The complete genome of the hyperthermophilic bacterium Aquifex aeolicus

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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, microaerophilic, 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

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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 NO_3^- 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

Genera

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)

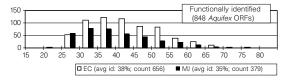
1,512 total (average length 956)

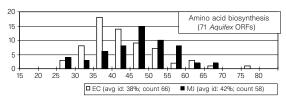
Extrachromosmal element (ECE)

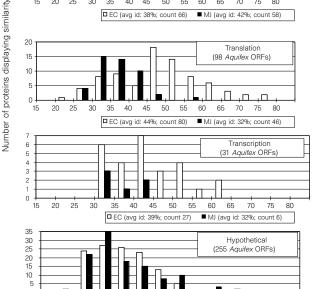
Length 39,456 bp G+C content 36.4% Protein-coding regions 53.5%

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

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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	
C	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	10.50	11.18	10.56	10.93	10.57	9.38	
M	2.44	2.28	2.86	2.12	1.92	2.33	
N	4.89	5.83	3.88	3.76	3.60	5.24	
Р	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	hiles		Thermophiles		
Charged residues (DEKRH)		24.1	1	=	29.84	1	
Polar/uncharged resid		31.7			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.

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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.

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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 $20-40\% \cdot \cdot \cdot , 40-60\% \cdot \cdot \cdot , 60-80\% \cdot \cdot \cdot \cdot , 80-100\% \cdot \cdot \cdot \cdot$

	Biosynthesis					1-carboxyvinyltransferase	45.7% ••••
Aromatic am Aq1536	ino 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 UDP-MurNac-tripeptide synthetase	29.3% 42.9%
Aq951	pheA	chorismate mutase/prephenate dehydratase	44.0% ••••	Aq821	murF	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 glycerol-3-phosphate cytidyltransferase	30.3% ···· 52.0% ····
Aq582	trpE	anthranilate synthase component I	50.0% ****	Aq185 Aq1368	tagD1 tagD2	glycerol-3-phosphate cytidyltransferase glycerol-3-phosphate cytidyltransferase	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 fan	nily			Aq1641 Aq1899	cap dmt	capsular polysaccharide biosynthesis protein dolichol-phosphate mannosyltransferase	30.8% ···· 40.2% ····
Aq1866	asd	aspartate-semialdehyde dehydrogenase	54.6% ••••	Aq1772	envA	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 Aq1143	aspC4 dapA	aminotransferase (AspC family) dihydrodipicolinate synthase	48.5% 53.1%	Aq1705	galF	UDP-glucose pyrophosphorylase	47.2% ****
Aq916	dapB	dihydrodipicolinate reductase	44.2% ••••	Aq908 Aq085	gmhA kdsA	phosphoheptose isomerase 3-deoxy-d-manno-octulosonic acid 8-phosphate	63.4% •••
Aq547	dapE	succinyl-diaminopimelate desuccinylase	25.8% 35.5%	71q003	KUS/1	synthase	52.0%
Aq1838 Aq1208	dapF lysA	diaminopimelate epimerase diaminopimelate decarboxylase	47.4%	Aq326	kdtA	3-deoxy-D-manno-2-octulosonic acid transferase	28.9% ••••
Aq1152	lysC	aspartokinase	52.2% ••••	Aq253 Aq1546	kdtB kpsF	lipopolysaccharide core biosynthesis protein polysialic acid capsule expression protein	46.5% •••• 45.9% ••••
Aq1710 Aq1812	metE thrA	tetrahydropteroyltriglutamate methyltransferase homoserine dehydrogenase	45.9% 40.4%	Aq692	kpsU	3-deoxy-manno-octulosonate cytidylyltransferase	41.3% ••••
Aq1309	thrB	homoserine kinase	38.3%	Aq1742 Aq604	lgtF lpxA	beta 1,4 glucosyltransferase acyl-[acyl-carrier-protein]-UDP-N-	35.2% ••••
Aq608	thrC1	threonine synthase	64.3% ••••	Aq004	ipxA	actylglucosamine acyltransferase	47.7%
Aq425	thrC2	threonine synthase	61.9% ••••	Aq1427	lpxB	lipid A disaccharide synthetase	31.6% ••••
Branched-ch	ain family ilvB	acetolactate conthace large cubunit	53 196	Aq538	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N acyltransferase	43.3%
Aq451 Aq1245	ilvC	acetolactate synthase large subunit acetohydroxy acid isomeroreductase	53.1% 64.3%	Aq718	mpg	mannose-1-phosphate guanyltransferase	34.1%
Aq837	ilvD ilvE	dihydroxyacid dehydratase	58.0% ••••	Aq1096	mtfA	mannosyltransferase A mannosyltransferase B	34.3% • • • • 29.0% • • • •
Aq1893 Aq1851	ilvH	branched-chain amino acid aminotransferase acetolactate synthase	40.3% 53.2%	Aq515 Aq516	mtfB mtfC	mannosyltransferase C	35.9%
Aq356	leuA1	2-isopropylmalate synthase	52,1%	Aq1335	nse	nucleotide sugar epimerase	45.8%
Aq2090 Aq244	leuA2 leuB	2-isopropylmalate synthase 3-isopropylmalate dehydrogenase	49.9% 58.7%	Aq505 Aq504	otnA otnA'	polysaccharide biosynthesis protein polysaccharide biosynthesis protein (fragment)	26.9% •••• 37.8% ••
Aq940	leuC	large subunit of isopropylmalate isomerase	52.3% ••••	Aq1543	rfaC1	ADP-heptose:LPS heptosyltransferase	30.7% ••••
Aq1398	leuD	3-isopropylmalate dehydratase	56.6% •••	Aq145	rfaC2	ADP-heptose:LPS heptosyltransferase	28.1% ****
Glutamate fa	mily			Aq344 Aq565	rfaD rfaE	ADP-L-glycero-D-manno-heptose-6-epimerase ADP-heptose synthase	39.6% 44.0%
Aq2068 Aq1879	argB argC	acetylglutamate kinase N-Acetyl-gamma-glutamylphosphate reductase	54.2% 40.6%	Aq2115	rfaG	glucosyl transferase I	27.1%
Aq023	argD	N-acetylornithine aminotransferase	49.5%	Aq1082	rfbD	GDP-D-mannose dehydratase	53.2%
Aq1711	argF	ornithine carbamoyltransferase	46.2%	Aq519	rfe	undecaprenyl-phosphate-alpha- N-acetylglucosaminyltransferase	24.870 ****
Aq1140 Aq1372	argG argH	argininosuccinate synthase argininosuccinate lyase	54.9% 46.4%	Aq1367	spsI	glucose-1-phosphate thymidylyltransferase	30.4% ••
Aq970	argJ	glutamate N-acetyltransferase	39.8% ••••	Aq518	spsK	spore coat polysaccharide biosynthesis protein SpsK	49.5% •••
Aq111	glnA	glutamine synthetase	57.6% ••••	Aq589	xanB	mannose-6-phosphate isomerase/mannose-1-	
Aq109 Aq1774	glnB glnE	nitrogen regulatory PII protein glutamate ammonia ligase adenylyl-transferase	73.2% 28.4%	•		phosphate guanyl transferase	40.9% ••••
Aq1565	gltB	glutamate synthase large subunit	44.3% ••••	Cellular Proces	ses		
Aq2064	gltD pro A	glutamate synthase small subunit gltD	37.7% ••••	Cell division	acrF	acriflavin resistance protein AcrE	24.8%
