).
- Altschul, S. F., Fish, W., Miller, W., Myers, E. W. & Lipman, D. J. Basic local alignment search tool. J. Mol. Biol. 215, 403–410 (1990).
- Pearson, W. R. & Lipman, D. J. Improved tools for biological sequence comparison. Proc. Natl Acad. Sci. USA 85, 2444–2448 (1988).
- 46. Gasterland, T. & Sensen, C. W. MAGPIE: automated genome interpretation. *Trends Genet.* 12, 76–78
- Gaasterland, T. & Sensen, C. W. Fully automated genome analysis that reflects user needs and preferences. A detailed introduction to the MAGPIE system architecture. *Biochimie* 78, 302–310 (1996).
- Gish, W. & States, D. J. Identification of protein coding regions by database similarity search. Nature Genet. 3, 266–272 (1993).
- Lowe, T. M. & Eddy, S. R. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25, 955–964 (1997).

Acknowledgements. This work was supported in part by Department of Energy Microbial Genome Program grants (to R.V.S., C. R. Woese and G.J.O.). We thank C. Woese for his cooperation in the analysis of the genome and interest in the project; K. Stetter for continuing interest; G. Frey, J. Holaska, S. Peralta, D. Hafenbrandl, S. Delk, T. Robinson, and J. Arnett for technical assistance; and D. Robertson, J. Stein, I. Sanyal, T. Richardson, G. Hauska, and K. Williams for discussions.

Correspondence should be addressed to R.V.S. (e-mail: rswanson@diversa.com). Requests for Aquifex aeolicus should be addressed to R.H. (e-mail: Robert.huber@biologie.uni-regensburg.de). The sequences have been deposited with GenBank and assigned accession numbers AE000657 (chromosome) and AE000667 (extrachromosomal element).

20 No. 100 No. \$100 KIN SOLUTION SOL 901 PB 201 20 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 One on the control of

The state of the s

Nature © Macmillan Publishers Ltd 1998

Table 1 Aquifex aeolicus Open Reading Frame Identifications. Gene numbers (Aq) correspond to those in Fig.1. Percentages refer to the identity found in the best FASTA alignment. The percentage of the sequence covered by the alignment is displayed with bullets as follows $20-40\% \cdot \cdot \cdot , 40-60\% \cdot \cdot \cdot , 60-80\% \cdot \cdot \cdot \cdot , 80-100\% \cdot \cdot \cdot \cdot$

Amino Acid Bi						1-carboxyvinyltransferase	45.7%
Aromatic amii Aq1536	no acids aroA	5-enolpyruvylshikimate-3-phosphate synthetase	43.0%	Aq520	murB1	UDP-N-acetylenolpyruvoylglucosamine reductase	35.6%
Aq081	aroC	chorismate synthase	55.2% ••••	Aq511 Aq1360	murB2 murC	UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetylmuramate-alanine ligase	38.9% 46.1%
Aq021 Aq901	aroD aroE	3-dehydroquinate dehydratase shikimate 5-dehydrogenase	33.3% •••• 46.1% ••••	Aq2075	murD	UDP-N-acetylmuramoylalanine-D-glutamate	
Aq2177	aroK	shikimate kinase	36.5%	Aq1747	murE	ligase	29.3% ···· 42.9% ····
Aq951	pheA	chorismate mutase/prephenate dehydratase	44.0% ••••	Aq821	murF	UDP-MurNac-tripeptide synthetase UDP-MURNAC-pentapeptide sythetase	32.3%
Aq1548 Aq706	trpA trpB1	tryptophan synthase alpha subunit tryptophan synthase beta subunit	44.5% 68.0%	Aq1177	murG	phospho-N-acetylmuramoyl-pentapeptide-	
Aq1410	trpB2	tryptophan synthase beta subunit	50.0% ****	Aq325	murI	transferase glutamate racemase	30.5% 43.4%
Aq1787 Aq196	trpC trpD1	indole-3-glycerol phosphate synthase phosphoribosylanthranilate transferase	43.3% 45.1%	Aq1189	pbpA1	penicillin binding protein 2	32.2%
Aq209	trpD2	phosphoribosylanthranilate transferase phosphoribosylanthranilate transferase	24.9%	Aq556	pbpA2	penicillin binding protein 2	30.3% ****
Aq582	trpE	anthranilate synthase component I	50.0% ****	Aq185 Aq1368	tagD1 tagD2	glycerol-3-phosphate cytidyltransferase glycerol-3-phosphate cytidyltransferase	52.0% ···· 67.2% ···
Aq2076 Aq549	trpF trpG	phosphoribosyl anthranilate isomerase anthranilate synthase component II	45.6% 59.2%			popolysaccharides	
Aq1755	tyrA	prephenate dehydrogenase	36.1% ••••	Aq1684	alg	alginate synthesis-related protein	37.2% ••
Aspartate fami	ily			Aq1641	cap dmt	capsular polysaccharide biosynthesis protein	30.8% ···· 40.2% ····
Aq1866	asd	aspartate-semialdehyde dehydrogenase	54.6% ••••	Aq1899 Aq1772	envA	dolichol-phosphate mannosyltransferase UDP-3-0-acyl N-acetylglcosamine deacetylase	36.5% ****
Aq1969 Aq2094	aspC1 aspC2	aspartate aminotransferase aminotransferase (AspC family)	53.5% 55.4%	Aq1757	exbB	biopolymer transport exbB	48.2%
Aq421	aspC3	aminotransferase (AspC family)	43.3% ••••	Aq1839 Aq1069	exbD galE	biopolymer transport ExbD UDP-glucose-4-epimerase	34.7% ···· 54.7% ····
Aq273	aspC4	aminotransferase (AspC family)	48.5%	Aq1705	galF	UDP-glucose pyrophosphorylase	47.2% ****
Aq1143 Aq916	dapA dapB	dihydrodipicolinate synthase dihydrodipicolinate reductase	53.1% •••• 44.2% ••••	Aq908	gmhA	phosphoheptose isomerase	63.4% •••
Aq547	dapE	succinyl-diaminopimelate desuccinylase	25.8% ••••	Aq085	kdsA	3-deoxy-d-manno-octulosonic acid 8-phosphate synthase	52.0%
Aq1838 Aq1208	dapF lysA	diaminopimelate epimerase	35.5% 47.4%	Aq326	kdtA	3-deoxy-D-manno-2-octulosonic acid transferase	28.9% ****
Aq1152	lysC	diaminopimelate decarboxylase aspartokinase	52.2%	Aq253	kdtB	lipopolysaccharide core biosynthesis protein	46.5% ••••
Aq1710	metE	tetrahydropteroyltriglutamate methyltransferase	45.9% ••••	Aq1546 Aq692	kpsF kpsU	polysialic acid capsule expression protein 3-deoxy-manno-octulosonate cytidylyltransferase	45.9% 41.3%
Aq1812 Aq1309	thrA thrB	homoserine dehydrogenase homoserine kinase	40.4% 38.3%	Aq1742	lgtF	beta 1,4 glucosyltransferase	35.2% ••••
Aq608	thrC1	threonine synthase	64.3%	Aq604	lpxA	acyl-[acyl-carrier-protein]-UDP-N-	47.70/
Aq425	thrC2	threonine synthase	61.9% ••••	Aq1427	lpxB	acetylglucosamine acyltransferase lipid A disaccharide synthetase	47.7% 31.6%
Branched-chai	in family			Aq538	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine	
Aq451	ilvB	acetolactate synthase large subunit	53.1%	1.0719	Page 2	N acyltransferase	43.3%
Aq1245 Aq837	ilvC ilvD	acetohydroxy acid isomeroreductase dihydroxyacid dehydratase	64.3% 58.0%	Aq718 Aq1096	mpg mtfA	mannose-1-phosphate guanyltransferase mannosyltransferase A	34.3% •••
Aq1893	ilvE	branched-chain amino acid aminotransferase	40.3% ••••	Aq515	mtfB	mannosyltransferase B	29.0% ••••
Aq1851	ilvH leuA1	acetolactate synthase 2-isopropylmalate synthase	53.2% • • • • 52.1% • • • •	Aq516 Aq1335	mtfC nse	mannosyltransferase C nucleotide sugar epimerase	35.9% 45.8%
Aq356 Aq2090	leuA2	2-isopropylmalate synthase 2-isopropylmalate synthase	49.9%	Aq505	otnA	polysaccharide biosynthesis protein	26.9%
Ag244	leuB	3-isopropylmalate dehydrogenase	58.7% ****	Aq504	otnA'	polysaccharide biosynthesis protein (fragment)	37.8% ••
Aq940	leuC leuD	large subunit of isopropylmalate isomerase	52.3% •••• 56.6% •••	Aq1543	rfaC1 rfaC2	ADP-heptose:LPS heptosyltransferase	30.7% ···· 28.1% ····
Aq1398		3-isopropylmalate dehydratase	30.070 ***	Aq145 Aq344	rfaD	ADP-heptose:LPS heptosyltransferase ADP-L-glycero-D-manno-heptose-6-epimerase	39.6% ••••
Glutamate fan Aq2068	nily argB	acetylglutamate kinase	54.2% ••••	Aq565	rfaE	ADP-heptose synthase	44.0%
Aq1879	argC	N-Acetyl-gamma-glutamylphosphate reductase	40.6% ••••	Aq2115 Aq1082	rfaG rfbD	glucosyl transférase I GDP-D-mannose dehydratase	27.1% •••• 53.2% ••••
Aq023	argD	N-acetylornithine aminotransferase	49.5% ••••	Aq519	rfe	undecaprenyl-phosphate-alpha-	24.8%
Aq1711 Aq1140	argF argG	ornithine carbamoyltransferase argininosuccinate synthase	46.2% 54.9%		_	N-acetylglucosaminyltransferase	
Aq1372	argH	argininosuccinate lyase	46.4% ••••	Aq1367 Aq518	spsI spsK	glucose-1-phosphate thymidylyltransferase spore coat polysaccharide biosynthesis protein	30.4% ••
Aq970	argJ	glutamate N-acetyltransferase	39.8% ••••	74Q510	spsik	SpsK	49.5% •••
Aq111 Aq109	glnA glnB	glutamine synthetase nitrogen regulatory PII protein	57.6% • • • • 73.2% • • • •	Aq589	xanB	mannose-6-phosphate isomerase/mannose-1-	
Aq1774	glnE	glutamate ammonia ligase adenylyl-transferase				phosphate guanyl transferase	40.9% ••••
			28.4% ****			1 -1 0 7	
Aq1565	gltB	glutamate synthase large subunit	44.3% ••••	Cellular Proces	ses	1 1 ,	
Aq1565 Aq2064	gltB gltD	glutamate synthase large subunit glutamate synthase small subunit gltD	44.3% 37.7%	Cell division	ses acrE		24.8%
Aq1565 Aq2064 Aq1071 Aq1134	gltB gltD proA proB	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase	44.3% 37.7% 47.9% 43.2%	Cell division Aq698 Aq1275	acrE cafA	acriflavin resistance protein AcrE cytoplasmic axial filament protein	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166	gltB gltD proA	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase	44.3% 37.7% 47.9%	Cell division Aq698 Aq1275 Aq523	acrE cafA ftsA	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein FtsA	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine	gltB gltD proA proB proC	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase	44.3% 37.7% 47.9% 43.2%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139	acrE cafA ftsA ftsH ftsW	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsH cell division protein PsH	28.5% 31.9% 51.1% 30.8%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166	gltB gltD proA proB	glutamate synthase lange subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole	44.3% 37.7% 47.9% 43.2% 35.1%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920	acrE cafA ftsA ftsH ftsW ftsY	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsaW cell division protein PsaW	28.5% 31.9% 51.1% 30.8% 35.2%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303	gltB gltD proA proB proC hisA	glutamate synthase lange subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazolegycrophosphate dehydratase	44.3% 37.7% 47.9% 43.2% 35.1%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525	acrE cafA ftsA ftsH ftsW ftsY ftsZ	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PSA cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSY cell division protein PSZ	28.5% 31.9% 51.1% 30.8% 35.2% 48.6%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084	gltB gltD proA proB proC hisA hisB hisC	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotramsferase istidion-loposphate amiotramsferase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PSA cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSZ glucose inhibited division protein A glucose inhibited division protein A	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782	gltB gltD proA proB proC hisA	glutamate synthase lange subunit gltD gamma-glutamyl phosphate reductase glutamate sk-ińase pyrroline carboxylate reductase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycorplohosphate dehydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase	44.396	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582	acrE cafA ftsA ftsH ftsW ftsY gidA1 gidA2 gidB	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG	glutamate synthase lange subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycorolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase	44.3%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PSA cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSY cell division protein PSY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.9%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH	44.3% 37.7% 47.9% 43.2% 55.1% 40.9% 46.4% 33.7% 49.9% 40.3% 47.7%	Cell division Aq688 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PtsA cell division protein PtsH cell division protein PtsH cell division protein PtsY cell division protein PtsY cell division protein PtsZ glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesJ septum site-determining protein MinC	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.9% 27.7% 39.4%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase lange subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycorolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase	44.3%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsV cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinC septum site-determining protein MinC septum site-determining protein MinD	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 57.5% 39.4% 44.9% 27.7% 39.4%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adotyntase histidinol-phosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase amidotransferase HisH phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 59.9% 40.3% 47.7% 43.8%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq878	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsH cell division protein PsH cell division protein PsY cell division protein PsY cell division protein PsY cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesI septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD	28.5% 31.9% 51.19% 30.8% 35.296 48.6% 50.29% 57.596 39.4% 44.99% 27.796 33.19% 54.596 55.49%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH	44.3% 37.7% 47.9% 43.2% 55.1% 40.9% 46.4% 33.7% 49.9% 40.3% 47.7%	Cell division Aq698 Aq1275 Aq523 Aq523 Aq523 Aq523 Aq521 Aq521 Aq521 Aq521 Aq521 Aq521 Aq521 Aq521 Aq521 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq878 Aq1217 Aq874 Aq875 Aq875 Aq875 Aq875 Aq875 Aq875 Aq875 Aq875	acrE cafA fisA fisH fisH fisW fisZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsH cell division protein PsY cell division protein PsY cell division protein PsY cell division protein PsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesI septum site-determining protein MinD septum site-determining protein MinD rod shape determining protein MreB rod shape determining protein RodA	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1030 Serine family	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate delhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosylransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 40.3%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1188 Aq1887 Aq12117 Aq878 Aq12117 Aq877 Aq845 Aq1025 Aq1130	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD od shape determining protein MreB	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase lange subunit gltD gamma-glutamyl phosphate reductase glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate dehydratase histidinol-cyhosphate aminotransferase histidinol-dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol)	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 42.7% 42.7% 42.7% 37.7% 42.7% 37.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq845 Aq025 Aq1130 Chaperones	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA sufI	acriflavin resistance protein AcrE cytoplasmic axial filament protein ell division protein PsA ell division protein PsH ell division protein PsH ell division protein PsY ell division protein PsY ell division protein PsY ell division protein PsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein ell cycle protein MesI septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD od shape determining protein RodA periplasmic cell division protein (Suff)	28.5% 31.9% 31.9% 51.196 30.896 35.296 48.696 50.296 57.596 39.496 27.796 33.196 54.596 57.496 37.696 28.196