Aq1071	proA proB	gamma-glutamyl phosphate reductase	47.9% ••••	Aq698	acrE cafA	acriflavin resistance protein AcrE cytoplasmic axial filament protein	24.8% 28.5%
Aq2064 Aq1071 Aq1134 Aq166	proA proB proC	glutamate synthase small subunit gltD gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase		Aq698 Aq1275 Aq523	cafA ftsA	cytoplasmic axial filament protein cell division protein FtsA	28.5%
Aq1071 Aq1134 Aq166 Histidine	proA proB proC	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase	47.9% 43.2%	Aq698 Aq1275 Aq523 Aq936	cafA ftsA ftsH	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH	28.5% 31.9% 51.1%
Aq1071 Aq1134 Aq166	proA proB	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole	47.9% 43.2% 35.1%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920	cafA ftsA ftsH ftsW ftsY	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsW cell division protein FtsY	28.5% 31.9% 51.1% 30.8% 35.2%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039	proA proB proC	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	47.9% 43.2% 35.1% 40.9% 46.4%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525	cafA ftsA ftsH ftsW ftsY ftsZ	cytoplasmic axial filament protein cell division protein PtsA cell division protein PtsH cell division protein PtsW cell division protein PtsY cell division protein PtsZ	28.5% 31.9% 51.1% 30.8% 35.2% 48.6%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084	proA proB proC hisA hisB hisC	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiortansferase histidinol-phosphate amiortansferase	47.996 43.296 35.1% 40.996 46.4% 33.796	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761	cafA ftsA ftsH ftsW ftsY ftsZ gidA1	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsW cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782	proA proB proC hisA hisB hisC hisD	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase midazoleglycrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phydrogenase	47.996 43.296 35.196 40.996 46.496 33.796 49.996	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582	cafA ftsA ftsH ftsW ftsY gtsZ gidA1 gidA2 gidB	cytoplasmic axial filament protein cell division protein FEA cell division protein FEH cell division protein FEH cell division protein FEY cell division protein FEY cell division protein FEY cell division protein FEY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein A	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613	proA proB proC hisA hisB hisC hisD hisF hisG	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase midazoleglycorplphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase	47.996 43.296 35.196 40.996 46.496 33.796 49.996 59.996	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf	cytoplasmic axial filament protein cell division protein PsA cell division protein PsA cell division protein PsH cell division protein PsW cell division protein PsY cell division protein PsC 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%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732	proA proB proC hisA hisB hisC hisD hisF hisG hisH	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide rihotide isomerase imidazoleglycrolphosphate dehydratase histidinol-ohosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH	47.996 43.296 35.196 40.996 46.496 33.796 49.996 49.996 40.396 47.796	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887	cafA ftsA ftsH ftsW ftsY gtsZ gidA1 gidA2 gidB	cytoplasmic axial filament protein cell division protein FbA cell division protein FbA cell division protein FbH cell division protein FbW cell division protein FbW cell division protein FbC glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes]	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 57.5% 39.4%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase midazoleglycorplphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase	47.996 43.296 35.196 40.996 46.496 33.796 49.996 59.996	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1	cytoplasmic axial filament protein cell division protein FbA cell division protein FbA cell division protein FbH cell division protein FbY cell division protein FbY cell division protein FbY cell division protein FbY 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 MinD	28.5% 31.9% 51.19% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.99% 27.7% 39.4%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotransferase histidinoi-ohosphate aminotransferase histidinoi dehydrogenase HisFi (cyclase) ATP phosphoribosyltransferase amidotransferase HisFi phosphoribosyltransferase amidotransferase HisFi phosphoribosyl-ATP pyrophosphohydrolase	47.996 43.296 35.196 40.996 46.496 33.796 49.996 59.996 40.396 47.796 43.896	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877	cafA fisA fisH fisH fisW fisY fisZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinD	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.9% 27.7% 39.4% 33.1%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide rihotide isomerase imidazoleglycrolphosphate dehydratase histidinol-ohosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH	47.996 43.296 35.196 40.996 46.496 33.796 49.996 49.996 40.396 47.796	Aq698 Aq1275 Aq523 Aq536 Aq139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq1887 Aq878 Aq1877 Aq877 Aq877 Aq877 Aq874 Aq877 Aq874	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsZ 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 rod shape determining protein MreB od shape determining protein RodA	28.5%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031 Aq1030 Serine family	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE selA	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase Hist-[cyclase] ATP phosphoribosylransferase amidotransferase Hist phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase	47.9% 43.2% 43.2% 40.9% 46.4% 33.7% 49.9% 40.3% 47.7% 43.8%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq1887 Aq1217 Aq878 Aq1217 Aq845 Aq945 Aq130	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein division protein B MAF protein cell cycle protein Mesl septum