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq1968 Selenocysteine Aq1030 Serine family Aq1556	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisH histE selA selD cysM	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate delhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosylransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 59.9% 40.3% 47.7% 43.8% 42.7% 37.7% 42.7% 37.7% 45.8% 62.7% 45.8% 62.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq12117 Aq877 Aq845 Aq025 Aq1713 Chaperones Aq154 Aq1735	acrE cafA fisA fisH fisW fisW fisW fisZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA suf1 ctaB dnaJ1	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsH cell division protein PsY cell division protein PsY cell division protein PsY cell division protein PsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesI septum site-determining protein MinD septum site-determining protein MinD rod shape determining protein MreB rod shape determining protein RodA	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1030 Serine family	gltB gltD proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate delhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosylransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B	44.3% 37.7% 47.9% 43.2% 35.1% 41.9% 43.2% 35.1% 44.9% 33.7% 49.9% 49.9% 49.9% 49.9% 43.3% 47.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq761 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq874 Aq1735 Aq1735 Aq1735 Aq1735 Aq1735 Aq1735 Aq1735 Aq1735 Aq033	acrE cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidA2 minD1 minD1 minD2 mreB rodA suf1 ctaB dna]1	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesJ septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MreB rod shape determining protein MreB rod shape determining protein fixe rod shape determining protein (Suff) cytochrome c oxidase assembly factor chaperone DnaJ	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq172 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cdl Envelope	gltB gltD proA proA proB proB proC hisA hisB hisC hisC hisC hisG hisH hisE hisH hisT cysM glyA serA	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate Sk-iánase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate adehydratase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase Hisf (cyclase) ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-scryl-IRNA(scr) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 59.9% 40.3% 47.7% 43.8% 42.7% 37.7% 42.7% 37.7% 45.8% 62.7% 45.8% 62.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1129 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq845 Aq1735 Aq025 Aq1735 Aq027 Aq154 Aq1735 Aq703 Aq996	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein ell division protein PsA ell division protein PsH ell division protein PsH ell division protein PsY ell division protein PsY ell division protein PsY ell division protein PsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein ell cycle protein MesI septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein fixed appear determining protein fixed of shape determining protein fixed of shape determining protein fixed haperone fixed division protein (Suff) cytochrome c oxidase assembly factor chaperone DnaJ chaperone DnaJ chaperone DnaJ haperone DnaJ	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 55.25% 48.6% 57.5% 39.4% 44.9% 27.7% 39.4% 33.1% 54.5% 57.4% 37.6% 28.1% 38.8% 45.1%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Serine family Aq1556 Aq479 Aq1905 Ccll Envelope Pili and fimbr	gltB gltD proA proA hisA hisB hisC hisB hisC hisB hisC hisH hisD hisF hisD hisF hisC hisH glyA serA ace	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase D-3-phosphoglycerate dehydrogenase	44.3% 37.7% 47.9% 43.2% 35.1% 440.9% 45.2% 46.4% 33.7% 49.9% 49.9% 49.9% 49.9% 49.9% 49.7% 47.7% 43.8% 42.7% 42.7% 45.8% 42.7% 44.1%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq9139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq025 Aq1735 Aq703 Aq996 Aq433 Aq996 Aq433 Aq192	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PstA cell division protein PstA cell division protein PstB cell division protein PstW cell division protein PstZ cell division protein PstZ cell division protein PstZ cell division protein PstZ diucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes acll cycle protein Miss septum site-determining protein MissC septum site-determining protein MissD septum site-determining protein MissD septum site-determining protein MissD od shape determining protein RodA periplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal chaperone Dnal chaperone Dnal hapsyo Chaperone Dnak heat shock protein GrpE chaperone Filstl	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq161 Aq7212 Aq1928 Selenocysteine Aq1031 Aq1031 Aq1030 Serine family Aq155 Aq479 Aq1905 Cell Envelope Pili and fimbr Aq1433	gltB gltD proA proA proB proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH glyA glyA glyA serA ae mmdDl	glutamate synthase large subunit glutamate synthase small subunit glutamate synthase small subunit glutamate synthase small subunit glutamate sykinase pyrroline carboxylate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoriboxylate reductase initialoxidelyocrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phydrogenase Hisf (cydase) ATP physophoriboxyl-transferase amidotransferase Histidinol dehydrogenase Hisf (cydase) ATP physophoriboxyl-transferase amidotransferase Histidinol dehydrogenase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase b-3-phosphorlycerate dehydrogenase minor pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.2% 35.1% 40.9% 46.4% 33.7% 49.9% 42.7% 42.7% 37.7% 42.7% 37.7% 42.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq91199 Aq9205 Aq725 Aq761 Aq691 Aq4178 Aq41718 Aq877 Aq877 Aq845 Aq1130 Clapseness Aq154 Aq1735 Aq123 Aq996 Aq433 Aq192 Aq1283	acrE cafA fish fish fish fish fish fisy fisy gidA1 gidA2 gidB minD1 minD2 minD2 mreB rodA sufl ctaB dnaj1 dnaj2 dnaK grpE hslU hspC	acriflavin reistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MreB rod shape determining	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 55.75% 39.4% 44.9% 42.94% 33.196 54.5% 54.5% 54.5% 54.5% 54.5% 55.74% 37.6% 28.196 38.8% 41.396
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1988 Selenocysteine Aq1031 Aq1030 Serine family Aq105 Cell Envelope Pili and fimbr Aq1433 Aq1434	gltB gltD proA proA proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH acl selD cysM glyA serA ac fimZ ppdD1 ppdD2	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate adelydratase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase Hisf (cyclase) ATP phosphoribosyl-transferase amidotransferase Hisf1 phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 44.7% 47.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq12117 Aq877 Aq845 Aq1215 Aq703 Aq996 Aq433 Aq192 Aq1283 Aq1991	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PstA cell division protein PstA cell division protein PstB cell division protein PstW cell division protein PstZ cell division protein PstZ cell division protein PstZ dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes get protein Mes del cycle protein Miss septum site-determining protein Miss septum site-determining protein Miss protein Mes dape determining protein Mes of shape determining protein RodA periplasmic cell division protein (Sufl) cytochrome c oxidase assembly factor chapteme Dnaj dhaptenoe Dnaj dhaptenoe Dnaj Hsy70 chaptenoe DnaK heat shock protein GrpE chaptenoe TsiU usmall heat shock protein (Cast I) heat shock protein (Sus I)	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1433 Aq1433 Aq1434 Aq1435	gltB gltD proA proA proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphorhydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase D-3-phosphoglycerate dehydrogenase minor pilin pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.6% 33.7% 49.9% 49.9% 43.8% 47.7% 43.8% 42.7% 37.7% 42.7% 43.8% 42.7% 44.1%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq91199 Aq9205 Aq725 Aq761 Aq691 Aq4178 Aq41718 Aq877 Aq877 Aq845 Aq1130 Clapseness Aq154 Aq1735 Aq123 Aq996 Aq433 Aq192 Aq1283	acrE cafA fish fish fish fish fish fisy fisy gidA1 gidA2 gidB minD1 minD2 minD2 mreB rodA sufl ctaB dnaj1 dnaj2 dnaK grpE hslU hspC	acriflavin reistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MreB rod shape determining	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 55.75% 39.4% 44.9% 42.94% 33.196 54.5% 54.5% 54.5% 54.5% 54.5% 55.74% 37.6% 28.196 38.8% 41.396
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq199 Aq1905 Cell Envelope Pili and fimbr Aq1433 Aq1432 Aq1434 Aq1435	gltB gltD proA proA proB proB proB proC hisA hisB hisC hisD hisC hisD hisF hisG hisH hisH hisH hisH priB glyA selD glyA serA ac fimZ ppdD1 ppdD2 ppdD2 ppdD2 ppdD2 ppdD3	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-ohsphate aminotransferase histidinol dehydrogenase HisFi (cyclase) ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq225 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq1217 Aq874 Aq674 Aq1735 Aq703 Aq996 Aq433 Aq1991 Aq2200 Aq2199	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MreB rod shape determining	28,5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq792 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1435 Lipoproteins a	gltB gltD proA proA proB proB proB proC hisA hisB hisC hisD hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH pidD cysM glyA serA ac fimZ ppdD1 ppdD2 ppdD2 ppdD3 ppdD3 nd porins lgt	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase subtamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate adiotrasferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase HisH phosphoribosyl-ATP pyrophosphorylodase Ls-eryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin pilin prolipoprotein diacylglyceryl transferase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.9% 35.1% 40.9% 44.9% 33.3.7% 49.9% 40.3% 47.7% 43.8% 47.7% 42.7% 42.7% 44.1	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq1217 Aq877 Aq847 Aq877 Aq847 Aq1217 Aq877 Aq847 Aq1217 Aq877 Aq847 Aq1217 Aq877 Aq847 Aq1217 Aq144 Aq1735 Aq703 Aq996 Aq4133 Aq192 Aq1283 Aq1991 Aq2200 Aq2199 Detoxification Aq486	acrE cafA fish fish fish fish fisy fisy gidA1 gidB mesj minC minD1 mreB rodA sufl dnal1 dnal2 dnal2 dnal2 dnal2 dnal2 dnal4 dnaM appE bapC appE bapC appC appC appC appC appC appC appC	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ cell division protein PsZ cell division protein PsZ cell division protein PsZ diucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MsB MAF protein cell cycle protein MsB Asp protein del cycle protein MsB Asp protein	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652	gltB gltD proA proA hisA hisB hisC hisD hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphorydrolase Ls-eryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin pilin prolipoprotein diacylglyceryl transferase apolipoprotein N-acyltransferase apolipoprotein N-acyltransferase apolipoprotein N-acyltransferase apolipoprotein N-acyltransferase apolipoprotein in A-acyltransferase apolipoprotein in A-acyltransferase apolipoprotein in Security (1997).	44.3% 37.7% 47.9% 43.2% 35.1% 440.9% 45.8% 45.8% 42.7% 42.7% 42.7% 44.1%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq225 Aq761 Aq611 A	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MesJ septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein ModA perplasmic cell division protein (Sufl) cytochrome c oxidase assembly factor chaperone DnaJ Hsp70 chaperone DnaJ Hsp70 chaperone DnaJ Hsp70 chaperone HsIU small heat shock protein (class I) heat shock protein GrpE chaperone HsIU small heat shock protein (class I) heat shock protein X GroEL GroES	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 50.296 57.5% 39.496 44.996 37.6% 33.1% 33.1% 55.74% 37.6% 38.8% 41.396 41.396 41.396 41.396 59.196 38.8% 57.5% 51.196 56.296 49.2%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq161 Aq732 Aq1986 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1995 Cell Envelope Pili and fimbr Aq1433 Aq1432 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652 Aq183	gltB gltD proA proA hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycorolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase Hisf (cyclase) ATP phosphoribosyl-tansferase amidotransferase Hisf1 phosphoribosyl-ATP pyrophosphohydrolase L-scryl-tRNA(scr) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 44.7% 43.2% 47.7%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq936 Aq139 Aq920 Aq225 Aq761 Aq691 Aq4178 Aq877 Aq877 Aq877 Aq878 Aq1130 Clapenoes Aq154 Aq1738 Aq192 Aq128 Aq128 Aq192 Aq128 Aq192 Aq133 Aq199 Aq220 Aq2199 Detosification Aq486 Aq888 Aq885 Aq136	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MreB rod shape determining rotein MreB rod shape determining	28.5% 31.9% 51.196 30.8% 35.296 48.6% 50.296 50.296 57.5% 39.4% 4.9% 32.7% 33.1% 53.1% 53.1% 54.5% 57.4% 37.6% 28.8% 41.3% 41.3% 41.3% 41.3% 41.3% 41.3% 41.1% 59.
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1434 Aq1435 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652 Aq1753 Aq529	gltB gltD proA proA proB proB proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH glyA serA ac fimZ ppdD1 ppdD2 ppdD2 ppdD1 ppdD2 lgt lint nlpD1 nlpD2 oprcC	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphorylosyl-ATP phosphoribosyl-ATP pyrophosphoryl-arabide selenophosphate synthase cleenophosphate synthase cleenophosphate synthase D-3-phosphoglycerate dehydrogenase D-3-phosphoglycerate dehydrogenase minor pilin pil	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.9% 33.5.1% 40.9% 44.9% 33.7% 49.9% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 42.7% 44.1	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq12117 Aq877 Aq845 Aq12130 Aq154 Aq1735 Aq703 Aq996 Aq433 Aq192 Aq1283 Aq192 Aq1283 Aq1991 Aq2200 Aq2199 Detoxification Aq486 Aq858 Aq136 Aq858 Aq136 Aq685	acrE cafA fish fish fish fish fisy fisy gidA1 gidB mesi minD1 minD1 minD1 minD1 minD1 minD1 dnal1 dnal2 dnal1 dnal2 dnal2 dnal2 dnal2 dnal2 ctaB dnaK grpE abpC1 abpC2 arsC cpx cpx cutA	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein F84 cell division protein F87 cell division protein F87 cell division protein F87 cell division protein F87 dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Ms1 septum site-determining protein MinD of shape determining protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal Chaperone F181 Lill small heat shock protein (class I) heat shock protein (class I) heat shock protein X GroEI GroES alkyl hydroperoxide reductase alkyl hydroperoxide reductase alkyl hydroperoxide reductase alkyl hydroperoxide reductase arsenate reductase cytochrome c peroxidase periplasmic divialent cation tolerance protein	28.5% 31.9% 51.196 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.9% 27.7% 33.196 57.5% 39.4% 44.9% 51.196 38.8% 45.196 38.8% 45.196 38.8% 45.196 44.9% 56.296
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1030 Aq1030 Serine family Aq1556 Aq479 Aq1995 Cell Envelope Pili and fimbr Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq1753 Aq2177	gltB gltD proA proA proB proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH pidD q glyA serA ac fimZ ppdD1 ppdD2 ppdD1 ppdD2 ppdD1 lpt lpt lint nlpD1 nlpD2 oprC pal rlpA1	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhordatase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphorylosyl-ATP pyrophosphorylosyl-ATP pyrophosphorylosyl-ATP pyrophosphorylosyl-ATP pyrophosphorylosyl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl-atphosphoryl	44.3% 37.7% 47.9% 43.2% 43.2% 44.9% 35.1% 44.9% 35.1% 49.9%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq936 Aq1199 Aq920 Aq525 Aq761 Aq691 Aq698 Aq1718 Aq691 Aq1718 Aq187 Aq887 Aq1718 Aq1877 Aq877 Aq877 Aq873 Aq1735 Aq188 Aq188 Aq188 Aq188 Aq188 Aq189 Aq180 Aq190 Aq190 Aq190 Aq190 Aq190 Aq190 Aq180 Aq180 Aq180 Aq190 Aq19	acrE cafA fisH fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MreB rod shape determining protein for B rod shape determining protein for S robe for the shape determining protein (Suff) cytochrome c potein GrpE chaperone HsIU small heat shock protein (class I) heat shock protein GrpE chaperone HsIU small heat shock protein (class I) heat shock protein GrpE chaperone diskuptoreroxide reductase alkyl hydroperoxide reductase arsenate reductase cytochrome c peroxidase periplasmic divalent cation tolerance protein superoxide diskumtase (Fe/Mr family)	28,5% 31,9% 51,19% 30,8% 35,29% 48,6% 50,29% 44,99% 34,5% 37,6% 37,6% 41,3% 41