site-determining protein MinG septum site-determining protein MinD septum site-determining protein MinD od shape determining protein MreB	28.5% 31.9% 51.1% 30.8% 35.2% 48.6% 50.2% 57.5% 39.4% 44.9% 27.7% 39.4% 33.1% 54.5% 57.4%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE sel	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 phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol)	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 59.9% 47.7% 43.8% 42.7% 37.796	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1718 Aq1878 Aq1877 Aq877 Aq845 Aq025 Aq1130 Chaperones	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA sufI	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septim site-determining protein MinD septum site-determining protein MinD rod shape determining protein MinD rod shape determining protein RodA periplasmic cell division protein (Suff)	28.5% 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
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031 Aq1030 Serine family Aq1556	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE ses estA selD	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ributide isomerase imidazoleglycrolphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisF (cyclase) ATP phosphoribosylransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase	47,996 43,296 35,196 40,996 46,496 33,796 49,996 40,396 47,796 43,896 42,796 37,796	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq1130 Chaperones Aq154	cafA ftsA ftsH ftsY ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA sufI	cytoplasmic axial filament protein cell division protein FBA cell division protein FBA cell division protein FBH cell division protein FBW cell division protein FBY cell division protein FBY dlucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mes] septum site-determining protein MinG septum site-determining protein MinD septum site-determining sprotein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining sprotein MinD septum site-determining	28.5% 31.9% 51.1% 30.8% 33.2% 48.6% 50.2% 49.6% 44.9% 44.9% 44.9% 37.6% 33.19% 54.5% 37.6% 38.8% 41.3%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031 Aq1030 Serine family	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisIE selA	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 phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol)	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 59.9% 47.7% 43.8% 42.7% 37.796	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq1130 Chaperones Aq154 Aq1735 Aq703	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA suff	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mesl septum site-determining protein MinG septum site-determining protein MinG septum site-determining protein MinD rod shape determining protein MreB rod shape determining protein foxIn) cytochrome c oxidase assembly factor chaperone Dnal	28.596 31.996 51.196 30.896 35.296 48.696 50.296 57.596 39.496 27.796 33.196 54.596 37.696 38.896 41.396
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031 Aq1030 Serine family Aq1556	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisH selD selD selD selA selD	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotransferase histidinoi-ohosphate amiotransferase histidinoi dehydrogenase Hisf (cyclase) ATP phosphoribosyltransferase amidotransferase Hisit phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 45.8% 62.7%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq845 Aq025 Aq1130 Chaperones Aq154 Aq1735 Aq703 Aq703 Aq703 Aq996	cafA fisA fisH fisW fisY fisZ gidA1 gidA2 gidB maf minD1 minD1 minD1 mreB rodA sufI ctaB dnaII dnaII dnaII	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY 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 rod shape determining protein food Apperiplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal chaperone Dnal chaperone Dnal Hsp70 chaperone Dnal Hsp70 chaperone Dnal	28.596 31.996 51.196 30.896 35.296 48.696 57.596 39.496 44.996 27.796 39.496 33.196 54.596 57.496 37.696 28.196
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocystein Aq1031 Aq1030 Serine family Aq1556 Aq479 Aq1905 Cell Envelope Pili and fimb	proA proB proC hisA hisB hisC hisD hisD hisD hisD hisG hisH hisGl hisH hisH e selA selD	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhydratase histidinol-phosphate aminotransferase histidinol dehydrogenase HisHF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphorhydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase	47.9%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq220 Aq761 Aq761 Aq1582 Aq11887 Aq1887 Aq1887 Aq1887 Aq1217 Aq845 Aq1217 Aq945 Aq133 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq134 Aq133 Aq132 Aq133 Aq133 Aq132	cafA ftsA ftsH ftsW ftsY ftsZ gidA1 gidA2 gidB maf mesJ minC minD1 minD2 mreB rodA suff	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mesl septum site-determining protein MinG septum site-determining protein MinG septum site-determining protein MinD rod shape determining protein MreB rod shape determining protein foxIn) cytochrome c oxidase assembly factor chaperone Dnal	28.5% 31.9% 31.9% 31.9% 31.9% 31.9% 35.2% 48.6% 50.2% 48.6% 50.2% 39.4% 44.9% 27.7% 39.4% 31.9% 54.5% 57.4% 31.9% 54.5% 57.4% 38.8% 45.1% 38.8% 45.1% 38.8% 57.5% 38.8% 57.5% 57.5%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq1303 Aq1303 Aq182 Aq181 Aq182 Aq181 Aq103 Aq103 Selmocysteir Aq103 Aq103 Aq103 Cell Envelope Pili and fimb Aq1433	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisH pisH hisH hisH selD ce selA selD glyA glyA glyA glyA glyA glyA glyA glyA	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphorihosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase Histi (cyclase) ATP phosphoribosyltransferase amidotransferase Histi 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	47.996 43.296 43.296 43.296 44.496 43.37.796 49.996 49.996 47.796 43.896 42.796 42.796 42.796 44.196 45.896 45.896 45.896 44.196 43.896 44.196 45.896 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 44.196 45.896 45.896 44.196 45.896 44.196 45.896 .	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq1210 Chaperones Aq154 Aq1735 Aq1733 Aq96 Aq433 Aq192 Aq192 Aq192 Aq192 Aq192 Aq192 Aq193 Aq192 Aq193 Aq193 Aq193 Aq193	cafA fish fish fish fish fisy gidA1 gidA2 gidA2 gidA2 gidA2 gidA2 minDC minDD1 mreB rodA sufl ctaB dnaj1 dnaj2 dnaj2 dnaj2 grpE hslU	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B cell cycle protein Mesl septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein MreB rod shape determining protein Mr	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 55.75% 39.4% 43.9% 52.4% 33.1% 54.5% 57.4% 37.6% 28.196 38.8% 41.396 41.396 45.196 59.196 38.8% 57.596 31.0%
Aq1071 Aq1134 Aq164 Aq1803 Aq0393 Aq0393 Aq0394 Aq2884 Aq782 Aq181 Aq1613 Aq1613 Aq1030 Serine family Aq1030 Serine family Aq1031 Aq1434	proA proB proC hisA hisA hisB hisC hisC hisP hisF hisH hisH hisH es eslA glyA serA 	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate amiotransferase histidinol-ohosphate amiotransferase histidinol-ohosphate amiotransferase histidinol dehydrogenase Hisf (cyclase) ATP phosphoribosyltransferase 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	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 45.8% 62.7% 44.1%	Aq698 Aq1275 Aq523 Aq523 Aq526 Aq1139 Aq520 Aq520 Aq520 Aq761 Aq691 Aq1582 Aq1887 Aq1887 Aq1887 Aq1887 Aq1887 Aq1130 Aq191 Aq194 Aq1217 Aq645 Aq1217 Aq645 Aq1217 Aq645 Aq123 Aq124 Aq128	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsZ 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 rod shape determining protein MinD rod shape determining protein (Suf) cytochrome c oxidase assembly factor chaperone Dnal chaperone Dnal chaperone Dnal chaperone Dnal heat shock protein Cass I) heat shock protein (Cass I) heat shock protein (Cass I) heat shock protein (Lass I)	28.5%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq0393 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1968 Selenocysteir Aq1031 Aq1030 Serine family Aq1556 Cell Encopteir Aq1905 Cell Encopteir Aq1905 Cell Encopteir Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434	proA proB proC hisA hisB hisC hisC hisD hisF hisG hisH hisH hisH esetA selD cysM glyA serA 	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate adhydratase histidinol-ohosphate aminotransferase histidinol dehydrogenase HisHF (cyclase) ATP phosphoribosyltransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphorhydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 45.8% 62.7% 44.1% 45.8% 62.7% 44.1%	Aq698 Aq1275 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq1210 Chaperones Aq154 Aq1735 Aq1733 Aq96 Aq433 Aq192 Aq192 Aq192 Aq192 Aq192 Aq192 Aq193 Aq192 Aq193 Aq193 Aq193 Aq193	cafA fish fish fish fish fisy gidA1 gidA2 gidA2 gidA2 gidA2 gidA2 minDC minDD1 mreB rodA sufl ctaB dnaj1 dnaj2 dnaj2 dnaj2 grpE hslU	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B cell cycle protein Mesl septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein Mino septum site-determining protein MreB rod shape determining protein Mr	28.5%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq039 Aq2084 Aq782 Aq181 Aq1613 Aq722 Aq1968 Selenocysteir Aq1031 Aq1030 Cell Envelope Pii and fimb Aq1433 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434	proA proB proC hisA hisB hisC hisC hisD hisF hisG hisH hisH ee ee glyA glyA glyA glyA erfa ppdD1 ppdD2 ppdD2 ppdD2 ppdD2 ppdD2 ppdD2 ppdD2	gamma-glutamyl phosphate reductase glutamate 5-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ributide isomerase imidazoleglycrolphosphate dehydratase 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 serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase	47.996 43.296 35.196 40.996 46.496 33.796 49.996 40.396 47.796 42.796 37.796 42.796 37.796 44.196 34.996 40.696 28.296	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq691 Aq158 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq845 Aq1217 Aq845 Aq123 Aq193 Aq192 Aq133 Aq192 Aq1283 Aq1991 Aq2200	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein B MAF protein MAF protein cell control of the many control ceptum site-determining protein MinD septum site-determining protein MreB rod shape determining protein for MreB rod shape determining protein for State control contr	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 57.5% 39.4% 34.4% 37.7% 39.4% 31.1% 54.5% 57.4% 37.6% 28.196 38.8% 41.3% 45.196 59.196 38.8% 57.5% 51.196 50.196
Aq1071 Aq1134 Aq1164 Aq1303 Aq0393 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1963 Serine family Aq153 Aq1903 Cell Envelope Pili and fimb Aq1432 Aq1434 Aq154 Aq164	proA proB proC hisA hisB hisC hisD hisF hisH hisH hisH es selA selD glyA serA 	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol dehydrogenase Histif-(cylase) ATP phosphoribosyltransferase amidotransferase Histi phosphoribosyl-ATP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin pilin prolipoprotein diacylglyceryl transferase	47.9%	Aq698 Aq1275 Aq523 Aq523 Aq526 Aq1139 Aq526 Aq1139 Aq7261 Aq691 Aq691 Aq182 Aq182 Aq1887 Aq1878 Aq1217 Aq887 Aq878 Aq1217 Aq845 Aq025 Aq1130 Chaperones Aq154 Aq703 Aq996 Aq433 Aq192 Aq1283 Aq192 Aq1283 Aq192 Aq1283 Aq1991 Aq2200 Aq2199 Detoxification Aq486	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsY 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 rod shape determining protein fixed haper determining protein fixed periplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal chaperone Dnal chaperone Dnal heat shock protein GrpE chaperone FtsH butter division division division for the set of the division of the division of the set of the division protein cytochrome c oxidase assembly factor chaperone Dnal chaperone FtsH butter shock protein GrpE chaperone FtsH butter droper dr	28.5%