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq1986 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Cell Envelope Pili and fimbr Aq1433 Aq1432 Aq1434 Aq1435 Lipoproteins a Aq270 Aq1652 Aq1753 Aq529 Aq652 Aq2147 Aq1370 Aq1174	gltB gltD proA proA proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glutamate synthase small subunit glU gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase amiotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.4% 33.7% 49.9% 44.4% 33.7% 49.9%	Cell division Aq698 Aq1275 Aq693 Aq1233 Aq936 Aq1139 Aq920 Aq1582 Aq761 Aq691 Aq698 Aq1718 Aq188 Aq188 Aq188 Aq188 Aq187 Aq845 Aq025 Aq173 Aq130 Chaperones Aq154 Aq1735 Aq123 Aq192 Aq1283 Aq199 Aq238 Aq199 Detection Aq186	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MreB rod shape determining rotein MreB rod shape determining protein MreB rod shape determining rotein MinD rod shape determining rotein MinD rod shape determining rotein MinD rod shape determining rot	28,5% 31,9% 51,19% 30,8% 35,29% 48,6% 50,29% 44,99% 39,4% 43,5% 37,6% 37,6% 41,3% 45,16% 51,19% 45,16% 51,19% 45,16% 51,19% 45,16% 56,29% 49,29% 50,09% 48,9% 47,09% 34,29% 39,5% 39,29% 59,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652 Aq1753 Aq292 Aq2147 Aq1753 Aq529 Aq2147 Aq1750 Aq1174 Aq166	gltB gltD proA proA proB proB proB proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH pidD q glyA serA ac fimZ ppdD1 ppdD2 ppdD3 ppdD4 ppdD3 ppdD4 ppdD3 ppd	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhoritase histidinol-phosphate aminotransferase histidinol dehydrogenase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphorylosyl-ATP phosphoribosyl-ATP pyrophosphoryl-amidotransferase HisF (pyclase) ATP phosphoribosyl-ATP pyrophosphohydrolase L-seyl-IRNA(sey) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin ratio protein N-acyltransferase apolipoprotein N-acyltransferase apolipoprotein N-acyltransferase ilipoprotein lipoprotein kingment outer membrane protein c peptidoglycan associated lipoprotein rare lipoprotein A rare lipoprotein A rare lipoprotein A rare lipoprotein A adhesion protein	44.3% 37.7% 47.9% 43.2% 43.2% 44.9% 35.1% 44.9% 43.8% 49.9%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq1217 Aq847 Aq847 Aq847 Aq4735 Aq703 Aq996 Aq433 Aq192 Aq1283 Aq199 Aq2200 Aq2199 Detoxification Aq486 Aq858 Aq136 Aq486 Aq136 Aq136 Aq136 Aq136 Aq136 Aq136 Aq136 Aq136 Aq858 Aq136 Aq1005 Aq1499 Aq1050	acrE cafA fish fish fish fish fish fish fisy fisy gidA1 gidB mesj minD minD minD mreB rodA sufl dnal1 dnal2 dnal2 dnal2 dnal2 dnapc apc ctaB dnaK grpE apc ctaB ctaB ctaB ctaB ctaB ctaB ctaB cta	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein F84 cell division protein F87 cell division protein F87 cell division protein F87 cell division protein F87 dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Ms1 septum site-determining protein MinD red spart determining protein MinD red shape determining protein MinD red shape determining protein Mref red shape determining protein for Septum S	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Cell Envelope Pili and fimbr Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq819 Aq829 Aq2147 Aq1753 Aq1529 Aq2147 Aq1730 Aq1730 Aq1730 Aq1730 Aq1730 Aq1730 Aq1730 Aq1731 Aq1620 Aq652 Aq1730 Aq1730 Aq1731 Aq1730 Aq1740 Aq1740 Aq1740 Aq1740 Aq1740 Aq1740 Aq1740 Aq1740 Aq1740	gltB gltD proA proA proA hisA hisB hisC hisD hisC hisD hisE hisG hisH hisH hisH hisH pidP glyA setA setB ac fmZ ppdD1 ppdD2 ppdD2 ppdD2 ppdD1 nlpD2 oprC pal nlpD1 nlpD1 nlpD2 oprC pal rlpA1 rlpA2 scbA yfeA	glutamate synthase large subunit glutamate synthase small subunit glU gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase amiotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.4% 33.7% 49.9% 44.4% 33.7% 49.9%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq936 Aq1139 Aq920 Aq1139 Aq921 Aq911	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein ModA periplasmic cell division protein (Suft) cytochrome c oxidase assembly factor chaperone DnaJ Hsp70 chaperone DnaJ Hsp70 chaperone DnaIA hsp70 chaperone DnaIA hsp870 chaperone fisU small heat shock protein (class I) heat shock protein GrpE chaperone HsU small heat shock protein (class I) heat shock protein X GroEL GroES alkyl hydroperoxide reductase alkyl hydroperoxide reductase arsenate reductase cytochrome c peroxidase periplasmic divalent cation tolerance protein superoxide dismutase (CuUZn) superoxide dismutase (CuUZn) thiol peroxidase	28,5% 31,9% 51,19% 30,8% 35,29% 48,6% 50,29% 44,99% 39,4% 43,5% 37,6% 37,6% 41,3% 45,16% 51,19% 45,16% 51,19% 45,16% 51,19% 45,16% 56,29% 49,29% 50,09% 48,9% 47,09% 34,29% 39,5% 39,29% 59,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq792 Aq1905 Serine family Aq1556 Cdl Envelope Pili and fimbr Aq1479 Aq1905 Cdl Envelope Aq14134 Aq1435 Lipoproteins a Aq270 Aq183 Aq1436 Aq1437 Aq1370 Aq1174 Aq2166 Aq619	gltB gltD proA proA hisA hisB hisB hisC hisD hisF hisG hisF hisG hisH hisH hisH hisH hisH glyA serA ac glyA serA ac in ffinZ ppdD1 ppdD2 ppdD3 md porins lig in tipn1 mpD2 schA yfeA	glutamate synthase lange subunit gltD gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase shistidinol-phosphate aminotransferase shistidinol-phosphate aminotransferase HisF (cyclase) ATP phosphoribosyl-transferase amidotransferase HisF (pyclase) L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pil	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.9% 33.7% 49.9%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq225 Aq7611 Aq691 Aq1582 Aq1718 Aq1887 Aq1217 Aq874 Aq1735 Aq703 Aq926 Aq133 Aq996 Aq433 Aq192 Aq128 Aq128 Aq1887 Aq1200 Aq2199 Detoxification Aq486 Aq888 Aq136 Aq105 Aq199 Aq238 Aq199 Aq238 Aq199 Aq238 Aq198 Aq885 Aq136 Aq105 Aq199 Aq238 Aq198 Aq685 Aq136 Aq105 Aq1499 Aq128 Aq188 Motility Aq833	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PstA cell division protein PstA cell division protein PstB cell division protein PstW cell division protein PstZ cell division protein PstZ cell division protein PstZ cell division protein PstZ diucose inhibited division protein A glucose inhibited division protein MinC septum site-determining protein MinC septum site-determining protein MinC septum site-determining protein MinD septum site-determining protein MinC septum site-determining protein MinD septum site-determining protein Road periplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal Control Contro	28,5% 31,9% 51,19% 30,8% 35,29% 48,6% 50,29% 44,99% 39,4% 43,5% 37,6% 37,6% 41,3% 45,16% 51,19% 45,16% 51,19% 45,16% 51,19% 45,16% 56,29% 49,29% 50,09% 48,9% 47,09% 34,29% 39,5% 39,29% 59,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5% 39,29% 59,5% 39,5
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Cell Envelope Pili and fimbr Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq829 Aq2147 Aq1753 Aq1754 Aq2176 Aq1754 Aq1754 Aq1754 Aq1754 Aq1754 Aq1754 Aq1755 Aq1757 Aq1757 Aq1757 Aq1757 Aq1770 Aq1774 Aq1774 Aq1774 Aq1774 Aq1776 Aq1777 Aq1776 Aq1777 Aq177	gltB gltD proA proA proA hisA hisB hisC hisD hisC hisD hisF hisG hisH hisH hisH hisH pidP glyA setA setB ac fmZ ppdD1 ppdD2 ppdD2 ppdD1 ppdD2 ppdD1 nlpD2 oprC pal nlpD1 nlpD2 oprC pal rlpA1 rlpA2 yfeA alr	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhoritase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisF (pyclase) ATP phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase Cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin pilin pilin prolipoprotein N-acyltransferase apolipoprotein N-acyltransferase apolipoprotein N-acyltransferase ilipoprotein N-acyltransferase ilipoprotein N-acyltransferase ilipoprotein ilipoprotein ilipoprotein A rare lipoprotein A adhesion protein adhesion B precursor	44.3% 37.7% 47.9% 43.2% 43.2% 44.2% 35.1% 40.9% 44.6% 33.7% 49.9% 49.9% 49.9% 49.9% 43.8% 47.7% 43.8% 42.7% 43.8% 42.7% 44.1%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq922 Aq726 Aq721 Aq691 Aq4178 Aq687 Aq41718 Aq877 Aq845 Aq1217 Aq878 Aq1217 Aq878 Aq1217 Aq878 Aq1218 Aq128 Aq128 Aq13 Aq199 Aq13 Aq199 Aq13 Aq199 Aq13 Aq199 Aq13 Aq199 Aq186 Aq858 Aq685 Aq136 Aq1486 Aq154 Aq154 Aq154 Aq154 Aq154 Aq154 Aq155 Aq13 Aq199 Aq169 Aq189 Aq188 Aq488 Aq184	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PsA cell division protein PsZ cell vision protein PsZ cell vision protein PsZ dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MsJ septum site-determining protein MinD septum site-determining protein Site site-determining protein MinD septum site-dete	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 48.6% 50.2% 49.9% 44.9% 37.6% 37.6% 37.6% 38.8% 41.3% 41.3% 41.3% 41.3% 45.1% 59.1%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq1988 Selenocysteine Aq1031 Aq1030 Serine family Aq195 Cell Envelope Pili and fimbr Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq1805 Aq819 Aq652 Aq1753 Aq2147 Aq1370 Aq1174 Aq2166 Aq619 Peptidoglycan Aq1827 Aq1681 Aq2195	gltB gltD proA proA proA hisA hisB hisC hisD hisF hisF hisF hisF hisF hisF hisF hisF	glutamate synthase large subunit glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate Skinase pyrroline carboxylate reductase glutamate Skinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol dehydrogenase Hisf (cytabe) ATP phosphoribosyl-transferase amidotransferase Hisf I phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin prolipoprotein Na-Cyltransferase lipoprotein NpD fragment outer membrane protein c peptidoglycan associated lipoprotein rare lipoprotein A rare lipoprotein A adhesion B precursor alanine racemase N-acetylmuramoyl-L-alanine amidase undecaprenol kinase	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.2% 35.1% 440.9% 44.2%	Cell division Aq698 Aq1275 Aq693 Aq1275 Aq936 Aq1139 Aq920 Aq1189 Aq921 Aq691 Aq691 Aq691 Aq691 Aq691 Aq691 Aq691 Aq691 Aq691 Aq697 Aq691 Aq697 Aq691 Aq697 Aq691 Aq697 Aq691 Aq697 Aq691 Aq698 Aq121 Aq697 Aq691 Aq696 Aq123 Aq123 Aq192 Aq1283 Aq1991 Aq696 Aq698 Aq189 Aq199 Aq1050 Aq238 Aq488 Aq688 Aq688 Aq688 Aq688 Aq698 Aq136 Aq1050 Aq238 Aq488 Aq698 Aq189 Aq188	acrE cafA fisH fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MreB rod shape determining protein for Shaperone DnaJ hsp70 chaperone DnaJ hsp70 chaperone DnaJ hsp70 chaperone DnaJ hsp70 chaperone HsIU small heat shock protein GrpE chaperone HsIU small heat shock protein (class I) heat shock protein GrpE chaperone HsIU small heat shock protein GrpE chaperone dissumtase (culzn) heat shock protein figure dissumtase (culzn) superoxide dissumtase (culzn)	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 48.6% 50.2% 49.9% 44.9% 37.6% 37.6% 37.6% 38.8% 41.3%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq181 Aq1613 Aq79 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1492 Aq1434 Aq1434 Aq1435 Aq1435 Aq1436 Aq1730 Aq1733 Aq1930 Paptidoglycan Aq1827 Aq1827 Aq18170 Aq1773 Aq1870 Aq1877 Aq1870 Aq1870 Aq1877 Aq1870 Aq1877 Aq1870 Aq1877	gltB gltD proA proA proA hisA hisB hisC hisD hisF hisG hisF hisG hisF hisG hisF hisG selD cysM glyA serA ac fmZ ppdD1 ppdD2 ppdD3 ad porins lig lint nlpD1 nlpD2 oprC pal rlpA1 rlpA1 rlpA1 rlpA2 sebA yfeA alr amiB bacA cybA1	glutamate synthase large subunit gltD gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase shistidinol-phosphate aminotransferase histidinol-phosphate aminotransferase HisF (cyclase) ATP phosphoribosyl-transferase amidotransferase HisF (phosphoribosyl-transferase selenophosphate synthase cycletine synthase, O-acetylserine (thiol) hyase B cycletine synthase, O-acetylserine (thiol) hyase B cycletine synthase, O-acetylserine (thiol) hyase B cycletine synthase cycletine synthase co-acetylserine phosphosphoglycerate dehydrogenase minor pilin p	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.6% 33.7% 49.9% 44.6% 33.7% 49.9% 43.8% 47.7% 43.8% 47.7% 44.1%	Cell division Aq698 Aq1275 Aq523 Aq936 Aq1275 Aq139 Aq220 Aq1199 Aq220 Aq1199 Aq220 Aq118 Aq1887 Aq878 Aq1217 Aq875 Aq121 Aq875 Aq121 Aq1925 Aq123 Aq129 Aq1	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSY cell division protein PSY cell division protein PSY cell division protein PSI glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MonD septum site-determining protein MonD septum site-determining protein MonD septum site-determining protein MonD of shape determining protein MonD of shape determining protein MonD cytochrome c oxidase assembly factor chaperone Dnal Hsp70 chaperone DnaK heat shock protein GapE thapeone FIsU detail site of the shock protein (class I) beat shock protein CapE GroES GroES Salval hydroperoxide reductase alkyl hydroperoxide reductase arsenate	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq181 Aq1613 Aq79 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1492 Aq1434 Aq1434 Aq1435 Aq1435 Aq1436 Aq1733 Aq1950 Aq1733 Aq1950 Aq1827 Aq819 Aq652 Aq1734 Aq1774	gltB gltD proA proA proB proB proB proC hisA hisB hisC hisD hisF hisG hisF hisG hisF hisG hisF hisH hisH hisH hisH hisH hisH hisH glyA serA ac fimZ ppdD1 ppdD2 ppdD3 ad dporins lig lint nlpD1 nlpD2 oprC pal rlpA1 rlpA2 ar ghA1 rdpA1 rdpA1 rdpA2 ddlA	glutamate synthase large subunit glut glutamate synthase small subunit glut gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase pyrroline carboxylate sindical carboxamide ribotide isomerase imidazoleglycerolphosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cycleine synthase (O-acetylserine (thiol) lyase B serine hydroxymethyl transferase cycleine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase minor pilin pil	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 44.2% 35.1% 440.9% 44.2%	Cell division Aq698 Aq1275 Aq936 Aq1275 Aq936 Aq129 Aq921 Aq	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcrE cytoplasmic axial filament protein cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSI dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein MSI septum site-determining protein MinD septum site-determining protein MonD red shape determining protein MonD cytochrome c oxidase assembly factor chaperone DnaJ Hsp70 chaperone DnaK heat shock protein GapE small heat shock protein (class I) heat shock protein X GroEI GroES allyl hydroperoxide reductase allyl hydroperoxide reductase allyl hydroperoxide reductase eytochrome c peroxidase periplasmic divalent cation tolerance protein superoxide dismutase (CulZn)	28.5%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq1988 Selenocysteine Aq1031 Aq1030 Serine family Aq195 Cell Envelope Pili and fimbr Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652 Aq1753 Aq529 Aq2147 Aq1370 Aq1753 Aq219 Aq1370 Aq1827 Aq1681 Aq2195 Aq1827 Aq1827 Aq1681 Aq2195 Aq1827	gltB gltD proA proA proA hisA hisB hisC hisD hisF hisF hisF hisF hisH hisE selD cysM glyA serA ac fimZ ppdD1 ppdD2 ppdD3 lgt lnt nlpD1 nlpD2 oprC oprC pdd alr amiB bacA cphA1 cphA1 cphA1	glutamate synthase large subunit glutamate synthase small subunit glU gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase Hisf (cyclase) ATP phosphoribosyl-transferase amidotransferase Hisf I phosphoribosyl-ATP pyrophosphohydrolase L-scryl-tRNA(scr) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin proticprotein NapD fragment outer membrane protein c peptidoglycan associated lipoprotein rare lipoprotein A rare lipoprotein A rare lipoprotein A adhesion protein adhesion B precursor salanine racenase N-acetylmuramoyl-L-alanine amidase undecaprenol kinase beta lactamase precursor beta lactamase precursor beta lactamase precursor D-alaninel jasse glucosminie-frictose-6-phosphate	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 43.2% 35.1% 40.9% 44.6% 33.7% 49.9% 40.5% 42.7%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq936 Aq1139 Aq920 Aq139 Aq920 Aq1582 Aq761 Aq691 Aq698 Aq1718 Aq4878 Aq1718 Aq4878 Aq1713 Aq875 Aq025 Aq171 Aq871 Aq1713 Aq1713 Aq1713 Aq1713 Aq1713 Aq1713 Aq1714 Aq1713 Aq1714 Aq1713 Aq188 Aq189 Aq2051 Aq189 Aq2051 Aq189 Aq288 Aq188 Aq188 Aq188 Aq188 Aq188 Aq188 Aq188 Aq1889 Aq2051 Aq894 Aq1714 Aq1713	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsW cell division protein PsW cell division protein PsW cell division protein PsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD septum site-determining protein MreB rod shape determining protein forth shaperone Dnal Hsp70 chaperone Dnal Hsp70 chaperone Dnal Hsp870 chaperone Hsp870 chaperone Hsp870 chaperone Hsp870 chaperone Hsp870 chaperone Hsp870 chaperone H	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 48.6% 50.2% 49.9% 44.9% 33.45% 33.45% 34.49% 33.45% 34.49% 34.9% 34.9% 49.9%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq188 Aq198 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1432 Aq1434 Aq1435 Lipoproteins a Aq270 Aq819 Aq652 Aq1753 Aq2195 Aq2170 Aq11774 Aq11774 Aq11774 Aq11777 Aq1177 Aq177 A	gltB gltD proA proA hisA hisB hisB hisC hisD hisF hisG hisF hisG hisF hisG hisF hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit gltD gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase pyroline carboxylate sk-kinase pyroline carboxylate sk-kinase pyroline sk-kinase sk-kinase pyroline sk-kinase sk-ki	44.3% 37.7% 47.9% 43.2% 48.2%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq723 Aq736 Aq1139 Aq722 Aq721 A	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSY cell division protein PSY cell division protein PSY cell division protein PSY cell division protein PSI glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinCI septum site-determining protein ModA periplasmic cell division protein MCEI rod shape determining protein function shape determining protein function shape determining protein function shape determining protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal Hsp70 chaperone Dnal Hsp70 chaperone Dnal K heat shock protein GrgE dhy hydroperoxide reductase alkyl hydroperoxide reductase arsenate reductase rychorhome c pereductase alkyl hydroperoxide reductase arsenate reductase rychorhome c pereductase alkyl hydroperoxide reductase arsenate reductase rychorhome c pereductase arsenate reductase rychorhome c pereductase arsenate reductase arsenate reductase rychorhome pereductase arsenate reductase rychorhome rychorhome rychorhome rychorhome rychorhome rychorhome rychorhome rychorhome	28.5% 31.9% 51.19% 30.8% 35.29% 48.69% 50.29% 50.29% 50.29% 50.29% 50.29% 50.39,4% 60.39,4% 60.39,4% 60.39,4% 60.39,4% 60.39,5% 6