Aq1071 Aq1134 Aq166 Aq1303 Aq0393 Aq0393 Aq2084 Aq782 Aq1881 Aq1613 Aq722 Aq1968 Serine family Aq1556 Cell Environment Aq1433 Aq1905 Cell Environment Aq1433 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq270 Aq819 Aq6522	proA proB proC hisA hisB hisC hisD hisF hisG hisH hisH hisH per selA selD cysM glyA serA serA serA serA serA serA serA ser	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase 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 minor pilin pilin pilin pilin prolipoprotein diacylglyceryl transferase apolipoprotein N-acyltransferase lipoprotein	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 43.8% 42.7% 33.7% 45.8% 42.7% 31.9% 45.8% 42.7% 43.8% 45.8% 42.7% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 45.8% 46.2% 46.5% 46	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq1582 Aq1718 Aq187 Aq187 Aq847 Aq847 Aq847 Aq847 Aq1130 Chaperones Aq154 Aq1735 Aq703 Aq996 Aq433 Aq1991 Aq1283 Aq1991 Aq229 Aq1299 Detoxification Aq486 Aq858	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsZ glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B cell cycle protein Mesl septum site-determining protein Mino septum site-determining protein Mesl rod shape determining protein MreB rod shape determining rotein MreB r	28.5% 31.9% 51.196 30.8% 35.296 48.6% 50.296 50.296 57.5% 39.4% 49.9% 33.1% 53.1% 53.1% 54.5% 57.4% 37.6% 28.8% 57.5% 38.8% 57.5% 31.0% 59.1% 59
Aq1071 Aq1134 Aq1164 Aq1303 Aq0393 Aq0393 Aq2084 Aq782 Aq181 Aq1613 Aq732 Aq1963 Serine family Aq1556 Cell Envelope Pili and fimb Aq1437 Aq1434 Aq1434 Aq1434 Aq1434 Aq1434 Aq1436 Aq146 Aq	proA proB proC hisA hisA hisB hisC hisC hisB hisB hisB hisB set selA setD cysM glyA serA serA serA serA serA serA setD setD setD setD setD setD setD setD	gamma-glutamyl phosphate reductase glutamate S-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 Histif phosphoribosyl-ATP pyrophosphohydrolase L-seryl-IRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	47,9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 40.35 40.35 43.8% 42.7% 43.8% 42.7% 43.8% 44.1% 45.8% 45.8% 42.6.4% 28.2% 30.1% 30.1% 30.1% 30.5% 43.2%	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq1582 Aq1718 Aq1887 Aq878 Aq1217 Aq877 Aq847 Aq023 Aq1130 Chaperones Aq154 Aq1735 Aq703 Aq996 Aq433 Aq192 Aq1283 Aq1991 Aq2209 Detoxification Aq486 Aq858 Aq885 Aq885 Aq885 Aq136	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cytic protein ftsH division protein ftsH septum site-determining protein finin septum site-determining protein ftsH protein ftsH cot shape determining protein ftsH dshape determining protein ftsH rod shape determining protein ftsH rot shape ftsH rot	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.696 50.296 57.596 39.496 44.996 37.696 32.796 33.196 34.996 37.696 38.896 41.396 41.396 45.196 59.196 38.896 41.196 59.196 38.896 41.196 59.19
Aq1071 Aq1134 Aq164 Aq1803 Aq0393 Aq0393 Aq0393 Aq0393 Aq1801 Aq1613 Aq1722 Aq1968 Aq1782 Aq1969 Aq1801 Aq1613 Aq1613 Aq1613 Aq1613 Aq1620 Aq1799 Aq1909 Cell Envelope Pili and fimb Aq1432 Aq1434 Aq1432 Aq1434 Aq1435 Lipoptotian Aq1819 Aq652 Aq1753 Aq529 Aq6753 Aq529 Aq2147	proA proB proC hisA hisA hisB hisC hisC hisD hisF hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-ohosphate aminotransferase histidinol-ohosphate aminotransferase histidinol dehydrogenase 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 minor pilin pilin pilin pilin prolipoprotein diacylglyceryl transferase apolipoprotein N-acyltransferase lipoprotein	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 43.8% 42.7% 33.7% 45.8% 42.7% 31.9% 45.8% 42.7% 43.8% 45.8% 42.7% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 42.7% 45.8% 45.8% 45.8% 46.2% 46.5% 46	Aq698 Aq1275 Aq523 Aq523 Aq526 Aq1139 Aq520 Aq525 Aq761 Aq691 Aq691 Aq1582 Aq1718 Aq1887 Aq1887 Aq1887 Aq1887 Aq187 Aq187 Aq187 Aq187 Aq197 Aq198 Aq199 Aq199 Aq200 Aq199 Detoxification Aq185 Aq185 Aq185 Aq186	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsY 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 rod shape determining protein Merl of shape determining protein food Aperiplasmic cell division protein (Suff) cytochrome c oxidase assembly factor chaperone Dnal chaperone Dnal chaperone Dnal chaperone Dnal chaperone fisU small heat shock protein (class I) heat shock protein (Cass I) heat shock protein X GroEE alkyl hydroperoxide reductase arsenate reductase cytochrome c peroxidase pretipalsmic divalent 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% 56.2% 49.2% 49.2% 49.2% 49.2%
Aq1071 Aq1134 Aq166 Histidine Aq1303 Aq0393 Aq0393 Aq2084 Aq782 Aq1881 Aq1613 Aq732 Aq1986 Selemocysteir Aq1031 Aq1030 Aq1030 Aq1434 Aq1905 Cell Enrel family Aq1435 Aq1434 Aq1435 Aq1434 Aq1435 Aq1434 Aq1435 Aq1435 Aq1732 Aq1733 Aq1734 Aq1734 Aq1734 Aq1734 Aq1734 Aq1734 Aq1734 Aq1734 Aq1734 Aq1735 Aq1734 Aq173	proA proB proB proC hisA hisB hisC hisD hisF hisG hisH hisH bisH cysM glyA glyA glyA glyA glyA glyA glyA glyA	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase amidotransferase HisH phosphoribosyl-ATP pyrophosphohydrolase L-seryl-IRNA(ser) selenium transferase selenophosphate synthase L-seryl-IRNA(ser) selenium transferase selenophosphate synthase D-3-phosphoglycerate dehydrogenase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin pilin pilin pilin pilin pilin prolipoprotein N-acyltransferase apolipoprotein N-acyltransferase lipoprotein N-acyltransferase lipoprotein N-acyltransferase lipoprotein N-proper in lipoprotein N-proper in lipoprotein plagment outer membrane protein c peptidoglycan associated lipoprotein rare lipoprotein A	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 43.8% 42.7% 37.7% 45.8% 42.7% 31.7% 45.8% 42.7% 45.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 44.1% 45.8% 44.1% 45.8% 45.8% 46.2% 46.6% 47.9% 48.2%	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq691 Aq158 Aq1718 Aq1887 Aq878 Aq1217 Aq847 Aq845 Aq1130 Chaperones Aq154 Aq1735 Aq193 Aq192 Aq1283 Aq192 Aq1283 Aq1991 Aq2200 Aq2199 Detoxification Aq486 Aq1858 Aq885 Aq885 Aq885 Aq136 Aq105 Aq136 Aq1005 Aq136 Aq1005 Aq1499	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein B MAF protein MAF protein division protein Mino septum site-determining protein MreB rod shape determining rotein MreB ro	28.5% 31.9% 51.196 30.8% 35.296 48.6% 50.296 50.296 57.5% 39.4% 4.9% 32.7% 33.4% 4.9% 33.4% 4.9% 37.6% 28.196 38.8% 51.196 51.196 54.49% 56.296
Aq1071 Aq1134 Aq164 Aq1803 Aq0393 Aq0393 Aq0393 Aq0393 Aq1801 Aq1613 Aq1722 Aq1968 Aq1782 Aq1969 Aq1801 Aq1613 Aq173 Aq173 Aq173 Aq173 Aq173 Aq173 Aq173 Aq170 Aq1174 Aq1170 Aq1174 Aq1170	proA proB proB proC hisA hisB hisC hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycrolphosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate 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 pil	47,996 43.296 35.196 40.996 46.496 33.796 49.996 40.396 47.796 43.896 42.796 37.796 44.196 44.196 34.996 44.196 34.996 40.696 25.596 22.296 30.196 25.596 27.296 30.72.96 61.196	Aq698 Aq1275 Aq523 Aq523 Aq936 Aq1139 Aq920 Aq525 Aq761 Aq691 Aq691 Aq158 Aq1718 Aq1887 Aq878 Aq1217 Aq847 Aq845 Aq1130 Chaperones Aq144 Aq1735 Aq133 Aq192 Aq1283 Aq192 Aq1283 Aq1991 Aq2200 Aq2199 Detoxification Aq486 Aq1056 Aq136 Aq1056 Aq1499 Aq1050 Aq238	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsH cell division protein FtsY cell division protein FtsY cell division protein FtsY cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cycle protein Mesl septiment site-determining protein MinD septum site-determining protein Septum septum site-determining protein Septum septum site-determining protein MinD septum site-determining protein Septum site septum site-determining septum site septum site-determi	28.5% 31.9% 51.196 30.8% 35.296 48.6% 50.296 57.5% 39.4% 49.9% 27.7% 33.4% 49.9% 37.6% 28.196 41.3% 41.3% 45.196 41.3% 41.3% 45.196 41.3% 41.196 42.196 43.88% 51.196 44.9% 56.296
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Aq1071 Aq1134 Aq1164 Aq1303 Aq0393 Aq0393 Aq0393 Aq0393 Aq1801 Aq1610 Aq1801 Aq1610 Aq1801 Aq1610 Aq	proA proB proC hisA hisB hisC hisC hisD hisF hisF hisF hisF hisF hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate 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 pi	47,9% 43,2% 35,1% 40,9% 46,4% 33,7% 49,9% 40,3% 47,7% 43,8% 42,7% 37,7% 41,8% 42,8% 42,8% 44,1% 45,8% 42,8% 44,1% 34,9% 41,1% 45,8% 41,1% 45,8% 41,1% 45,8% 41,1% 41,1% 45,8% 41,1% 41,1% 45,8% 41,1%	Aq698 Aq1275 Aq523 Aq523 Aq523 Aq526 Aq1139 Aq526 Aq1139 Aq526 Aq1582 Aq1718 Aq1887 Aq1887 Aq1887 Aq1173 Aq187 Aq1735 Aq1735 Aq1735 Aq1736 Aq1838 Aq488	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsY 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 MinG septum site-determining protein MinG septum site-determining protein MinD septum site-determining protein Septum septum site-determining protein Septum septum site-determining protein Septum septum site-determining septum site septum septum site septum site septum septum site septum septum site septum septum site septum septu	28.5% 31.9% 51.196 30.8% 35.296 48.6% 50.296 55.296 49.9% 49
Aq1071 Aq1134 Aq1164 Aq1303 Aq0393 Aq0393 Aq0393 Aq0393 Aq1801 Aq1613 Aq1614 Aq1614 Aq1614 Aq1614 Aq1616 Aq1619 Aq	proA proB proB proC hisA hisB hisC hisC hisD hisF hisF hisF hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphate aminotransferase histidinoi-phosphoribosyltransferase amidotransferase HisH phosphoribosyl-AIP pyrophosphohydrolase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thioi) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin pilin pilin prolipoprotein N-acyltransferase lipoprotein N-acyltransferase lipoprotein lipoprotein N-acyltransferase lipoprotein asociated lipoprotein rare lipoprotein A rare lipoprotein A adhesion protein adhesion B precursor alanine racemase N-acetylmuramoyl-L-alanine amidase undecaprenol kinase than the same and th	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 40.3% 47.7% 43.8% 42.7% 37.7% 43.8% 42.7% 37.7% 45.8% 62.7% 44.1% 45.8% 62.7% 45.8% 62.7% 62.1% 60.6% 62.8.2% 30.1% 60.6%	Aq698 Aq1275 Aq523 Aq523 Aq523 Aq526 Aq1139 Aq761 Aq761 Aq761 Aq761 Aq761 Aq1582 Aq1788 Aq1217 Aq878 Aq1217 Aq878 Aq1217 Aq877 Aq845 Aq123 Aq124 Aq1735 Aq703 Aq296 Aq433 Aq192 Aq1283 Aq192 Aq1283 Aq192 Aq1283 Aq193 Aq209 Detoxification Aq486 Aq858 Aq136 Aq488 Aq136 Aq1050 Aq1499 Aq1290 Aq1299 Aq1299 Aq1299 Aq1299 Aq1299 Aq1299 Aq1299 Aq1299 Aq1299 Aq138 Aq191 Aq2091 Aq2091 Aq2091 Aq2091 Aq2091 Aq2091 Aq1050 Aq1184 Aq883 Aq1184 Aq883 Aq1184 Aq183 Aq1184 Aq183 Aq1184 Aq183 Aq1184 Aq1931 Aq2031 Aq2031 Aq2031 Aq2031 Aq2031 Aq2031 Aq2031 Aq2031 Aq1114 Aq1662 Aq1663	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsY 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 MinG septum site-determining protein MinG septum site-determining protein MinD septum site-determining protein Septum septum site-determining protein MinD septum site-determining protein Septum septum site-determining protein Septum site septum site-determining septum site septum site site site site site site site site	28.5% 31.9% 51.196 51.196 30.8% 35.2% 48.6% 50.296 57.5% 39.4% 43.9% 27.7% 33.196 33.196 34.5% 35.2% 44.996 28.196 38.8% 45.196 38.8% 45.196 45.196 49.2% 49
Aq1071 Aq1134 Aq164 Aq1303 Aq0393 Aq0393 Aq0393 Aq181 Aq1613 Aq1783 Aq181 Aq1613 Aq178 Aq181 Aq1613 Aq178 Aq178 Aq181 Aq1613 Aq178 Aq181 Aq161 Aq178 Aq181 Aq178 Aq181 Aq182 Aq182 Aq182 Aq181 A	proA proB proB proB proC hisA hisB hisC hisC hisD hisF hisG hisH hisH bisH set selA setA setA glyA setA setA setA setA setA setA setA set	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase listif (volase) ATP phosphoribosyl-transferase amidotransferase HisH phosphoribosyl-ATP pyrophosphodylorlase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase D-3-phosphoglycerate dehydrogenase minor pilin p	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 41.38% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 43.9% 44.1% 44.1% 44.1% 44.1% 44.1% 45.8% 36.2% 36.1% 36.2% 37.6% 38.2% 33.2%	Aq698 Aq1275 Aq523 Aq523 Aq523 Aq526 Aq1139 Aq526 Aq1139 Aq526 Aq1781 Aq1887 Aq1887 Aq1887 Aq1217 Aq845 Aq1217 Aq845 Aq1217 Aq184 Aq1217 Aq130 Aq130 Aq130 Aq1413 Aq1413 Aq1413 Aq1413 Aq1413 Aq1413 Aq1413 Aq1414 A	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B cell cycle protein Mes cell cycle protein Mes septum site-determining protein MinG septum site-determining protein MinG septum site-determining protein MinD septum site-determining protein MreB rod shape determining protein