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq181 Aq1613 Aq79 Aq1905 Cell Envelope Pili and fimbr. Aq1433 Aq1492 Aq1434 Aq1434 Aq1435 Aq1435 Aq1436 Aq1733 Aq1950 Aq1733 Aq1950 Aq1827 Aq819 Aq652 Aq1734 Aq1774	gltB gltD proA proA proA hisA hisB hisC hisD hisC hisD hisF hisG hisF hisG hisF hisG selD cysM glyA serA ac fimZ ppdD1 ppdD1 ppdD2 ppdD3 and porins lig lint nlpD1 nlpD2 oprC pal ripA1 ripA2 aripA1 ripA2 aripA1 ripA2 ddlA	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphohydrolase Ls-eryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase selenophosphate synthase cysteine synthase pyrophosphosphosphosphosphosphosphosphospho	44.3% 37.7% 47.9% 43.2% 35.1% 440.9% 43.2% 45.9% 45.8% 47.7%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq723 Aq726 Aq1139 Aq220 Aq721 A	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSW cell division protein PSW cell division protein PSY cell division protein PSZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mss] septum site-determining protein MinC septum site-determining protein MinD nod shape determining protein MinD septum site-determining protein MinD septum site-determining protein Mod periplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal hap-rote division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal hap-rote Dnal hap-rote Dnal hap-rotein CpE chaperone FMSU small heat shock protein (class I) heat shock protein GrpE chaperone HSU small heat shock protein (class I) heat shock protein X GroEL G	28.5% 31.9% 51.19% 30.8% 35.29% 48.6% 50.29% 50.29% 50.29% 50.29% 50.27% 50.39,4% 50.39,4% 50.39,4% 50.39,4% 50.39,4% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.39,5% 50.4% 50.9% 50.4% 50.9% 50.4% 50.9% 50.4% 50.9%
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq782 Aq1986 Selenocysteine Aq1031 Aq1030 Serine family Aq1556 Cell Envelope Pili and fimbr. Aq1433 Aq1432 Aq1434 Aq1435 Lipoproteins a Aq270 Aq1652 Aq1753 Aq2147 Aq1370 Aq1753 Aq2147 Aq1370 Aq1754 Aq2166 Aq619 Peptidoglycan Aq1827 Aq1619 Peptidoglycan Aq1827 Aq1619 Aq619 Aq619 Aq619 Aq619 Aq619 Aq619 Aq619 Aq1827 Aq1734 Aq2166 Aq619	gltB gltD proA proA hisA hisB hisB hisC hisD hisF hisG hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glutamate synthase small subunit glU gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyroline carboxylate reductase phosphoribosylfromimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	44.3% 37.7% 47.9% 43.2% 35.1% 40.9% 43.2% 35.1% 40.9% 44.1% 33.7.7% 49.9% 49.9% 49.9% 49.9% 49.9% 49.9% 49.9% 49.9% 49.9% 49.9% 41.7% 42.7% 37.7% 42.7% 37.7% 42.7% 37.7% 42.7% 37.7% 42.8% 42.9% 41.1	Cell division Aq698 Aq1275 Aq936 Aq1275 Aq936 Aq1139 Aq9205 Aq761 1 Aq691 Aq698 Aq1718 Aq188 Aq188 Aq188 Aq188 Aq188 Aq188 Aq188 Aq189 Aq173 Aq183 Aq188 Aq1	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PsA cell division protein PsZ cell division protein PsZ cell division protein PsZ cell division protein PsZ ducose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes cell cycle protein Misc septum site-determinian protein Misc septum site-determinian protein Misc septum site-determinian protein Misc of shape determining protein Misc of shape determining protein Misc of shape determining protein RodA periplasmic cell division protein (Sufl) cytochrome c oxidase assembly factor chaperone Dna] chaperone Dna] chaperone Dna] chaperone Dna; chaperone TsAll usmall heat shock protein (class I) heat shock protein (class I) heat shock protein (class I) heat shock protein X GroEI. GroES alkyl hydroperoxide reductase alkyl hydroperoxide reductase alkyl hydroperoxide reductase eyrochrome c peroxidase periplasmic divalent cation tolerance protein superoxide dismutase (CulZn)	28.5% 31.9% 51.196 30.8% 35.296 48.696 50.296 57.596 39.496 44.996 27.796 33.196 35.296 44.996 45.196 38.896 45.196 45.196 45.196 45.196 45.196 46.296 49.296
Aq1565 Aq2064 Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq161 Aq782 Aq1986 Selenocysteine Aq1031 Aq1030 Serine family Aq1056 Aq479 Aq1995 Cell Envelope Pili and fimbr. Aq1433 Aq1434 Aq1435 Lipoproteins a Aq270 Aq1652 Aq1753 Aq2147 Aq1370 Aq1753 Aq2166 Aq619 Peptidoglycan Aq181 Aq219 Aq652 Aq1753 Aq529 Aq2147 Aq1370 Aq1174 Aq2166 Aq619 Peptidoglycan Aq181 Aq181 Aq2195 Aq621 Aq41798 Aq181 Aq2195 Aq627 Aq1798 Aq181 Aq2195 Aq5211 Aq301 Aq607	gltB gltD proA proA hisA hisB hisB hisC hisD hisF hisG hisH hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	glutamate synthase large subunit glut gamma-glutamyl phosphate reductase glutamate sk-kinase pyrroline carboxylate reductase glutamate sk-kinase pyrroline carboxylate reductase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase HisF (cyclase) ATP phosphoribosyl-ATP pyrophosphohydrolase Ls-eryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase selenophosphate synthase cysteine synthase pyrophosphosphosphosphosphosphosphosphospho	44.3% 37.7% 47.9% 43.2% 35.1% 440.9% 43.2% 45.9% 45.8% 47.7%	Cell division Aq698 Aq1275 Aq698 Aq1275 Aq723 Aq726 Aq1139 Aq220 Aq721 A	acrE cafA fish fish fish fish fish fish fish fish	acriflavin resistance protein AcE cytoplasmic axial filament protein cell division protein PSH cell division protein PSH cell division protein PSH cell division protein PSW cell division protein PSW cell division protein PSY cell division protein PSZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mss] septum site-determining protein MinC septum site-determining protein MinD nod shape determining protein MinD septum site-determining protein MinD septum site-determining protein Mod periplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal hap-rote division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal hap-rote Dnal hap-rote Dnal hap-rotein CpE chaperone FMSU small heat shock protein (class I) heat shock protein GrpE chaperone HSU small heat shock protein (class I) heat shock protein X GroEL G	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 55.25% 39.4% 45.196 31.9% 31.9% 31.9% 31.9% 54.596 57.496 31.9% 31.9% 59.196 38.8% 41.396 45.196 50.296 51.196 56.296 39.296 39.296 39.596 39.596 39.596 39.596

1 2001	din.	4 H 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	24.20/	1 505		111 6 11 1 1 0	45.00/
Aq2001	fliD	flagellar hook associated protein FliD	24.3% ••	Aq527	moaC	molybdenum cofactor biosynthesis moaC	45.0% ••
Aq1182	fliF	Flagellar M-ring protein	32.0% ••••	Aq2181	moaE	molybdopterin converting factor subunit 2	39.3% •••
Aq653	fliG	flagellar switch protein FliG	35.9% ••••	Aq1326	mobB	molybdopterin-guainine dinucleotide	44.407
Aq1595	fliI	flagellar export protein	44.6% ••••			biosynthesis protein B	44.4% •
Aq1860	fliL	flagellar biosynthesis FliL	30.6% ••••	Aq030	moeA1	molybdenum cofactor biosynthesis protein A	36.8% ••••
Aq1539	fliN	flagellar switch protein FliN	42.9% •••	Aq1329	moeB	molybdopterin biosynthesis protein MoeB	54.1% ••••
Aq1920	fliP	flagellar biosynthetic protein FliP	47.7% ****	Aq061	mog	molybdenum cofactor biosynthesis MOG	55.5% ****
Aq1962	fliQ	flagellar biosynthesis protein FliQ	45.5% ••••	Aq049	phhB	pterin-4a-carbinolamine dehydratase	37.9% ••••
Aq1961	fliR	flagellar biosynthetic protein FliR	29.7% ••••	Panthenate			
Aq2002	fliS	flagellar protein FliS	30.8% ••••	Aq815	dfp	pantothenate metabolism flavoprotein	41.2%
Aq1003	motA	flagellar motor protein MotA	35.0%	A-1072		3-methyl-2-oxobutanoate	41.270 ****
Aq1002	motB1	flagellar motor protein MotB	36.8%	Aq1973	panB	3-methyl-2-oxobutanoate	
Aq1001	motB2	flagellar motor protein MotB-like	27.5% ••••			hydroxymethyltransferase	45.5%
	mous	ingenia motor proteir moto inc	27.570	Aq2132	panC	pantothenate synthetase	47.4%
Secretion				Aq476	panD	aspartate 1-decarboxylase	46.0% ****
Aq1720	ffh	signal recognition particle receptor protein	49.1%		-	· ·	
Aq1288	gspD	general secretion pathway protein D	27.5%	Pyridine nu			
Aq1474	genE		48.8%	Aq1889	nadA	quinolinate synthetase A	44.3%
Aq14/4	gspE	general secretion pathway protein E		Aq777	nadB	L-aspartate oxidase	36.7% •••
Aq418	gspG	general secretion pathway protein G	50.7%	Aq869	nadC	quinolinate phosphoribosyl transferase	47.0% ••••
Aq955	lepB	type-I signal peptidase	33.9% ••••	Aq959	nadE	NH(3)-dependent NAD+ synthetase	39.6%
Aq1837	lsp	lipoprotein signal peptidase	37.4% ••••				
Aq1271	mpp	processing protease	28.7% ••••	Pyridoxal pl			
Aq747	pilC1	fimbrial assembly protein PilC	37.4% ••••	Aq852	pdxA	pyridoxal phosphate biosynthetic protein PdxA	36.8% ****
Aq1285	pilC2	fimbrial assembly protein PilC	28.9%	Aq1423	pdxJ	pyridoxal phosphate synthetase	88.2% ****
Aq1601	pilD	type 4 prepilin peptidase	34.8%		-		
Aq745	pilT	twitching motility protein PilT	51.4%	Quinones			
Aq2151	pilU	twitching mobility protein	41.6%	Aq895	ispB	octoprenyl-diphosphate synthase	35.7% ••••
Aq1870	secA	preprotein translocase SecA subunit	44.9%	Aq052	ubiA	4-hydroxybenzoate octaprenyltransferase	41.4%
Aq973	secD	protein export membrane protein SecD	36.0%	Riboflavin			
Aq1602	secF	protein-export membrane protein	41.4%	Aq350	ribA	GTP cyclohydrolase II	61.7%
Aq1002				Aqoou	TIDA		
Aq079	secY	preprotein translocase SecY	44.2% ••••	Aq1707	ribC	riboflavin synthase alpha chain	45.3% ••••
Aq2080	sppA	proteinase IV	43.4% ••••	Aq138	ribD1	riboflavin specific deaminase	46.0% ••••
Aq1971	tapB	type IV pilus assembly protein TapB	42.2% ••••	Aq436	ribD2	riboflavin specific deaminase	42.9% ****
Aq1340	tig	trigger factor	27.4% ••••	Aq139	ribF	riboflavin kinase	38.4%
				Aq132	ribH	riboflavin synthase beta subunit	51.0% ••••
Central Inter	mediary Metabo	dism				, ,	
One-carbon	metabolism			Thiamine			
Aq1429	metF	5,10-methylenetetrahydrofolate reductase	43.3% ••••	Aq1204	thiC	thiamine biosynthesis protein	67.1% ••••
Aq1154	metK	S-adenosylmethionine synthetase	49.2% ••••	Aq1960	thiD	HMP-P kinase	40.5% ****
Aq1180	sahH	S-adenosylhomocysteine hydrolase	60.9% ••••	Aq1366	thiE1	thiamine phosphate synthase	36.3% ****
				Aq558	thiE2	thiamine phosphate synthase	39.5% ••••
	polysaccharides			Aq2178	thiG	thiamine biosynthesis, thiazole moiety	52.5%
Aq1407	bcsA	cellulose synthase catalytic subunit	39.5% ••••	Aq2119	thiL	thiamine monophosphate kinase	34.5%
Aq1401	celY	endoglucanase fragment	33.0% ••			инанине топорнозрнае кшазе	J4.J /0 ****
Aq721	glgA	glycogen synthase	38.1%	Thio- and g	lutaredoxin		
Aq722	glgB	1,4-alpha-glucan branching enzyme	56.5% ••••	Aq443	gua	glutaredoxin-like protein	33.8%
Aq717	glgP	glycogen phosphorylase	37.0%	Aq1916	trxAl	thioredoxin	58.9% •••
A 0722	malM	4-alpha-glucanotransferase (amylomaltase)	42 404	Aq1811	trxA2	thioredoxin	32.2% ••
Aq723		4-aipha-gidcanotransierase (amyiomanase)	43.4% ••••	A-500			
Tri-carboxyli	ic acid cycle			Aq500	trxB	thioredoxin reductase	39.8% ••••
Aq1784	aco	aconitase	36.1% •••	Energy Meta	abolism		
Aq1195	forA1	ferredoxin oxidoreductase alpha subunit	31.5% •••	Aq1342	gph	phosphoglycolate phosphatase	33.9%
Aq1167	forA2	ferredoxin oxidoreductase alpha subunit	32.3%			prospriogryconic prosprintisc	33.5 /0 ****
	forB1	ferredoxin oxidoreductase aipiia subunit	29.6%	ATP-Proton	Motive Force		
Aq1196			31.5%	Aq679	atpA	ATP synthase F1 alpha subunit	64.3% ****
Aq1168	forB2	ferredoxin oxidoreductase beta subunit		Aq179	atpB	ATP synthase F0 subunit a	36.4%
Aq1200	forG1	ferredoxin oxidoreductase gamma subunit	34.5% ••••	Aq673	atpC	ATP synthase F1 epsilon subunit	37.4%
Aq1169	forG2	ferredoxin oxidoreductase gamma subunit	34.5% •••	Aq2038	atpD	ATP synthase F1 beta subunit	67.4% ••••
Aq594	frdA	fumarate reductase flavoprotein subunit	51.4%	Aq177	atpD	ATP synthase F1 beta subunit ATP synthase F0 subunit c	53.8% •••
Aq553	frdB1	reductase iron-sulfur subunit	35.2% ****	A-1500	atpE	ATP synthase F0 subunit b	26.3%
Aq655	frdB2	fumarate reductase iron-sulfur subunit	35.1%	Aq1586	atpF1		20.5% ****
Aq1780	fumB	fumarate hydratase (fumarase)	46.4%	Aq1587	atpF2	ATP synthase F0 subunit b	25.5% ••••
Aq1679	fumX	C-terminal fumarate hydratase, class I	40.4%	Aq2041	atpG	ATP synthase F1 gamma subunit	39.9%
Aq150	gltA	citrate synthase	33.0%	Aq1588	atpH	ATP synthase F1 delta chain	28.1% ****
A-1512	gith	citrate synthase		D.I			
Aq1512	icd	isocitrate dehydrogenase	46.0% ••••	Dehydroger	iases	1 1 1 1 1 1	25 404
Aq1782	mdh1	malate dehydrogenase	49.8% ****	Aq1362	adh1	alcohol dehydrogenase	35.4% ••••
Aq1665	mdh2	malate dehydrogenase	46.9% •••	Aq1240	adh2	alcohol dehydrogenase	28.8%
Aq1614	oadA	oxaloacetate decarboxylase alpha chain	50.1%	Aq186	aldH1	aldehyde dehydrogenase	41.9%
Aq1306	sucC1	succinyl-CoA ligase beta subunit	35.1%	Aq227	aldH2	aldehyde dehydrogenase	28.0% ****
Aq1620	sucC2	succinyl-CoA ligase beta subunit	52.9%	Aq1145	dhaT	1,3 propanediol dehydrogenase	36.6% ****
Aq1888	sucD1	succinyl-CoA ligase alpha subunit	41.7% •••	Aq232	dhsU	flavocytochrome C sulfide dehydrogenase	33.6%
Aq1622	sucD2	succinyl-CoA ligase alpha subunit	65.7%	Aq1769	dld1	D-lactate dehydrogenase	45.3%
	Suc172	succinyi-CoA ngase aipna subunit	03.770 ****	A-1224		D-factate denydrogenase	
Phosphate				Aq1234	dmsA	DMSO reductase chain A	25.0% ••••
Aq1351	phoH	phosphate starvation-inducible protein	47.1%	Aq1232	dmsB	DMSO reductase chain B	38.4% •••
Aq1547	ppa	inorganic pyrophosphatase	56.5% ****	Aq1231	dmsC	DMSO reductase chain C	29.5% •
Aq891	ppx	exopolyphosphatase	33.6%	Aq1051	fdhE	formate dehydrogenase formation protein FdhE	25.9% ••••
	PPA	скорогурнооргимизс	33.070 ****	Aq1039	fdoG	formate dehydrogenase alpha subunit	50.0%
Polyamines				Aq1046	fdoH	formate dehydrogenase beta subunit	45.7% ****
Aq728	speC	ornithine decarboxylase	30.9% ••••	Aq1049	fdoI	formate dehydrogenase gamma subunit	38.4%
Aq062	speE	spermidine synthase	48.4%	Aq1903	gcsP1	glycine dehydrogenase (decarboxylating)	49.6%
	-F	-F		Aq1109	gcsP2	glycine dehydrogenase (decarboxylating)	46.8%
Sulfur				Aq1639	glpC	oxido/reductase iron sulfur protein	27.1%
Aq1081	cysD	sulfate adenylyltransferase	46.7% ••••	Aq395	hdrA	heterodisulfide reductase subunit A	39.7%
Aq1076	rhdA	thiosulfate sulfurtransferase	32.3% ••••	A-400	hdrB	heterodisulfide reductase subunit A	32.5% ••••
Aq1799	rhdA	thiosulfate sulfurtransferase	31.7% ••••	Aq400			
Aq455	sor	sulfur oxygenase reductase	36.7%	Aq398	hdrC	heterodisulfide reductase subunit C	35.7% •
Aq1803	soxB	sulfur oxidation protein SoxB	41.3%	Aq961	hdrD	heterodisulfide reductase	29.5% ••••
		sultui oxidation protein 30xb	41.570 ****				
Cofactor Bios	synthesis			Aq038	hibD	3-hydroxyisobutyrate dehydrogenase	34.6% ****
Lipoic acid b				Aq038 Aq727	hibD ldhA	D-lactate dehydrogenase	34.6%
Aq1355				Aq727	ldhA	D-lactate dehydrogenase	34.6%
	lipA	Lipoic acid synthetase	48.9%	Aq727 Aq736	ldhA lpdA	D-lactate dehydrogenase dihydrolipoamide dehydrogenase	34.6% 33.5% 37.0%
	lipA	Lipoic acid synthetase	48.9% •••	Aq727 Aq736 Aq217	ldhA lpdA narB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB	34.6% 33.5% 37.0% 39.1%
Biotin				Aq727 Aq736 Aq217 Aq206	ldhA lpdA narB nirB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit	34.6% 33.5% 37.0% 39.1% 35.3%
Biotin Aq170	bioA	DAPA aminotransferase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835	ldhA lpdA narB nirB nox	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase	34.6% 33.5% 37.0% 39.1% 35.3%
Biotin Aq170				Aq727 Aq736 Aq217 Aq206 Aq835 Aq024	ldhA lpdA narB nirB nox nsd	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase	34.6% 33.5% 37.0% 39.1% 35.3% 33.1% 47.0%
Biotin Aq170 Aq975	bioA	DAPA aminotransferase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135	ldhA lpdA narB nirB nox nsd nueM	D-lactate dehydrogenase dihydrollpoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone)	34.6% 33.5% 37.0% 39.1% 35.3% 33.1% 47.0%
Biotin Aq170 Aq975 Aq557	bioA bioB bioD	DAPA aminotransferase biotin synthetase dethiobiotin synthetase	51.7% 42.0% 41.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024	ldhA lpdA narB nirB nox nsd	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase	34.6% 33.5% 37.0% 39.1% 35.3% 33.1% 47.0%
Biotin Aq170 Aq975 Aq557 Aq626	bioA bioB bioD bioF	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-oxononanoate synthase	51.7% 42.0%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010	ldhA lpdA narB nirB nox nsd nueM udh	D-lactate dehydrogenase dihydrollpoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone)	34.6% 33.5% 37.0% 39.1% 35.3% 33.1% 47.0%
Biotin Aq170 Aq975 Aq557	bioA bioB bioD	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyhexanoate-CoA ligase	51.7% 42.0% 41.5% 45.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra	ldhA lpdA narB nirB nox nsd nueM udh	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NADP)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase	34.6% 33.5% 37.0% 39.1% 35.3% 33.19 47.0% 28.2% 29.7%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659	bioA bioB bioD bioF bioW	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-xoononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyl CoA synthase)	51.7% 42.0% 41.5% 45.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I	34.6% 33.5% 37.0% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 42.4%
Biotin Aq170 Aq975 Aq557 Aq626	bioA bioB bioD bioF	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyhexanoate-CoA ligase	51.7% 42.0% 41.5% 45.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit I	34.6%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566	bioA bioB bioD bioF bioW	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-xoononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyl CoA synthase)	51.7% 42.0% 41.5% 45.1% 47.3% 37.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II	34.6% 33.5% 37.0% 39.1% 39.1% 31.1% 47.0% 28.2% 29.7% 42.4% 27.4%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid	bioA bioB bioD bioF bioW	DAPA aminotransferase biotin synthetase dethicibiotin synthetase 8-amino-7-osononanoate synthase 6-carboxyhezanoate-CoA ligase (pimedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase	51.7% 42.0% 41.5% 45.1% 47.3% 37.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NADP)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III	34.6%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045	bioA bioB bioD bioF bioW birA	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyhexanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase	51.7% 42.0% 41.5% 45.1% 47.3% 37.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II chem O oxygenase	34.6%
Biotin Aq170 Aq975 Aq557 Aq656 Aq1659 Aq566 Folic acid Aq2045 Aq1898	bioA bioB bioD bioF bioW birA folC folD	DAPA aminotransferase biotin synthetase dethioliotin synthetase 8-amino-7-exononanoate synthase 6-carboxyhezanoate-CoA ligase (pimedoy GoA synthase) biotin [acetyl-CoA-carboxylase] ligase folypolyglutamate synthetase methylenetetrahydrofolate dehydrogenase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153	ldhA lpdA narB nirB nox nsd nueM udh ansport coxA1 coxA2 coxB coxC	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NADP)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III	34.6%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239	bioA bioB bioD bioF bioW birA folC folD folE	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyi CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cydolydrolase I	51.7% 42.0% 41.5% 45.1% 47.3% 37.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2199 Aq2188 Aq153 Aq042	ldhA lpdA narB nirB nox nsd nueM udh insport coxA1 coxA2 coxB coxC ctaA cyc	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrate reductase (NADP)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III heme O oxygenase cytochrome c	34.6% 33.5% 37.0% 39.1% 35.3% 31.9% 47.0% 28.2% 29.7% 42.4% 28.6% 28.6% 28.6% 28.6% 25.8%
Biotin Aq170 Aq975 Aq557 Aq656 Aq1659 Aq566 Folic acid Aq2045 Aq1898	bioA bioB bioD bioF bioW birA folC folD	DAPA aminotransferase biotin synthetase dethioliotin synthetase 8-amino-7-exononanoate synthase 6-carboxyhezanoate-CoA ligase (pimedoy GoA synthase) biotin Jacetyl-CoA-carboxylase] ligase folypolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153 Aq042 Aq792	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxB coxC ctaA cyc	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III chem O oxygenase cytochrome c cytochrome	34.6% 33.5% 33.196 35.3% 31.196 35.3% 31.196 47.0% 28.2% 29.7% 22.4% 28.6% 22.4% 28.6% 28.196 25.8% 29.9% 29.9%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162	bioA bioB bioD bioF bioW birA folC folD folE folK	DAPA aminotransferase biotin symhetase dethiobiotin symhetase 8-mino-7-oxonoanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyi CoA synthase) biotin [aceyl-CoA-carboxylase] ligase follylpolyglutamate synthetase methyleneterlaylvafolate dehydrogenase GTP cyclohydroase I folate biosynthesis 7,8-dihydro-6- hydroxymethylpterin-pyrophosphokinase	51.7% 42.0% 41.5% 45.196 47.396 37.596 31.8% 53.2% 57.196	Aq727 Aq736 Aq217 Aq206 Aq885 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2198 Aq153 Aq042 Aq792 Aq1550	ldhA lpdA narB nirB nox nsd nueM udh insport coxA1 coxA2 coxB coxC ctaA cyc cycB1	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrate reductase (NADP)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit III heme O oxygenase cytochrome c cytochrome c cytochrome c cytochrome c cytochrome CS52	34.6% 33.5% 33.5% 33.1% 35.3% 35.3% 33.1% 47.0% 28.2% 29.7% 29.7% 29.7% 22.8.6% 22.4% 38.1% 27.4% 28.6% 28.1% 29.9% 38.7% 38.7% 38.7%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162	bioA bioB bioF bioF bioW birA folC folD folE folK	DAPA aminotransferase biotin synthetase delchiobiotin synthetase delchiobiotin synthetase 8-amino-7-exononanoate synthase 6-earboxyhezanoate-CoA ligase (pimeloyl GoA synthase) biotin [acetyl-CoA-earboxylase] ligase folypolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropterate synthase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1550 Aq1550	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase oxidase subunit II cytochrome c oxidase o	34.6% 33.5% 37.0% 39.1% 39.1% 39.1% 35.3% 31.9% 47.0% 28.2% 29.7% 42.4% 38.1% 27.4% 28.6% 28.8% 29.9% 38.7% 38.8% 38.8% 38.8%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB	DAPA aminotransferase boint symbetase dechiobiotin symbetase dechiobiotin symbetase 8-amino-7-oxononanoate Synthase 6-carboxyheanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylaolyglutamate synthetase methylenetertanlydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylterin-pyrophosphokinase dihydropteroate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1357 Aq1358	ldhA lpdA narB nirB nirB nox nsd nueM udh insport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydA	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II	34.6% 33.5% 37.0% 39.1% 39.1% 31.3% 31.2% 31.2% 31.2%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1144	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB	DAPA aminotransferase boint symbetase dechiobiotin symbetase dechiobiotin symbetase 8-amino-7-oxononanoate Synthase 6-carboxyheanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylaolyglutamate synthetase methylenetertanlydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylterin-pyrophosphokinase dihydropteroate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1358 Aq1358 Aq1358 Aq067	ldhA lpdA narB nirB nirB nox nsd nueM udh ansport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydB dmsB	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD/PH) large subunit NADH oxidase nuclotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase da subunit II cytochrome coxidase d subunit I cytochrome coxidase d subunit I cytochrome oxidase d subunit I dimethylsulfoxide reductase chain B	34.6% 33.5% 33.5% 39.1% 39.1% 39.1% 35.3% 33.1% 47.0% 28.2% 29.7% 42.4% 38.1% 27.4% 28.6% 28.1% 25.8% 29.9% 38.7% 38.8% 31.2% 40.2%
Biotin Aq170 Aq975 Aq557 Aq557 Aq626 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1468 Aq1144 Aq1606	bioA bioB bioF bioF bioW birA folC folD folE folK	DAPA aminotransferase biotin synthetase delchiobiotin synthetase delchiobiotin synthetase 8-amino-7-exononanoate synthase 6-earboxyhezanoate-CoA ligase (pimeloyl GoA synthase) biotin [acetyl-CoA-earboxylase] ligase folypolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropterate synthase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq004 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1357 Aq1357 Aq1358 Aq067 Aq235	ldhA lpdA narB nirB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydB dmsB fccB'	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c S2 cytochrome c S2 cytochrome c S2 cytochrome c S2 cytochrome c S3 cytochrome c S4 cytochrom	34.6% 33.5% 33.5% 37.0% 39.1% 39.1% 33.3% 33.1% 47.0% 28.2% 29.7% 22.4% 22.4% 38.1% 27.4% 28.6% 28.6% 29.9% 38.8% 38.8% 31.2% 38.9%
Biotin Aq170 Aq975 Aq557 Aq557 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1066 Heme	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-xononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyl CoA synthase) biotin Jacetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetterlaydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydrogynethylerin-pyrophosphokinase dihydropteroate synthese p-aminoderozote synthese p-aminoderozote synthesis aminoderoxychorismate lysse	51.7% 42.0% 41.5% 45.1% 47.3% 37.5% 31.8% 53.2% 57.1% 43.7% 43.7% 45.8% 41.5% 29.0% 61.5% 29.0% 61.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq1024 Aq1135 Aq1010 Electron tra Aq2191 Aq2199 Aq2188 Aq153 Aq153 Aq152 Aq1550 Aq1358 Aq1550 Aq150 Aq15	ldhA lpdA narB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydB dmsB fccB' fdx1	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrate reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c S52 cytochrome c532 cytochrome oxidase d subunit I dimethylsulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin	34.6% 33.5% 33.5% 33.5% 35.3% 39.1% 35.3% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 38.1% 27.4% 28.6% 29.9% 38.2%
Biotin Aq170 Aq975 Aq557 Aq557 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1066 Heme	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB	DAPA aminotransferase boint symbetase dechiobiotin symbetase dechiobiotin symbetase 8-amino-7-oxononanoate Synthase 6-carboxyheanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylaolyglutamate synthetase methylenetertanlydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylterin-pyrophosphokinase dihydropteroate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase p-aminoberoate synthase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq1024 Aq1135 Aq1010 Electron tra Aq2191 Aq2199 Aq2188 Aq153 Aq153 Aq152 Aq1550 Aq1358 Aq1550 Aq150 Aq15	ldhA lpdA narB nirB nirB nox nsd nueM udh unsport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydB dmsB fccB'	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (vlochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit I cytochrome coxidase d subunit I cytochrome coxidase d subunit I dimethylsulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin ferredoxin	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.3% 33.1% 47.0% 28.2% 29.7% 22.4% 22.4% 38.1% 27.4% 28.6% 28.6% 29.9% 38.8% 31.2% 38.7% 38.8% 31.2% 38.9% 31.2% 38.9%
Biotin Aq170 Aq975 Aq557 Aq557 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1606 Heme Aq207	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB pabC	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 8-amino-7-xononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyl CoA synthase) biotin Jacetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetterlaydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydrogynethylerin-pyrophosphokinase dihydropteroate synthese p-aminoderozote synthese p-aminoderozote synthese aminoderozote synthesis aminoderoxychorismate lysse	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2192 Aq2190 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1358 Aq067 Aq1358 Aq067 Aq235 Aq919A Aq1171a	ldhA lpdA narB nirB nox nsd nueM udh ansport coxA1 coxA1 coxA2 coxB coxC ctaA cyc cycB1 cycB2 cydA cydA dydB dmsB fccB' fdx1 fdx2	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (vlochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit I cytochrome coxidase d subunit I cytochrome coxidase d subunit I dimethylsulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin ferredoxin	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 35.3% 33.1% 47.0% 28.2% 29.7% 22.4% 22.4% 38.1% 27.4% 28.6% 29.9% 29.9% 38.8% 31.2% 38.7%
Biotin Aq170 Aq975 Aq955 Aq557 Aq526 Aq1659 Aq566 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB pabC cobA cysG	DAPA aminotransferase biotin symthetase dechiobiotin symthetase dechiobiotin symthetase 8-amino-7-oxononanoate synthase 6-carboxyhexanoate-CoA ligase (pimeloyi CoA synthase) biotin [acceyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methyleneterlanlydrofolate dehydrogenase GTP cyclohydroase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthases aminodeoxychorismate lyase uroporphyrin-III c-methyltransferase sirohene synthase	51.7% 42.0% 41.5% 45.1% 47.3% 37.5% 53.2% 57.1% 43.7% 29.0% 52.2% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.9% 55.2.9% 55.2.9% 55	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq792 Aq1550 Aq1357 Aq1358 Aq067 Aq235 Aq919a Aq1171a Aq11912a	ldhA lpdA narB nirB nox nsd mueM udh msport coxA1 coxA2 coxB coxC cyc lydA cydB fccB' fdx1 fdx1 fdx2 fdx2 fdx3	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (valoriment oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase dubunit II cytochrome coxidase d subunit I cytochrome coxidase d subunit I cytochrome oxidase flavoprotein subunit ferredoxin ferredoxin ferredoxin	34.6% 33.5% 33.5% 33.5% 35.3% 35.3% 35.3% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 38.1% 27.4% 28.6% 29.9% 38.2%
Biotin Aq170 Aq975 Aq957 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq334	bioA bioB bioD bioF bioW birA folC folID folE folK folP pabB pabC	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminoberoxote synthase aminodecoxytorismate lyase uroporphyrin-III c-methyltransferase siroheme synthase uroporphyrinoen decarboxylase	51.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 tra Aq2191 Aq2190 Aq2189 Aq2189 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq153 Aq153 Aq153 Aq153 Aq153 Aq153 Aq153 Aq153 Aq153 Aq167 Aq1357 Aq1358 Aq167 Aq235 Aq919a Aq1171a Aq1192a Aq1192a Aq1192a	ldhA narB nirB nox nsd nueM udh usport coxA1 coxA2 coxB coxC ctaA cyc cycB1 cydB dmsB fccB' fcdb' fdk2 fdk3 fdk4	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ushquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II dimethylsulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 22.4% 22.4% 22.4% 38.1% 27.4% 28.1% 29.9% 38.8% 38.8% 38.8% 38.8% 39.3% 38.9% 31.2% 38.9% 31.2% 40.2% 38.9% 31.2% 39.0% 35.0% 56.6% 56.6%