forth lasperone Dnal Hsp?0 chaperone Dnal Hsp?0 chaperone Dnal Hsp?0 chaperone FtsIU small heat shock protein (class I) heat shock protein GrpE chaperone FtsIU small heat shock protein (class I) heat shock protein S GroEL GroES alkyl hydroperoxide reductase alkyl hydroperoxide reductase alkyl hydroperoxide reductase arsenate reductase cytochrome c peroxidase periplasmic divalent cation tolerance protein superoxide dismutase (CulZn) superoxide dismutase (CulZn) superoxide dismutase (CulZn) thiol peroxidase flagellar protein FlgA flagellar book basal-body protein FlgG flagellar hook basal-body protein FlgG flagellar hook saso-dated protein FlgL flagellar hook associated protein FlgL flagellar hook assoc	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.696 50.296 57.596 39.496 34.796 33.196 54.596 57.496 33.196 34.896 41.396 45.196 59.196 38.896 41.396 50.296 50.296 50.296 39.496 39.596 39.596 39.596 39.596 39.596
Aq1071 Aq1134 Aq1184 Aq181 Aq1803 Aq0393 Aq0393 Aq0393 Aq1801 Aq1811 Aq1613 Aq1722 Aq1968 Aq1782 Aq1969 Aq1903 Serine family Aq1631 Aq1631 Aq1631 Aq1630 Serine family Aq1631 Aq175 Aq175 Aq175 Aq175 Aq176 Aq177 A	proA proB proB proC hisA hisB hisC hisC hisD hisF hisF hisF hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase histidinol-phosphate aminotransferase amidotransferase HisH phosphoribosyl-AIP pyrophosphohydrolase L-seryl-IRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase minor pilin	47.9% 43.2% 35.1% 40.9% 46.4% 33.7% 49.9% 49.9% 41.38% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 42.7% 43.8% 45.8% 42.7% 45.8% 42.7% 45.8% 46.2% 46.6% 47.7% 41.1%	Aq698 Aq1275 Aq523 Aq523 Aq523 Aq526 Aq1139 Aq525 Aq521 Aq691 Aq691 Aq1582 Aq1718 Aq1887 Aq1887 Aq1887 Aq1887 Aq1817 Aq845 Aq1025 Aq1130 Chaperones Aq144 Aq1735 Aq193 A	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsA cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B cell cycle protein Mes cell cycle protein Mes septum site-determining protein Mino septum site-determining protein MreB rod shape determining protein fyga haperone Dnal haperone Dnal haperone Dnal haperone Dnal haperone Dnal haperone protein (class I) heat shock protein (class	28.5% 31.9% 51.196 51.196 30.8% 35.296 48.6% 50.296 55.25% 39.4% 47.9% 31.9% 31.9% 41.396
Aq1071 Aq1134 Aq1164 Aq1303 Aq0393 Aq0393 Aq0393 Aq0393 Aq1801 Aq1613 Aq1614 Aq1614 Aq1614 Aq1614 Aq1616 Aq1619 Aq	proA proB proB proC hisA hisB hisC hisC hisD hisF hisG hisH hisH hisH hisH hisH hisH hisH hisH	gamma-glutamyl phosphate reductase glutamate S-kinase pyrroline carboxylate reductase phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase imidazoleglycerolphosphate dehydratase histidinol-phosphate aminotransferase listif (volase) ATP phosphoribosyl-transferase amidotransferase HisH phosphoribosyl-ATP pyrophosphodylorlase L-seryl-tRNA(ser) selenium transferase selenophosphate synthase cysteine synthase, O-acetylserine (thiol) lyase B serine hydroxymethyl transferase D-3-phosphoglycerate dehydrogenase D-3-phosphoglycerate dehydrogenase minor pilin p	47.5% 413.2% 43.2% 35.19 40.996 46.496 33.796 49.996 40.396 47.796 43.896 42.796 37.796 44.196 34.996 44.196 34.996 44.196 34.996 44.196 34.996 44.196 35.196 30.196 25.596 25.496 43.296 33.196 61.196 25.796 28.596 33.296 33.296 33.296 43.296	Aq698 Aq1275 Aq523 Aq523 Aq523 Aq526 Aq1139 Aq761 Aq620 Aq761 Aq611	cafA fish fish fish fish fish fish fish fish	cytoplasmic axial filament protein cell division protein FtsA cell division protein FtsH cell division protein FtsY glucose inhibited division protein A glucose inhibited division protein A glucose inhibited division protein B MAF protein cell cytle protein Mes] septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD septum site-determining protein MinD rot shape determining protein MinD rot shape determining protein MeB od shape determining protein MeB rot shape determining protein Septum rot shape determining protein FtgB flagellar protein FtgB flagellar book basel-body protein FtgB flagellar book basel-body protein FtgB flagellar protein FtgB	28.5% 31.9% 51.196 30.8% 35.2% 48.6% 50.296 57.5% 39.4% 43.9% 27.7% 33.196 33.196 34.5% 35.2% 44.996 45.196 38.8% 45.196 45.196 45.196 45.196 46.2% 49

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 Aq1595	fliG fliI	flagellar switch protein FliG flagellar export protein	35.9% 44.6%	Aq1326	mobB	molybdopterin-guainine dinucleotide biosynthesis protein B	44.4% •
Aq1860	fliL	flagellar biosynthesis FliL	30.6% ••••	Aq030	moeA1	molybdenum cofactor biosynthesis protein A	36.8% ****
Aq1539	fliN fliP	flagellar switch protein FliN	42.9% •••	Aq1329	moeB	molybdopterin biosynthesis protein MoeB	54.1%
Aq1920 Aq1962	fliQ	flagellar biosynthetic protein FliP flagellar biosynthesis protein FliQ	47.7% ···· 45.5% ····	Aq061 Aq049	mog phhB	molybdenum cofactor biosynthesis MOG pterin-4a-carbinolamine dehydratase	55.5% •••• 37.9% ••••
Aq1961	fliR	flagellar biosynthetic protein FliR	29.7% ••••	Panthenate	F	F	
Aq2002	fliS motA	flagellar protein FliS flagellar motor protein MotA	30.8% ···· 35.0% ····	Aq815	dfp	pantothenate metabolism flavoprotein	41.2%
Aq1003 Aq1002	motA motB1	flagellar motor protein MotA	36.8%	Aq1973	panB	3-methyl-2-oxobutanoate	
Aq1001	motB2	flagellar motor protein MotB-like	27.5% ••••	Aq2132	panC	hydroxymethyltransferase pantothenate synthetase	45.5% 47.4%
Secretion				Aq476	panD	aspartate 1-decarboxylase	46.0%
Aq1720	ffh	signal recognition particle receptor protein	49.1%	Pyridine nucl	eotides		
Aq1288 Aq1474	gspD gspE	general secretion pathway protein D general secretion pathway protein E	27.5% ···· 48.8% ····	Aq1889	nadA	quinolinate synthetase A	44.3%
Aq418	gspG	general secretion pathway protein G	50.7% ••••	Aq777 Aq869	nadB nadC	L-aspartate oxidase quinolinate phosphoribosyl transferase	36.7% ••• 47.0% ••••
Aq955	lepB	type-I signal peptidase lipoprotein signal peptidase	33.9% •••• 37.4% ••••	Aq959	nadE	NH(3)-dependent NAD+ synthetase	39.6%
Aq1837 Aq1271	lsp mpp	processing protease	28.7%	Pyridoxal pho	osphate		
Aq747	pilC1	fimbrial assembly protein PilC	37.4% ••••	Aq852	pdxA	pyridoxal phosphate biosynthetic protein PdxA	36.8%