Biotin Aq170 Aq975 Aq957 Aq557 Aq626 Aq1659 Aq1666 Folic acid Aq2045 Aq1898 Aq239 Aq162 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq334 Aq816	bioA bioB bioD bioF bioW birA folC folD folE folB pabB pabC cobA cysG dcuP gsa	DAPA aminotransferase botion symbetase dechiobiotin symbetase dechiobiotin symbetase 8-amino-7-oxononanoate Symbase 6-carboxyheanoate-CoA ligase (pimeloyi CoA symbase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate symbetase methylenetertahydrofolate dehydrogenase GTP cyclohydroase I folate biosymbesis 7,8-dihydro-6-hydroxymethylterin-pyrophosphokinase dihydropteroate symbases aminodeoxychorismate lyase uroporphyrin-III c-methyltransferase sirohene symbase uroporphyrinogen decarboxylase uroporphyrinogen decarboxylase gutuamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase glutamate-1-semiladehyde aminotransferase	51.7% 42.0% 41.5% 45.1% 47.3% 37.5% 53.2% 57.1% 43.7% 29.0% 52.2% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.2.9% 55.9% 55.2.9% 55.2.9% 55	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq1550 Aq1358 Aq1550 Aq1358 Aq1550 Aq1358 Aq1550 Aq1358 Aq162 Aq192 Aq192 Aq192 Aq1171a Aq11912 Aq108a Aq108a Aq108a	ldhA narB nirB nox nsd nueM udh udh usport coxA1 coxA2 coxB coxC ctaA cyCB1 cyCB2 cydA dmsB fccB' fdx1 fdx2 fdx3 fdx4 fhp	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrate reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (Vathorme c oxidase subunit I cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase d subunit I cytochrome coxidase d subunit I cytochrome oxidase flavorite subunit formedoxin ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.2% 29.7% 38.1% 28.6% 29.9% 38.7% 38.7% 38.7% 38.7% 38.7% 38.7% 38.7% 38.7% 38.7% 38.7% 39.6% 43.9% 37.1% 43.9% 35.0%
Biotin Aq170 Aq975 Aq957 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1898 Aq239 Aq162 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq334	bioA bioB bioD bioF bioW birA folC folID folE folK folP pabB pabC	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-oxononanoate synthase 6-ariboxyhezanoate-CoA ligase (pinedoji CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase ethylenetetralpydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodexoxytorismate lyase uroporphyrin-III c-methyltransferase siroheme synthase uroporphyrinogen decarboxylase glutamate-1-semialdehyde aminotransferase glutamyl (RMA reductase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 37.5% 57.1% 43.7% 43.7% 43.7% 43.8% 41.5% 52.0% 52.1% 36.9% 41.4% 56.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2189 Aq2189 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq1537 Aq153 Aq163 Aq153 Aq163 Aq163 Aq163 Aq163 Aq1192 Aq	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase nucleotide sugar dehydrogenase (usiquinone) dehydrogenase votochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase d subunit II cytochrome coxidase d subunit II cytochrome	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 22.4% 22.4% 22.4% 38.1% 27.4% 28.1% 29.9% 29.9% 38.1% 29.9% 38.8% 31.2% 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 39.6 35.0% 56.6% 43.4% 32.5%
Biotin Aq170 Aq975 Aq957 Aq626 Aq1659 Aq1669 Aq1698 Aq239 Aq168 Aq1144 Aq1608 Aq1144 Aq1608 Aq1239 Aq162 Aq144 Aq169 Aq1239 Aq169 Aq1239 Aq169 Aq1239 Aq169 Aq169 Aq17 Aq17 Aq189 Aq	bioA bioB bioD bioF bioW birA folC folD folE folP pabB pabC cobA cysG dcuP gsa hemA	DAPA aminotransferase botion symbetase dechiobiotin symbetase dechiobiotin symbetase 8-amino-7-oxononanoate Synthase 6-carboxyheanoate-CoA ligase (pimeloyi CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetertanlydrofolate dehydrogenase GTP cyclohydroase I folate biosynthesis 7,8-dihydro-6-hydroxymethylenise pynophosphoshokinase dihydropteroate synthase aminodeoxychorismate lyase uuroporphyrin-III c-methyltransferase sinchene synthase uroporphyrinogen decarboxylase uroporphyrinogen decarboxylase glutamate1-semiddehyde aminotransferase glutamyl IRNA reductase (delta-aminotransferase glutamyl IRNA reductase (delta-aminotevulnates)	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 31.8% 53.2% 57.1% 43.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq902 Aq1550 Aq1357 Aq1358 Aq067 Aq235 Aq919a Aq1171a Aq1192a Aq108a Aq2191 Aq2108 Aq211 Aq2096 Aq045	ldhA narB nirB nox nsd nueM udh umsport coxA1 coxA2 coxB coxC ctaA cycB1 cycB2 cydA dmsB fccB' fdx1 fdx3 fdx4 ffdx3 fdx4 ffdx4 pfloX petA	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitriate reductase narB nitriate reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase da subunit II cytochrome c oxidase da subunit II cytochrome coxidase d subunit II cytochrome oxidase d subunit I cytochrome oxidase d subunit II cytochrome oxidase d subunit I cytochrome oxi	34.6% 33.5% 33.5% 33.5% 35.3% 35.3% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 22.4% 28.1% 28.6% 28.1% 28.6% 29.9% 38.8% 31.2% 48.0% 37.1% 43.9% 35.0%
Biotin Aq170 Aq1975 Aq1975 Aq1975 Aq1976 Aq1626 Aq1626 Aq1626 Aq2045 Aq1898 Aq239 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq234 Aq344 Aq816 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279	bioA bioB bioD bioF bioW birA folC folID folE folK folP pabB pabC cobA cysG dcuP gsa hemA hemB	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxynthosimate lyase uroporphyrin-III c-methyltransferase sinoheme synthase uroporphyrinogen decarboxylase glutamate-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblinogen synthase)	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 57.1% 47.396 57.196 52.1% 43.7% 43.7% 43.8% 41.5% 52.196 56.5% 38.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2189 Aq153 Aq042 Aq154 Aq194 Aq194 Aq194 Aq194 Aq194 Aq194 Aq195 Aq194 Aq194 Aq194 Aq194 Aq194 Aq194 Aq194 Aq211 Aq2096 Aq045 Aq044	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NADIPH) large subunit NADH oxidase nucleotide sugar dehydrogenase (usliquinone) dehydrogenase (usliquinone) dehydrogenase (usliquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase dubunit III cytochrome c oxidase dubunit II cytochrome c oxidase c ubunit II cytochrome c	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 22.4% 38.1% 27.4% 28.1% 22.86% 29.9% 38.1% 29.9% 38.8% 38.8% 31.2% 38.9% 31.2% 39.0% 37.1% 38.9% 31.2% 39.0% 37.1% 38.9% 31.2% 38.9% 31.2% 31.2% 38.9% 31.2% 31.3%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1689 Aq1898 Aq1398 Aq139 Aq1146 Aq1146 Aq1146 Aq1606 Henne Aq207 Aq146 Aq207 Aq134 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17	bioA bioB bioD bioF bioW folC folC folD folK folP pabB pabC cobA cysG dcuP gsa hemA	DAPA aminotransferase boint synthese dechiobiotin synthetase dechiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyheanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase (pimeloyl CoA synthase) complete the synthetase methyleneter tanhydrofolate dehydrogenase (TP cycloplydrolase) 1 folate biosynthesis 7.8-dihydro-6-hydroxymethyletein-prynphosphokinase dihydropteroate synthase aminodeoxychorismate lyase uuroporphyrin-III c-methyltransferase sirohene synthase uroporphyrinogen decarboxylase glutameti-1-serniadehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphobilinogen synthase porphobilinogen synthase porphobilinogen synthase porphobilinogen synthase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 31.8% 53.2% 57.1% 43.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq902 Aq1550 Aq1358 Aq1650 Aq1358 Aq067 Aq235 Aq1171a Aq1192a Aq108a Aq2111 Aq2096 Aq045 Aq044 Aq244	ldhA narB nirB nox nsd nueM udh umsport coxA1 coxA2 coxB coxC ctaA cycB1 cycB2 cydA dmsB fccB' fdx1 fdx3 fdx4 ffdx3 fdx4 ffdx4 pfloX petA	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitriate reductase narB nitriate reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase subunit II cytochrome c oxidase da subunit II cytochrome c oxidase da subunit II cytochrome c oxidase da subunit II cytochrome oxidase da subunit II cytochrome coxidase da subunit II cytochrome oxidase da subunit II dimethyslulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin	34.6% 33.5% 33.5% 33.5% 33.1% 34.7% 33.1% 34.7% 35.3% 33.1% 34.7% 35.3%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1689 Aq1898 Aq1398 Aq139 Aq1146 Aq1146 Aq1146 Aq1606 Henne Aq207 Aq146 Aq207 Aq134 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17 Aq17	bioA bioB bioD bioF bioW birA folC folID folE folK folP pabB pabC cobA cysG dcuP gsa hemA hemB	DAPA aminotransferase boint synthese dechiobiotin synthetase dechiobiotin synthetase 8-amino-7-oxononanoate synthase 6-carboxyheanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase (pimeloyl CoA synthase) complete the synthetase methyleneter tanhydrofolate dehydrogenase (TP cycloplydrolase) 1 folate biosynthesis 7.8-dihydro-6-hydroxymethyletein-prynphosphokinase dihydropteroate synthase aminodeoxychorismate lyase uuroporphyrin-III c-methyltransferase sirohene synthase uroporphyrinogen decarboxylase glutameti-1-serniadehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphobilinogen synthase porphobilinogen synthase porphobilinogen synthase porphobilinogen synthase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 53.2% 57.1% 43.7% 43.8% 45.8% 41.5% 52.0% 52.1% 56.5% 56.5% 58.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq902 Aq1550 Aq1358 Aq1650 Aq1358 Aq067 Aq235 Aq1171a Aq1192a Aq108a Aq2111 Aq2096 Aq045 Aq044 Aq244	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mirite reductase (NAD/PH) Harge subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase (volothrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase dubunit II cytochrome coxidase dubunit II cytochrome coxidase dubunit II dimethylsulfoxide reductase chain B sulfide dehydrogenase, flavoprotein subunit ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin flavohemoprotein flavodoxin Rieske-I iron sulfur protein cytochrome b Rieske-I iron sulfur protein	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 22.4% 38.1% 27.4% 28.1% 22.86% 29.9% 38.1% 29.9% 38.8% 38.8% 31.2% 38.9% 31.2% 39.0% 37.1% 38.9% 31.2% 39.0% 37.1% 38.9% 31.2% 38.9% 31.2% 31.2% 38.9% 31.2% 31.3%
Biotin Aq170 Aq1975 Aq1975 Aq1975 Aq1976 Aq1626 Aq1626 Aq1626 Aq2045 Aq1898 Aq239 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq234 Aq344 Aq816 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279 Aq1279	bioA bioB bioD bioF bioW folC folC folD folK folP pabB pabC cobA cysG dcuP gsa hemA	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxynthosimate lyase uroporphyrin-III c-methyltransferase sinoheme synthase uroporphyrinogen decarboxylase glutamate-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblinogen synthase)	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 53.2% 57.1% 43.7% 43.8% 45.8% 41.5% 52.0% 52.1% 56.5% 56.5% 58.7%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2189 Aq188 Aq153 Aq042 Aq792 Aq189 Aq1357 Aq108 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1193 Aq067 Aq1357 Aq235 Aq919 Aq1192 Aq119	ldhA narB lpdA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrate reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase (ytochrome coxidase subunit II cytochrome coxidase subunit III dimethydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) dehydrogenase (ubiquinone) ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin Riseke-l iron sulfur protein cytochrome b Riseke-l iron sulfur protein sulfur protein sulfur protein sulfur protein erductase	34.6% 33.5% 33.5% 33.5% 33.1% 34.7% 33.1% 34.7% 35.3% 33.1% 34.7% 35.3%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1659 Aq1045 Aq148 Aq1144 Aq1606 Heme Aq207 Aq134 Aq1247 Aq1279 Aq1279 Aq1279 Aq1279 Aq1299 Aq1299 Aq1299 Aq1299 Aq2199 Aq2199 Aq2199 Aq263 Aq1424	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB pabC cobA cyxG dcuP gs hemA hemB hemC hemF	DAPA aminotransferase boint synthese dethiohoint synthetase dethiohoint synthetase 8-amino-7-oxononanoate synthase 8-amino-7-oxononanoate synthase (-narboxyl-kanoate-CoA ligase (pimeloyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folyloolyglutamate synthetase methylenetertarlydrofolate dehydrogenase methylenetertarlydrofolate dehydrogenase synthesis 7.8-dihydro-6-hydroxymethyletein-pyrophosphokinase dihydropteroate synthase aminodeoxychorismate lyase uroporphyrin-III c-methyltransferase sindenes synthase uroporphyrinogen decarboxylase glutamatei -la-ernialdehyde aminotransferase glutamyl tRNA reductase glutamyl tRNA reductase glutamyl tRNA reductase porphoblimogen synthase porphoblimogen synthase porphoblimogen synthase porphoblimogen deaminase oxygen-independent coproporphyrinogen III oxidase	51.7% 42.0% 41.5% 41.5% 47.3% 47.3% 37.5% 47.3% 47.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq042 Aq1550 Aq1358 Aq042 Aq150 Aq1358 Aq067 Aq235 Aq108a Aq1171a Aq108a Aq2101 Aq2096 Aq042 Aq108a Aq2184 Aq2186 Aq044 Aq234 Aq2186 Aq045 Aq0466 Aq047	ldhA narB nirB nox nsd nueM udh umsport coxA1 coxA2 coxB coxC taA cyc cycB1 cycB2 cydA cydB fdx1 fdx1 fdx1 fdx2 fdx3 fdx4 fdx2 fdx3 fdx4 petB soxF soxF soxF soxF soxF soxF soxF soxF	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase (NADH dehydrogenase (Usiquinone) dehydrogenase (Usiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome c oxidase d subunit II cytochrome c oxidase c d subunit II cytochrome c oxidase subunit II cytochrome c oxidase c d subunit II cytochrome c oxidase c d subunit II cytochrome c oxidase d subunit II cytochrome c oxidase d subunit II cytochrome c oxidase c d subunit II cytochrome c c d subuni	34.6% 33.5% 33.5% 33.5% 35.3% 35.3% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 29.9% 38.1% 29.9% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.2% 38.3% 396 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 36.3% 38.3% 396 38.3% 39.0% 39.0%
Biotin Aq170 Aq175 Aq527 Aq527 Aq626 Aq1626 Aq1626 Aq1626 Aq2045 Aq2045 Aq1898 Aq239 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq1237 Aq1237 Aq1237 Aq1244 Aq816 Aq1279 Aq263 Aq1279 Aq263 Aq1424 Aq2015	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB pabC cobA cysG dcuP gsa hemA hemB hemC hemF	DAPA aminotransferase biotin synthetase delchiobiotin synthetase delchiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folypolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxychorismate lyase uroporphyrinogen decarboxylase glutaminetense sinchem eynthase uroporphyrinogen decarboxylase glutamate-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblimogen synthase porphoblimogen synthase porphoblimogen deaminase oxygen-independent copropopyrinogen III oxidase	51.796 42.096 41.596 41.596 47.396 37.596 47.396 57.596 57.196 47.796 43.796 41.596 41.596 45.896 41.596 41.596 41.596 57.196 41.596 57.596	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2189 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq153 Aq162 Aq193 Aq153 Aq167 Aq235 Aq193 Aq1192 Aq1193 Aq1192 Aq	ldhA narb lpdA narb nirB nox nsd nueM udh nsport coxA1 coxA2 coxA2 cyc ctaA cyc cycB1 cycB2 cydA ddb fccB' fdx1 fdx1 fdx2 fdx3 fdx4 fhp ptB soxF aqr and gluconeogen and gluconeogen eno eno	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (Votchrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit III cytochrome c oxidase subunit II cytochrome coxidase dubunit I cytochrome coxidase dubunit II cytochrome coxidase subunit II cytochrome coxidase su	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 28.6% 29.9% 38.1% 28.6% 29.9% 38.7% 38.8% 31.2% 38.2% 31.2% 39.5%
Biotin Aq170 Aq175 Aq557 Aq526 Aq1659 Aq626 Folic acid Aq2045 Aq1898 Aq139 Aq168 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq1237 Aq127 Aq127 Aq127 Aq127 Aq127 Aq127 Aq128 Aq189 Aq129 Aq109 Aq109 Aq109 Aq109 Aq109 Aq104 Aq104 Aq144 Aq144 Aq144 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq144 Aq166 Aq144 Aq166 Aq146 Aq166 A	bioA bioB bioD bioF bioW birA folC folD folK folP pabB pabC cobA cyvG dcuP gs hemA hemB hemC hemF hemG	DAPA aminotransferase biotin symthese composition symthese composition symthese seems of the composition of	51.7% 42.0% 41.5% 41.5% 47.3% 47.3% 47.3% 47.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2189 Aq2188 Aq153 Aq042 Aq792 Aq1550 Aq1358 Aq067 Aq235 Aq108a Aq1171a Aq108a Aq2111 Aq2096 Aq042 Aq236 Aq108a Aq211 Aq2096 Aq044 Aq234 Aq2186 Aq044 Aq234 Aq2186 Aq044 Aq234 Aq2186 Aq044 Aq2384 Aq2186 Aq044 Aq2384 Aq2186	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase (NADH) dehydrogenase (SADH) dehydrogenase (Usiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase da subunit II cytochrome c oxidase da subunit II cytochrome c oxidase da subunit I cytochrome c oxidase da subunit I cytochrome coxidase da subunit I cytochrome coxidase da subunit I cytochrome oxidase da subunit I cytochrome coxidase da subunit I cytochrome oxidase da subunit I cytochrome coxidase (navoprotein subunit ferredoxin ferredo	34.6% 33.5% 33.5% 33.5% 33.1% 34.7% 35.3% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 27.4% 28.1% 28.6% 29.9% 38.7%
Biotin Aq170 Aq175 Aq527 Aq527 Aq626 Aq1626 Aq1626 Aq1626 Aq2045 Aq2045 Aq1898 Aq239 Aq1468 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq1237 Aq1237 Aq1237 Aq1244 Aq816 Aq1279 Aq263 Aq1424 Aq2015 Aq948 Aq909	bioA bioB bioD bioF bioW birA folC folD folE folK folP pabB pabC cobA cysG dcuP gsa hemA hemB hemC hemF hemG hemH	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase 1 folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxyntosirante lyase uroporphyrinogen decarboxylase glutaminetense synthase uroporphyrinogen decarboxylase glutamite-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblinogen synthase porphoblinogen synthase porphoblinogen deaminase oxygen-independent copropophyrinogen lill oxidase protoporphyrinogen oxidase ferrochelatase protoporphyrinogen oxidase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 57.1% 47.3% 52.2% 57.1% 43.7% 43.7% 45.8% 41.5% 52.0% 56.5% 56.5% 56.5% 56.5% 57.1% 57.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2180 Aq188 Aq153 Aq042 Aq792 Aq1530 Aq153 Aq042 Aq1530 Aq153 Aq042 Aq1530 Aq1354 Aq1530 Aq1650 Aq1650 Aq188 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1193 Aq1192 Aq1193 Aq1194 Aq214	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit II dimed to oxidase dubunit II dim	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 28.2% 29.9% 38.1% 29.9% 38.8% 31.2% 40.2% 38.7% 38.6% 31.2% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.9%
Biotin Aq170 Aq175 Aq557 Aq526 Aq1659 Aq626 Folic acid Aq2045 Aq1898 Aq139 Aq168 Aq1144 Aq1606 Heme Aq207 Aq1237 Aq1237 Aq127 Aq127 Aq127 Aq127 Aq127 Aq127 Aq128 Aq189 Aq129 Aq109 Aq109 Aq109 Aq109 Aq109 Aq104 Aq104 Aq144 Aq144 Aq144 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq201 Aq1424 Aq144 Aq166 Aq144 Aq166 Aq146 Aq166 A	bioA bioB bioD bioF bioW birA folC folD folK folP pabB pabC cobA cyvG dcuP gs hemA hemB hemC hemF hemG	DAPA aminotransferase biotin symthese composition symthese composition symthese seems of the composition of	51.7% 42.0% 41.5% 41.5% 47.3% 47.3% 47.3% 47.5%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2180 Aq188 Aq153 Aq042 Aq792 Aq1530 Aq153 Aq042 Aq1530 Aq153 Aq042 Aq1530 Aq1354 Aq1530 Aq1650 Aq1650 Aq188 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1193 Aq1192 Aq1193 Aq1194 Aq214	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase subunit II dimed to oxidase dubunit II dim	34.6% 33.5% 33.5% 33.5% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 28.2% 29.9% 38.1% 29.9% 38.8% 31.2% 40.2% 38.7% 38.6% 31.2% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.5% 39.9%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1898 Aq2045 Aq1898 Aq162 Aq1484 Aq1606 Heme Aq207 Aq1237 Aq314 Aq1279 Aq2148 Aq1279 Aq2109 Aq2109 Aq205 Aq205 Aq206 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq208 Aq20	bioA bioB bioD bioF bioW birA folC folD folB folK folP pabB pabC cobA cysG dcuP gsa hemA hemB hemC hemF hemG hemH hemH	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase 1 folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxyntosirante lyase uroporphyrinogen decarboxylase glutaminetense synthase uroporphyrinogen decarboxylase glutamite-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblinogen synthase porphoblinogen synthase porphoblinogen deaminase oxygen-independent copropophyrinogen lill oxidase protoporphyrinogen oxidase ferrochelatase protoporphyrinogen oxidase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 57.1% 47.3% 52.2% 57.1% 43.7% 43.7% 45.8% 41.5% 52.0% 56.5% 56.5% 56.5% 56.5% 57.1% 57.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq792 Aq1550 Aq1357 Aq1358 Aq067 Aq235 Aq1171a Aq1191a Aq1191a Aq1194 Aq108a Aq2186 Aq2186 Aq044 Aq234 Aq2186 Aq044 Aq235 Aq0159 Aq108a Aq1171a Aq108a Aq211 Aq2096 Aq044 Aq234 Aq2186 Aq044 Aq2384 Aq2186 Aq044 Aq2384 Aq2186 Aq044 Aq2384 Aq2186 Aq484 Aq3390 Aq1065 Aq484	ldhA narB nirB nirB nirB nox nsd nueM udh nssport coxA1 coxA2 coxA2 cyc ttaA cyc cytB1 cytB2 cydA cydB fdx1 fdx1 fdx2 fdx3 fdx4 fdx4 fdx4 petB soxF soxF soxF soxF soxF soxF soxF soxF	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase (NADH dehydrogenase (Usiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase da subunit I cytochrome c oxidase da subunit I cytochrome coxidase da subunit I cytochrome oxidase chase II giveraldehyde -3-pholosphate aldolase class II glyceraldehyde -3-pholosphate dehydrogenase glycerol kinase	34.6%
Biotin Aq170 Aq170 Aq1577 Aq557 Aq1626 Aq1659 Aq266 Folic acid Aq2045 Aq1898 Aq2199 Aq160 Aq1468 Aq1146 Aq1160 Aq1606 Heme Aq207 Aq1237 Aq1237 Aq1237 Aq1237 Aq1237 Aq1248 Aq1606 Aq129 Aq205 Aq129 Aq205 Aq1609 Aq206 Aq1609 Aq207 Aq1609 Aq208 Aq1609 Aq209 Aq209 Aq209 Aq209 Aq1609 Aq209 Aq1609 Aq209 Aq1609 Aq209 Aq209 Aq1609 Aq20 Aq20 Aq20 Aq20 Aq20 Aq20 Aq20 Aq20	bioA bioB bioD bioF bioW birA folC folD folB folK folP pabB pabC cobA cysG dcuP gsa hemA hemB hemG hemH hemF	DAPA aminotransferase biotin synthetase dethiobiotin synthetase 48-mino-7-conomanate synthase 6-emo-7-conomanate synthase 6-emo-7-conomanate synthase 6-emo-7-conomanate synthase 6-emo-7-conomanate synthase policial pacetyl-CoA-carbonylase] ligase folylpolyglutamate synthetase aminotemosterating synthetase aminotemosterating synthetase p-aminotemoster synthetase aminodemoster synthetase aminodemoster synthase uroporphyrinogen decarbonylase glutamate-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminotewolfare synthase porphobilinogen deaminase opythobilinogen synthase porphobilinogen synthase porphobilinogen deaminase onygen-independent opproporphyrinogen III oxidase protoporphyrinogen oxidase ferrochelatase protoporphyrinogen oxidase ferrochelatase protoporphyrinogen oxidase oxygen-independent opproporphyrinogen III oxidase oxygen-independent oxygen-independe	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 31.8% 55.2% 57.1% 43.7% 43.7% 44.5% 55.1% 56.5% 57.1% 57.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq024 Aq135 Aq1010 Electron tra Aq2191 Aq2190 Aq2189 Aq1150 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq153 Aq042 Aq153 Aq163 Aq163 Aq163 Aq163 Aq163 Aq191 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1192 Aq1193 Aq1193 Aq1193 Aq1194 Aq214 Aq218 Aq216 Aq045 Aq045 Aq045 Aq045 Aq045 Aq1390 Aq144 Aq214 Aq218 Aq180 Aq180 Aq180 Aq180 Aq194 Aq214 Aq214 Aq218 Aq194 Aq218 Aq199 Aq105 Aq045 Aq045 Aq144 Aq214	ldhA narB nirB nirB nirB nirB nirB nirB nirB ni	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB nitrite reductase (NAD(P)H) large subunit NADH oxidase nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase subunit II cytochrome c oxidase subunit III cytochrome c oxidase d subunit II cytochrome c oxidase d subunit II cytochrome c oxidase d subunit II cytochrome coxidase d subunit II cytochrome in cytochrome in the cytochrome in ferredoxin ferredoxin ferredoxin fieredoxin fieredox	34.6% 33.5% 33.5% 39.1% 39.1% 39.1% 33.1% 47.0% 28.2% 29.7% 28.2% 29.7% 28.1% 28.2% 29.9% 38.1% 29.9% 38.2% 38.2% 38.2% 39.2%
Biotin Aq170 Aq975 Aq557 Aq626 Aq1659 Aq1659 Aq1659 Aq1898 Aq2045 Aq1898 Aq162 Aq1484 Aq1606 Heme Aq207 Aq1237 Aq314 Aq1279 Aq2148 Aq1279 Aq2109 Aq2109 Aq205 Aq205 Aq206 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq207 Aq208 Aq20	bioA bioB bioD bioF bioW birA folC folD folB folK folP pabB pabC cobA cysG dcuP gsa hemA hemB hemC hemF hemG hemH hemH	DAPA aminotransferase biotin synthetase delhiobiotin synthetase delhiobiotin synthetase 8-amino-7-exononanoate synthase 6-arrboxyhezanoate-CoA ligase (pinedoyl CoA synthase) biotin [acetyl-CoA-carboxylase] ligase folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase 1 folate biosynthesis 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase p-aminobenzoate synthetase aminodeoxyntosirante lyase uroporphyrinogen decarboxylase glutaminetense synthase uroporphyrinogen decarboxylase glutamite-1-semialdehyde aminotransferase glutamyl tRNA reductase (delta-aminolevulinate synthase) porphoblinogen synthase porphoblinogen synthase porphoblinogen deaminase oxygen-independent copropophyrinogen lill oxidase protoporphyrinogen oxidase ferrochelatase protoporphyrinogen oxidase	51.7% 42.0% 41.5% 41.5% 47.3% 37.5% 57.1% 47.3% 52.2% 57.1% 43.7% 43.7% 45.8% 41.5% 52.0% 56.5% 56.5% 56.5% 56.5% 57.1% 57.1%	Aq727 Aq736 Aq217 Aq206 Aq835 Aq0024 Aq135 Aq1010 Electron tra Aq2191 Aq2199 Aq2199 Aq2188 Aq153 Aq162 Aq792 Aq1550 Aq1357 Aq1358 Aq067 Aq235 Aq1171a Aq1191a Aq1191a Aq1194 Aq108a Aq2186 Aq2186 Aq044 Aq234 Aq2186 Aq044 Aq235 Aq0159 Aq108a Aq1171a Aq108a Aq211 Aq2096 Aq044 Aq234 Aq2186 Aq044 Aq2384 Aq2186 Aq044 Aq2384 Aq3484	ldhA narB nirB nirB nirB nox nsd nueM udh nssport coxA1 coxA2 coxA2 cyc ttaA cyc cytB1 cytB2 cydA cydB fdx1 fdx1 fdx2 fdx3 fdx4 fdx4 fdx4 petB soxF soxF soxF soxF soxF soxF soxF soxF	D-lactate dehydrogenase dihydrolipoamide dehydrogenase nitrate reductase narB mitrite reductase (NAD/PH) large subunit NADH oxidase nucleotide sugar dehydrogenase (NADH dehydrogenase (Usiquinone) dehydrogenase cytochrome c oxidase subunit I cytochrome c oxidase subunit II cytochrome c oxidase da subunit I cytochrome c oxidase da subunit I cytochrome coxidase da subunit I cytochrome oxidase chase II giveraldehyde -3-pholosphate aldolase class II glyceraldehyde -3-pholosphate dehydrogenase glycerol kinase	34.6% 33.5% 37.0% 39.1% 39.1% 35.3% 31.1% 47.0% 28.2% 29.7% 42.4% 38.1% 27.4% 28.1% 28.1% 29.7% 38.8% 38.1% 38.3% 39.3% 31.9% 35.0% 35.0% 35.0% 35.0% 36.0% 31.3% 36.3% 36.3% 36.3% 37.1% 38.3%

Aq1708	pfkA	phosphofructokinase	49.4%	Aq046	pyrD	dihydroorotase dehydrogenase	50.5%
Aq750 Aq118	pgi pgk	glucose-6-phosphate isomerase phosphoglycerate kinase	37.8% •••• 54.5% ••••	Aq1305	pyrDB	dihydroorotate dehydrogenase electron transfer subunit	34.7%
Aq1990	pgmA	phosphoglycerate mutase	33.2% ••••	Aq1580	pyrF	orotidine-5'-phosphate decarboxylase	37.2% ****
Aq501 Aq2142	pmu ppsA	phosphoglucomutase/phosphomannomutase phosphoenolpyruvate synthase	37.8% · · · · · 56.3% · · · ·	Aq1334 Aq713	pyrG pyrH	CTP synthetase UMP kinase	57.5% •••• 62.1% ••••
Aq1520	pycA	pyruvate carboxylase c-terminal domain	46.6% ••••	Aq640	thy	thymidylate synthase complementing protein	30.5% •••
Aq1517 Aq360	pycB timA	pyruvate carboxylase n-terminal domain triose phophate isomerase	57.1% · · · · · 52.2% · · · ·	Aq969 Aq1907	tmk umpS	thymidylate kinase uridine 5-monophosphate synthase	35.1% 42.1%
		ti tose pitopitate isomerase	32.270 ****	Aq2163	uraP	uracil phosphoribosyltransferase	42.170
Hydrogenase Aq665	hoxZ	Ni/Fe hydrogenase B-type cytochrome subunit	40.4%	Regulation			
Aq667	hupD	HupD hydrogenase related function	40.9%	Aq1058	acrR1	transcriptional regulator (TetR/AcrR family)	34.1%
Aq666 Aq1021	hupE hypA	HupE hydrogenase related function hydrogenase accessory protein HypA	38.3%	Aq2179 Aq281	acrR2 acrR3	transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family)	31.0%
Aq671	hypB	hydrogenase expression/formation protein B	50.6%	Aq1387	arsR	transcriptional regulator (ArsR family)	35.3% ••••
Aq1157 Aq662	hypD mbhL1	hydrogenase expression/formation protein HypD hydrogenase large subunit	56.1% · · · · · 50.6% · · · ·	Aq1724	degT	transcriptional regulator (DegT/DnrJ/Eryc1 family)	34.1%
Aa960	mbhL2	hydrogenase large subunit	44.3% ••••	Aq534	draG	ADP-ribosylglycohydrolase	32.1% ••••
Aq804 Aq660	mbhL3 mbhS1	hydrogenase large subunit hydrogenase small subunit	27.9%	Aq831 Aq490	exsB fnr	trans-regulatory protein ExsB transcriptional regulator (Crp/Fnr family)	38.5% ···· 29.5% ····
Aq965	mbhS2	hydrogenase small subunit	51.3% ••••	Aq1207	furR1	transcriptional regulator (FurR family)	37.9%
Aq802 Aq1591	mbhS3 shyS	hydrogenase small subunit soluble hydrogenase small subunit	36.7% · · · · · 41.6% · · · ·	Aq1418 Aq213	furR2 glnBi	transcriptional regulator (FurR family) PII-like protein GlnBi	48.0% ••
Sugar metab		, 5		Aq1908	hflX	GTP-binding protein HflX	40.3%
Aq968	cbbE2	ribulose-5-phosphate 3-epimerase	47.2% ••••	Aq1115 Aq316	hksP1 hksP2	histidine kinase sensor protein histidine kinase sensor protein	27.7% •• 28.1% •••
Aq1658 Aq1979	fucA1 fucA2	fuculose-1-phosphate aldolase fuculose-1-phosphate aldolase	31.8% · · · · · 29.7% · · · ·	Aq905	hksP3	histidine kinase sensor protein	23.6% •••
Aq498	gnd	6-phosphogluconate dehydrogenase	45.2% ••••	Aq231 Aq1156	hksP4 hoxX	histidine kinase sensor protein hydrogenase regulation HoxX	28.2% ···· 46.7% ····
Aq497 Aq1138	gsdA rpiB	glucose-6-phosphate 1-dehydrogenase ribose 5-phosphate isomerase B	32.3% ···· 54.5% ····	Aq093	hth	transcriptional regulator (H-T-H)	50.2% ****
Aq119	talC	transaldolase	71.1% ••••	Aq1019 Aq672	hypE hypF	hydrogenase expression/formation protein transcriptional regulatory protein HypF	44.8%
Aq1765	tktA	transketolase	52.4% ••••	Aq764	iclR	transcriptional regulator (IclR family)	30.4%
NADH dehy Aq1385	drogenase nuoA1	NADH dehydrogenase I chain A	42.0%	Aq638 Aq1038	lysR1 lysR2	transcriptional regulator (LysR family) transcriptional regulator (LysR family)	32.8% ···· 28.9% ····
Aq1310	nuoA2	NADH dehydrogenase I chain A	44.9% ••••	Aq702	merR	transcriptional regulator (MerR family)	32.8% ****
Aq1312 Aq551	nuoB nuoD1	NADH dehydrogenase I chain B NADH dehydrogenase I chain D	60.1% 37.7%	Aq218 Aq1117	nifA ntrCl	transcriptional regulator (NifA family) transcriptional regulator (NtrC family)	42.8%
Aq1314	nuoD1	NADH dehydrogenase I chain D	42.2% ****	Aq1792	ntrC2	transcriptional regulator (NtrC family)	40.2% ••••
Aq574	nuoE	NADH dehydrogenase I chain E	36.8% · · · · · 20.5% · · ·	Aq230	ntrC3	transcriptional regulator (NtrC family)	40.0%
Aq573 Aq437	nuoF nuoG	NADH dehydrogenase I chain F NADH dehydrogenase I chain G	35.4%	Aq164 Aq2069	ntrC4 obg	transcriptional regulator (NtrC family) GTP-binding protein	38.3% •••• 54.9% ••
Aq1315	nuoHl	NADH dehydrogenase I chain H	41.0%	Aq319	phoB	transcriptional regulator (PhoB-like)	41.6% ****
Aq1373 Aq1374	nuoH2 nuoH3	NADH dehydrogenase I chain H NADH dehydrogenase I chain H	42.1% 38.9%	Aq906 Aq844	phoU spoT	transcriptional regulator (PhoU-like) (p)ppGpp 3-pyrophosphohydrolase	41.9% • • • • 47.2% • • • •
Aq1317	nuoIl	NADH dehydrogenase I chain I	30.5% •••	Aq1496	xylR	transcriptional regulator (NagC/XylR family)	29.3%
Aq1375 Aq1318	nuoI2 nuoI1	NADH dehydrogenase I chain I NADH dehydrogenase I chain J	29.2% 35.4%	DNA Replica	tion and Repair		
Aq1377	nuoJ2	NADH dehydrogenase I chain J	30.6%	Aq358 Aq322	dinG dnaA	ATP-dependent helicase (DinG family) chromosome replication initiator protein DnaA	27.9%
Aq1319 Aq1378	nuoK1 nuoK2	NADH dehydrogenase I chain K NADH dehydrogenase I chain K	51.1% 48.4%	Aq1472	dnaB	replicative DNA helicase	40.3%
Aq1320	nuoLl	NADH dehydrogenase I chain L	39.0% ••••	Aq910 Aq1008	dnaC dnaE	DNA replication protein DnaC DNA polymerase III alpha subunit	26.4%
Aq866 Aq1379	nuoL2 nuoL3	NADH dehydrogenase I chain L NADH dehydrogenase I chain L	30.2% • • • 43.1% • • • •	Aq1493	dnaG	DNA primase	39.8% •••
Aq1321	nuoM1	NADH dehydrogenase I chain M	43.6% ••••	Aq1882 Aq932	dnaN dnaQ	DNA polymerase III beta chain DNA polymerase III epsilon subunit	32.1% ···· 40.0% ····
Aq1382	nuoM2 nuoN1	NADH dehydrogenase I chain M	36.9% ···· 34.1% ····	Aq1855	dnaX	DNA polymerase III gamma subunit	36.6%
Aq1322 Aq1383	nuoN2	NADH dehydrogenase I chain N NADH dehydrogenase I chain N	32.8%	Aq1422 Aq1693	dpbF dplF	DNA polymerase beta family	39.1%
Lipid metabo	olism			Aq980	gyrA	N-terminus of phage SPO1 DNA polymerase DNA gyrase A subunit	43.6%
Aq2058	aas	2-acylglycerophosphoethanolamine	27.10/	Aq1026	gyrB	gyrase B	55.2% ••
Aq1206	accA	acyltransferase acetyl-CoA carboxylase alpha subunit	37.1% •••• 57.1% •••	Aq2057 Aq1484a	helX himA	DNA helicase DNA binding protein HU	49.7%
Aq1363	accB	biotin carboxyl carrier protein	44.6% ••••	Aq2174	ihfB	integration host factor beta subunit	35.8%
Aq1664 Aq1470	accC1 accC2	biotin carboxylase biotin carboxylase	54.4% · · · · · 56.5% · · · ·	Aq1394 Aq633	lig ligA	DNA ligase (ATP dependent) DNA ligase (NAD dependent)	50.8% ···· 45.7% ····
Aq445	accD	acetyl-CoA carboxyltransferase beta subunit	56.9% ••••	Aq1578	mutL	DNA mismatch repair protein MutL	72.3% ••••
Aq1717a Aq813	acpP acpS	acyl carrier protein holo-[acyl-carrier protein] synthase	71.2%	Aq308 Aq1242	mutS1 mutS2	DNA mismatch repair protein MutS DNA mismatch repair protein MutS	77.5% •••• 37.0% ••••
Aq2104	acs	acetyl-coenzyme A synthetase	54.0%	Aq1449	mutT	8-OXO-dGTPase domain (mutT domain)	46.3% ••••
Aq2103	acs'	acetyl-coenzyme A synthetase c-terminal fragment	61.2%	Aq282 Aq172	mutY1 mutY2	endonuclease III endonuclease III	53.6% ···· 51.8% ····
Aq1249	cds	phosphatidate cytidylyltransferase	29.2% ••••	Aq496	mutY3	endonuclease III	43.4% ****
Aq1737 Aq892	cfa fabD	cyclopropane-fatty-acyl-phospholipid synthase malonyl-CoA:Acyl carrier protein transacylase	37.5% •••• 42.1% ••••	Aq1629 Aq710	nfo nucI	deoxyribonuclease IV thermococcal nuclease homolog	39.0%
Aq1717	fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	58.4% ••••	Aq1495	ogt	O-6-methylguanine-DNA-alkyltransferase	36.9% •••
Aq1716 Aq1099	fabG fabH	3-oxoacyl-[acyl-carrier-protein] reductase 3-oxoacyl-[acyl-carrier-protein] synthase III	52.9% ···· 47.0% ····	Aq1628 Aq1967	pol polA	DNA polymerase I 3'-5' exo domain DNA polymerase I (PolI)	43.2%
Aq1552	fabI	enoyl-[acyl-carrier-protein] reductase (NADH)	49.6%	Aq1610	radC	DNA repair protein RadC	39.0% ••••
Aq056	fabZ	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase	58.7% ••••	Aq2150	recA recG	recombination protein RecA	88.5% ···· 38.9% ····
Aq999	fadD	long-chain-fatty-acid CoA ligase	30.0% •••	Aq2053 Aq2155	recJ	ATP-dependent DNA helicase RecG single-strand-DNA-specific exonuclease RecJ	31.8% ****
Aq1638	lplA	lipoate-protein ligase A	28.1%	Aq561	recN	recombination protein RecN	27.7% ••••
Aq958 Aq2154	pgsA pgsA	phosphotidylglycerophosphate synthase phosphotidylglycerophosphate synthase	37.3% • • 38.9% • • •	Aq1478 Aq793	recR rep	recombination protein RecR ATP-dependent DNA helicase REP	38.3%
Aq1101	plsX	PlsX protein	43.7% ••••	Aq1886	sbcD	ATP-dependent dsDNA exonuclease	29.9% ••••
		eotides and Nucleosides	35.004	Aq064 Aq657	ssb topA	single stranded DNA-binding protein topoisomerase I	39.4%
Aq094 Aq1505	nrdA nrdF	ribonucleotide reductase alpha chain ribonucleotide reductase beta chain	35.0% • • • • 36.2% •	Aq1159	topG1	reverse gyrase	41.6% ••••
Purines				Aq886 Aq686	topG2 uvrA	reverse gyrase repair excision nuclease subunit A	35.1%
Aq568 Aq236	deoD	purine nucleoside phosphorylase	33.1% ••••	Aq1856	uvrB	repair excision nuclease subunit B	53.9%
Aq2023	guaA guaB	GMP synthase inosine monophosphate dehydrogenase	58.4% 65.4%	Aq2126	uvrC	repair excision nuclease subunit C	32.5% ••••
Aq544	hpt	hypoxanthine-guanine phosphoribosyltransferase	48.2% ••••	Transcription RNA polyme	1 erase and transcr	rintion factors	
Aq078 Aq1590	kad ndk	adenylate kinase nucleoside diphosphate kinase	50.0% 48.2%	Aq613	deaD	ATP-dependent RNA helicase DeaD	42.3%
Aq1636	prs	phosphoribosylpyrophosphate synthetase	55.2% ••••	Aq357a Aq1218	flgM fliA	anti sigma factor FlgM RNA polymerase sigma factorFliA	20.6%
Aq1290 Aq597	purA purB	adenylosuccinate synthetase adenylosuccinate lyase	49.2% ···· 52.4% ····	Aq259	nusA	transcription termination NusA	45.4% •••
Aq2117	purC	phosphoribosylaminoimidazole-		Aq133 Aq1931	nusB nusG	transcription termination NusB transcription antitermination protein NusG	32.3% •••• 46.3% ••
Aq742	purD	succinocarboxamide synthase phosphoribosylamine-glycine ligase	52.5% ···· 54.2% ····	Aq873	rho	transcriptional terminator Rho	59.6%
Aq1178	purE	phosphoribosylaminoimidazole carboxylase	64.6% ••••	Aq070 Aq1939	rpoA rpoB	RNA polymerase alpha subunit RNA polymerase beta subunit	40.4%
Aq1175 Aq1963	purF purH	amidophosphoribosyltransferase phosphoribosylaminoimidazolecarboxamide	42.7% ••••	Aq1945	rpoC	RNA polymerase beta prime subunit	46.9% ••••
		formyltransferase	48.2%	Aq1490 Aq599	rpoD rpoN	RNA polymerase sigma factor RpoD RNA polymerase sigma factor RpoN	41.6%
Aq245	purK	phosphoribosyl aminoimidazole carboxylase	35.6% • • • • 49.3% • • • •	Aq599 Aq1452	rpoN rpoS	RNA polymerase sigma factor RpoN RNA polymerase sigma factor RpoS	40.5%
Aq1836 Aq769	purL purM	phosphoribosylformylglycinamidine synthase II phosphoribosylformylglycinamidine cyclo-ligase	50.0% ••••	RNA modific	cation		
Aq857	purN	phosphoribosylglycinamide formyltransferase	48.3% 51.1%	Aq1816	ksgA	dimethyladenosine transferase	36.1% ••••
Aq1105 Aq1818	purQ purU	phosphoribosyl formylglycinamidine synthase I formyltetrahydrofolate deformylase	51.1% ••••	Aq1067	miaA	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase	38.2%
Pyrimidines		• •		Aq411	pcnB1	poly A polymerase	28.5% ****
Aq410	carA	carbamoyl phosphate synthese small subunit	52.2% ••••	Aq2158 Aq221	pcnB2 phpA	poly A polymerase polyribonucleotide nucleotidyltransferase	33.9% • • · · · · · · · · · · · · · · · · ·
Aq1172 Aq2101	carB carB	carbamoyl-phosphate synthase large subunit carbamoyl-phosphate synthase, large subunit	60.7%	Aq894	queA	queuosine biosynthesis protein	46.9%
Aq2153	cmk	cytidylate kinase	38.5% ****	Aq946 Aq1955	rnc rnhB	RNase III RNase HII	35.8% ···· 48.4% ····
Aq1607 Aq220	dcd dut	deoxycytidine triphosphate deaminase deoxyuridine 5'triphosphate nucleotidohydrolase	39.5% ••••	Aq924	rnpH	RNase PH	64.0%
Aq409	pyrB	aspartate carbamoyltransferase catalytic chain	42.0% ••••	Aq1661 Aq1308	spoU tgt	rRNA methylase SpoU queuine tRNA-ribosyltransferase	44.0% ···· 52.6% ····
Aq806	pyrC	dihydroorotase	37.3% •••	Aq841	trm1	N2,N2-dimethylguanosine tRNA	J2.0/U ****

A a 1 490	terna D	methyltransferase	34.6% ••••	Aq1671	hslV	heat shock protein HsLV	57.6% ****
Aq1489 Aq749	trmD truA	tRNA guanine-N1 methyltransferase pseudouridine synthase I	42.9% ···· 33.1% ····	Aq1450 Aq242	htrA lon	periplasmic serine protease Lon protease	38.3% ···· 50.6% ····
Aq705	truB	tRNA pseudouridine 55 synthase	38.2% ···· 36.4% ····	Aq076	map	methionyl aminopeptidase	44.1% •••• 27.7% ••
Aq1890 Aq2046	tsnR vacB	rRNA methylase VacB protein (ribonuclease II family)	37.9% ••••	Aq1459 Aq2099	npr pepA	neutral protease leucine aminopeptidase	39.5% ****
Aq257	ygcA	RNA methyltransferase (TrmA-family)	28.8% ••••	Aq1535 Aq618	pepQ	xaa-pro dipeptidase protease I	31.9% 41.8%
Translation Aq2131	fmt	methionyl-tRNA formyltransferase	45.7%	Aq797	pfpI prc	carboxyl-terminal protease	41.8%
Aq2151 Aq247	gatA	glutamyl-tRNA(Gln) amidotransferase subunit A	53.6% ••••	Aq552 Aq2204	sms	ATP-dependent protease sms	46.2%
Aq461	gatB	glutamyl-tRNA(Gln) amidotransferase subunit B	48.8% 41.1%		ymxG	processing protease	28.3%
Aq2147a Aq346	gatC pth	glutamyl-tRNA(Gln) amidotransferase subunit C peptidyl-tRNA hydrolase	48.8%	Transport Aq1222	abcT1	ABC transporter	34.7%
Aminoacyl tRN				Aq620	abcT2	ABC transporter	36.8%
Aq1293	alaS	alanyl-tRNA synthetase	46.6% ••••	Aq1095 Aq1094	abcT3 abcT4	ABC transporter (ABC-2 subfamily) ABC transporter	34.4%
Aq923 Aq1677	argS aspS	arginyl-tRNA synthetase aspartyl-tRNA synthetase	39.4% ···· 51.3% ····	Aq1097	abcT5	ABC transporter (hlyB subfamily)	45.5%
Aq1068	cysS	cysteinyl-tRNA synthetase	45.0% ••••	Aq417 Aq413	abcT6 abcT7	ABC transporter ABC transporter	51.8% 51.5%
Aq763 Aq1221	genX gltX	lysyl-tRNA synthetase (genX) homolog glutamyl-tRNA synthetase	38.6% 48.5%	Aq297	abcT8	ABC transporter	49.3% ••••
Aq945	glyQ	glycyl-tRNA synthetase alpha subunit	61.9% ••••	Aq2160 Aq1531	abcT9 abcT10	ABC transporter ABC transporter	45.3%
Aq2141 Aq122	glyS hisS1	glycyl-tRNA synthetase beta subunit histidyl-tRNA synthetase	37.1% 43.3%	Aq2122	abcT11	ABC transporter	42.5% ****
Aq1155	hisS2	histidyl-tRNA synthetase	34.9% ••••	Aq2137 Aq1563	abcT12 abcT13	ABC transporter ABC transporter (MsbA subfamily)	38.2%
Aq305 Aq351	ileS leuS	isoleucyl-tRNA synthetase leucyl-tRNA synthetase alpha subunit	82.1% •• 50.7% •••	Aq695	acrD1	cation efflux system (AcrB/AcrD/AcrF family)	22.7% ••••
Aq1770	leuS'	leucyl-tRNA synthetase beta subunit	47.2% ••••	Aq1122 Aq469	acrD2 acrD3	cation efflux system (AcrB/AcrD/AcrF family) cation efflux system (AcrB/AcrD/AcrF family)	32.0%
Aq1202 Aq1257	lysU metG	lysyl-tRNA synthetase methionyl-tRNA synthetase alpha subunit	53.2% ••• 45.0% •••	Aq786	acrD4	cation efflux (AcrB/AcrD/AcrF family)	27.7% ••••
Aq422	metG'	methionyl-tRNA synthetase beta subunit	64.2% ••••	Aq112	amtB arsA1	ammonium transporter	49.0% 41.5%
Aq953	pheS pheT	phenylalanyl-tRNA synthetase alpha subunit	51.9%	Aq682 Aq343	arsA2	anion transporting ATPase anion transporting ATPase	33.9%
Aq1730 Aq365	proS	phenylalanyl-tRNA synthetase beta subunit proline-tRNA synthetase	44.1%	Aq851	corA	Mg(2+) and Co(2+) transport protein	31.1% ****
Aq298	serS	seryl-tRNA synthetase	59.4% ••••	Aq724 Aq1445	ctrA1 ctrA2	cation transporting ATPase (E1-E2 family) cation transporting ATPase (E1-E2 family)	30.7% ···· 28.1% ····
Aq1667 Aq992	thrS trpS	threonyl-tRNA synthetase tryptophanyl-tRNA synthetase	48.5% ···· 38.4% ····	Aq1125	ctrA3	cation transporting ATPase (E1-E2 family)	43.8% ****
Aq1751	tyrS	tyrosyl tRNA synthetase	56.2% ••••	Aq1132 Aq1331	czcB1 czcB2	cation efflux system (czcB-like) cation efflux system (czcB-like)	23.7%
Aq1413	valS	valyl-tRNA synthetase	33.2% ••••	Aq468	czcB2	cation efflux system (czcB-like)	28.5% ****
Ribosomal Pro Aq1935	teins rplA	ribosomal protein L01	57.9%	Aq1073 Aq911	czcD ebs	cation efflux system (CzcD-like) erythrocyte band 7 homolog	43.4%
Aq013	rplB	ribosomal protein L02	46.9% ••••	Aq1062	emrB	major facilitator family transporter	28.3% ••••
Aq009 Aq011	rplC rplD	ribosomal protein L03 ribosomal protein L04	53.8% 51.3%	Aq1255 Aq1330	feoB gltP	ferrous iron transport protein B proton/sodium-glutamate symport protein	32.6%
Aq1652	rplE	ribosomal protein L05	67.0% ••••	Aq1268	hvsT	high affinity sulfate transporter	29.4%
Aq1649 Aq2042	rplF rplI	ribosomal protein L06 ribosomal protein L09	46.2% 35.6%	Aq1863 Aq1725	kch lepA	potassium channel protein G-protein LepA	30.1% ••• 59.8% ••••
Aq1936	rplJ	ribosomal protein L10	36.5% ••••	Aq1229	mffT	transporter (major facilitator family)	37.2% ••••
Aq1933 Aq1937	rplK	ribosomal protein L11 ribosomal protein L7/L12	71.4%	Aq447	mgtC	Mg(2+) transport ATPase	36.2%
Aq1877	rplL rplM	ribosomal protein L1/L12 ribosomal protein L13	60.6% ••••	Aq1609 Aq086	modA modC	molybdate periplasmic binding protein Molybdenum transport system permease	44.8%
Aq1654	rplN	ribosomal protein L14	59.5% •••• 57.4% ••••	Aq415	napA1	Na(+)/H(+) antiporter	27.6% ••••
Aq1642 Aq018	rplO rplP	ribosomal protein L15 ribosomal protein L16	59.3% ••••	Aq929 Aq2030	napA2 napA3	Na(+)/H(+) antiporter Na(+)/H(+) antiporter	32.7% ···· 26.8% ····
Aq069	rplQ	ribosomal protein L17	48.7%	Aq215	nasA	nitrate transporter	35.8% •••
Aq1648 Aq1954	rplR rplS	ribosomal protein L18 ribosomal protein L19	62.7% ···· 59.8% ···	Aq1441	oppA	transporter (extracellular solute binding protein family 5)	37.0%
Aq952	rplT	ribosomal protein L20	63.5% ••••	Aq481	oppB	transporter (OppBC family)	46.2% ••••
Aq016a Aq012	rplV rplW	ribosomal protein L22 ribosomal protein L23	47.3% 52.2%	Aq1509 Aq2019	oppC pstA	oligopeptide transport system permease phosphate transport system permease PstA	46.2% ···· 43.5% ····
Aq1653	rplX	ribosomal protein L24	50.8% ••••	Aq1055	pstB	phosphate transport ATP binding protein	68.1% ****
Aq1644 Aq1930a	rpmD rpmG	ribosomal protein L30 ribosomal protein L33	46.4% •• 67.9% ••••	Aq2018 Aq2016	pstC pstS	phosphate transport system permease protein C phosphate-binding periplasmic protein	45.2% •••• 52.4% ••••
Aq792a	rpmI	ribosomal protein L35	48.3% ••••	Aq2129	sbf	Na(+) dependent transporter (Sbf family)	34.9% ••••
Aq1485 Aq2007	rpsA rpsB	ribosomal protein S01 ribosomal protein S02	32.6% ···· 60.3% ····	Aq098 Aq2077	secG snf	protein export membrane protein SecG Na(+):neurotransmitter symporter (Snf family)	35.7% ···· 25.7% ····
Aq017	rpsC	ribosomal protein S03	54.0% ••••	Aq2106	ssf	Na(+):solute symporter (Ssf family)	47.4% •
Aq072 Aq1645	rpsD rpsE	ribosomal protein S04 ribosomal protein S05	51.9%	Aq1988 Aq1504	tolQ trk1	TolQ homolog K+ transport protein homolog	32.5% • 40.6% ••••
Aq063	rpsF	ribosomal protein S06	32.7% ••••	Aq031	trnS	transporter (Pho87 family)	46.8% ••••
Aq1832 Aq734	rpsG1 rpsG2	ribosomal protein S07 ribosomal protein S07	52.5% ···· 51.9% ····	Uncategorized	C1	and the second second	25.00/
Aq1651	rpsH	ribosomal protein S08	39.9% ••••	Aq1023 Aq2110	acuC1 acuC2	acetoin utilization protein acetoin utilization protein	36.9%
Aq1878 Aq008	rpsI rpsJ	ribosomal protein S09 ribosomal protein S10	50.5% ••• 55.9% ••••	Aq158	apfA	AP4A hydrolase	36.6% ****
Aq073	rpsK	ribosomal protein S11	60.7% ••••	Aq458 Aq542	bcp bcpC	bacterioferritin comigratory protein phosphonopyruvate decarboxylase	40.6% ···· 37.4% ····
Aq735 Aq1834	rpsL1 rpsL2	ribosomal protein S12 ribosomal protein S12	78.9% ···· 78.9% ····	Aq147	cobW	cobalamin synthesis related protein CobW	29.5% •••
Aq074	rpsM	ribosomal protein S13	61.9% ••••	Aq1303a Aq1265	cspC cstA	cold shock protein carbon starvation protein A	67.2% •••• 33.0% ••••
Aq1651a Aq226a	rpsN rpsO	ribosomal protein S14 ribosomal protein S15	51.6% 61.6%	Aq348	ctc	general stress protein Ctc	34.7% ••••
Aq123	rpsP	ribosomal protein S16	36.6% •••	Aq212 Aq337	cynS cysQ	cyanate hydrolase CysQ protein	39.5% ···· 47.4% ····
Aq020 Aq064a	rpsQ rpsR	ribosomal protein S17 ribosomal protein S18	59.6% •••• 48.5% ••••	Aq528	dedF	phenylacrylic acid decarboxylase	52.4% ••••
Aq015	rpsS	ribosomal protein S19	63.1% ••	Aq148 Aq2095	deoC dksA	deoxyribose-phosphate aldolase dnaK suppressor protein	46.6% ···· 35.1% ····
Aq1767 Aq867a	rpsT rpsU	ribosomal protein S20 ribosomal protein S21	40.0%	Aq1994	eral	GTP-binding protein Era	49.7% ••••
Translation fac				Aq1919 Aq1540	era2 gcpE	GTP binding protein Era GcpE protein	43.0%
Aq1364	efp	elongation factor P	48.6%	Aq1052	gcsH1	glycine cleavage system protein H	28.6% ••••
Aq2114 Aq712	frr	initiation factor eIF-2B alpha subunit ribosome recycling factor	43.0%	Aq1657 Aq944	gcsH2 gcsH3	glycine cleavage system protein H glycine cleavage system protein H	39.8% •••
Aq001	fusA	elongation factor EF-G	91.9% ••••	Aq1108	gcsH4	glycine cleavage system protein H	44.8% •••
Aq075a Aq2032	infA infB	initiation factor IF-1 initiation factor IF-2	69.1% •••• 48.5% ••••	Aq1458	gcvT	aminomethyltransferase (glycine cleavage system T protein)	42.2%
Aq1777	infC	initiation factor IF-3	53.6% ••••	Aq108b	hfq	host factor I	53.5% ••••
Aq876 Aq1840	prfA prfB	peptide chain release factor RF-1 peptide chain release factor RF-2	54.8% ···· 49.9% ····	Aq101 Aq2120	hly hlyC	hemolysin hemolysin homolog protein	33.7% ••• 29.3% ••••
Aq1033	selB	elongation factor SelB	30.4% ••••	Aq1091	hýlA	hemolysin	33.5% •••
Aq715 Aq005	tsf tufA1	elongation factor EF-Ts elongation factor EF-Tu	35.8% ···· 74.4% ····	Aq708 Aq1925	hyuA hyuB	N-methylhydantoinase A N-methylhydantoinase B	39.8% 43.1%
Aq1928	tufA2	elongation Factor EF-Tu	73.9%	Aq1579	iagB	invasion protein IagB	38.3% •••
Protein modifie		_		Aq1983	imp2	myo-inositol-1(or 4)-monophosphatase	36.0% ****
Aq731 Aq579	ccdA def	cytochrome c-type biogenesis protein	32.0% 41.4%	Aq748 Aq1739	ispA lytB	geranylgeranyl pyrophosphate synthase LytB protein	40.7%
Aq2093	dsbC	polypeptide deformylase thiol:disulfide interchange protein	27.6% ••••	Aq1977	masA	enolase-phosphatase E-1	42.3% ••••
Aa055	hemX1 hemX2	cytochrome c biogenesis protein cytochrome c biogenesis protein	26.2% 36.2%	Aq1560 Aq1823	mglA1 mglA2	gliding motility protein gliding motility protein MglA	42.4%
Aq2043 Aq1053	nifS1	FeS cluster formation protein NifS	38.5% ••••	Aq1789 Aq587	mviB neaC	'virulence factor' homolog MviB	29.7% 42.8%
Aq739	nifS2	FeS cluster formation protein NifS	45.5% ****	Aq587 Aq1820	neaC nfeD	N-ethylammeline chlorohydrolase nodulation competitiveness protein NfeD	42.8%
Aq1871 Aq2102	pmbA prmA	peptide maturation ribosomal protein L11 methyltransferase	25.6% 35.1%	Aq896	nifU	NifU protein	48.3% ****
Aq567	rimI	ribosomal-protein-alanine acetyltransferase	37.9% ••••	Aq1300 Aq1507	omp omt	outer membrane protein O-methyltransferase	25.5%
Aq576 Aq152	stpK tlpA	ser/thr protein kinase thiol disulfide interchange protein	30.8% 37.6%	Aq967	ostA	organic solvent tolerance protein	22.0% ****
Proteases	•	. 0.1	***	Aq141 Aq994	pkcI pncA	protein kinase C inhibitor (HIT family) pyrazinamidase/nicotinamidase	59.0% ···· 39.1% ····
Aa1950	aprV	serine protease	26.5% •••	Aq057	sfsA	sugar fermentation stimulation protein	27.3% ••••
Aq1672 Aq1296	clpB clpC	ATP-ase subunit of ATP-dependent protease ATP-dependent Clp protease	46.8% 54.9%	Aq287 Aq832	smb surE	small protein B stationary phase survival protein SurE	52.0% 44.1%
Aq1339	clpP	ATP-dependent Clp protease proteolytic subunit	65.4% ••••	Aq871	thdF	thiophene and furan oxidation protein	45.4% ****
Aq1337 Aq1015	clpX col	ATP-dependent protease ATPase subunit clpX collagenase	66.1% ···· 41.3% ····	Aq2021 Aq773	tldD tly	TldD protein hemolysin	40.9%
Aq801	gcp	sialoglycoprotease	45.5% ••••	Aq629	xcpC	chromosome assembly protein homolog	33.3% ••••