Aq1285	pilC2 pilD	fimbrial assembly protein PilC	28.9%	Aq1423	pdxJ	pyridoxal phosphate synthetase	88.2%
Aq1601 Aq745	pilT	type 4 prepilin peptidase twitching motility protein PilT	51.4%	Quinones			
Aq2151	pilU	twitching mobility protein	41.6% ••••	Aq895 Aq052	ispB ubiA	octoprenyl-diphosphate synthase 4-hydroxybenzoate octaprenyltransferase	35.7% 41.4%
Aq1870	secA secD	preprotein translocase SecA subunit	44.9% 36.0%	Riboflavin	don't	4-nydroxybenzoate octapienytransierase	41.470 ****
Aq973 Aq1602	secF	protein export membrane protein SecD protein-export membrane protein	41.4%	Aq350	ribA	GTP cyclohydrolase II	61.7%
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 Aq1340	tapB tig	type IV pilus assembly protein TapB trigger factor	42.2% ···· 27.4% ····	Aq436 Aq139	ribD2 ribF	riboflavin specific deaminase riboflavin kinase	42.9% ···· 38.4% ····
			27.170	Aq132	ribH	riboflavin synthase beta subunit	51.0%
One-carbon me	etabolism	iii		Thiamine			
Aq1429	metF	5,10-methylenetetrahydrofolate reductase	43.3% ••••	Aq1204	thiC	thiamine biosynthesis protein	67.1%
Aq1154	metK	S-adenosylmethionine synthetase	49.2%	Aq1960 Aq1366	thiD thiE1	HMP-P kinase thiamine phosphate synthase	40.5%
Aq1180	sahH	S-adenosylhomocysteine hydrolase	00.9% ••••	Aq558	thiE2	thiamine phosphate synthase	39.5%
Cytoplasmic po Aq1407	lysaccharides bcsA	cellulose synthase catalytic subunit	39.5% ••••	Aq2178	thiG	thiamine biosynthesis, thiazole moiety	52.5% ••••
Aq1401	celY	endoglucanase fragment	33.0% ••	Aq2119	thiL	thiamine monophosphate kinase	34.5% ••••
Aq721	glgA	glycogen synthase	38.1%	Thio- and glu			
Aq722 Aq717	glgB	1,4-alpha-glucan branching enzyme glycogen phosphorylase	56.5% 37.0%	Aq443 Aq1916	gua trxA1	glutaredoxin-like protein thioredoxin	33.8% •••• 58.9% •••
Aq723	glgP malM	4-alpha-glucanotransferase (amylomaltase)	43.4%	Aq1811	trxA2	thioredoxin	32.2%
Tri-carboxylic a		•		Aq500	trxB	thioredoxin reductase	39.8% ••••
Aq1784	aco	aconitase	36.1% •••	Energy Metab			
Aq1195	forA1 forA2	ferredoxin oxidoreductase alpha subunit ferredoxin oxidoreductase alpha subunit	31.5% 32.3%	Aq1342	gph	phosphoglycolate phosphatase	33.9% ••••
Aq1167 Aq1196	forB1	ferredoxin oxidoreductase aipna subunit ferredoxin oxidoreductase beta subunit	29.6%	ATP-Proton N			
Aq1168	forB2	ferredoxin oxidoreductase beta subunit	31.5% •••	Aq679 Aq179	atpA atpB	ATP synthase F1 alpha subunit ATP synthase F0 subunit a	64.3% ···· 36.4% ····
Aq1200	forG1 forG2	ferredoxin oxidoreductase gamma subunit	34.5% •••• 34.5% •••	Aq673	atpC	ATP synthase F1 epsilon subunit	37.4%
Aq1169 Aq594	frdA	ferredoxin oxidoreductase gamma subunit fumarate reductase flavoprotein subunit	51.4%	Aq2038	atpD	ATP synthase F1 beta subunit	67.4% ****
Aq553	frdB1	reductase iron-sulfur subunit	35.2% ••••	Aq177 Aq1586	atpE atpF1	ATP synthase F0 subunit c ATP synthase F0 subunit b	53.8% • • • • 26.3% • • • •
Aq655	frdB2 fumB	fumarate reductase iron-sulfur subunit	35.1% •••• 46.4% ••••	Aq1587	atpF2	ATP synthase F0 subunit b	25.5%
Aq1780 Aq1679	fumX	fumarate hydratase (fumarase) 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% ••••
Aq1512	icd mdh1	isocitrate dehydrogenase	46.0% 49.8%	Dehydrogena	ses adh1	dark d Adrida array	35.4%
Aq1782 Aq1665	mdh1 mdh2	malate dehydrogenase malate dehydrogenase	46.9%	Aq1362 Aq1240	adh1 adh2	alcohol dehydrogenase 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% •••• 52.9% ••••	Aq227	aldH2 dhaT	aldehyde dehydrogenase	28.0% ···· 36.6% ····
Aq1620 Aq1888	sucC2 sucD1	succinyl-CoA ligase beta subunit succinyl-CoA ligase alpha subunit	41.7%	Aq1145 Aq232	dhsU	1,3 propanediol dehydrogenase flavocytochrome C sulfide dehydrogenase	33.6%
Aq1622	sucD2	succinyl-CoA ligase alpha subunit	65.7% ••••	Aq1769	dld1	D-lactate dehydrogenase	45.3% ****
Phosphate				Aq1234	dmsA dmsB	DMSO reductase chain A DMSO reductase chain B	25.0% ···· 38.4% ···
Aq1351	phoH	phosphate starvation-inducible protein	47.1% ••••	Aq1232 Aq1231	dmsC	DMSO reductase chain B DMSO reductase chain C	29.5% •
Aq1547 Aq891	ppa	inorganic pyrophosphatase exopolyphosphatase	56.5% •••• 33.6% ••••	Aq1051	fdhE	formate dehydrogenase formation protein FdhE	25.9%
Polyamines	ppx	cxoporypriospriatase	33.070 ****	Aq1039	fdoG fdoH	formate dehydrogenase alpha subunit	50.0% ···· 45.7% ····
Aq728	speC	ornithine decarboxylase	30.9% ****	Aq1046 Aq1049	fdoI	formate dehydrogenase beta subunit formate dehydrogenase gamma subunit	38.4%
Aq062	speE	spermidine synthase	48.4%	Aq1903	gcsP1	glycine dehydrogenase (decarboxylating)	49.6% ••••
Sulfur				Aq1109	gcsP2	glycine dehydrogenase (decarboxylating)	46.8% •••• 27.1% ••••
Aq1081	cysD	sulfate adenylyltransferase	46.7% ••••	Aq1639 Aq395	glpC hdrA	oxido/reductase iron sulfur protein heterodisulfide reductase subunit A	39.7%
Aq1076 Aq1799	rhdA rhdA	thiosulfate sulfurtransferase thiosulfate sulfurtransferase	32.3%	Aq400	hdrB	heterodisulfide reductase subunit B	32.5% ••••
Aq455	sor	sulfur oxygenase reductase	36.7% ••••	Aq398 Aq961	hdrC hdrD	heterodisulfide reductase subunit C heterodisulfide reductase	35.7% • 29.5% ••••
Aq1803	soxB	sulfur oxidation protein SoxB	41.3% ••••	Aq038	hibD	3-hydroxyisobutyrate dehydrogenase	34.6% ••••
Cofactor Biosyn				Aq727	ldhA	D-lactate dehydrogenase	33.5% ••••
Lipoic acid bios Aq1355	synthesis lipA	Lipoic acid synthetase	48.9%	Aq736 Aq217	lpdA narB	dihydrolipoamide dehydrogenase nitrate reductase narB	37.0%
	£***	1		Aq206	nirB	nitrite reductase (NAD(P)H) large subunit	35.3% •••
Biotin Aq170	bioA	DAPA aminotransferase	51.7%	Aq835	nox	NADH oxidase	33.1% ****
Aq975	bioB	biotin synthetase	42.0% ••••	Aq024 Aq135	nsd nueM	nucleotide sugar dehydrogenase NADH dehydrogenase (ubiquinone)	47.0%
Aq557 Aq626	bioD bioF	dethiobiotin synthetase 8-amino-7-oxononanoate synthase	41.5% •••• 45.1% ••••	Aq1010	udh	dehydrogenase	29.7%
Aq1659	bioW	6-carboxyhexanoate-CoA ligase		Electron trans	sport		
		(pimeloyl CoA synthase)	47.3% ••••	Aq2191	coxA1	cytochrome c oxidase subunit I	42.4%
-	birA	biotin [acetyl-CoA-carboxylase] ligase	37.5% ••••	Aq2192 Aq2190	coxA2 coxB	cytochrome c oxidase subunit I cytochrome c oxidase subunit II	38.1% 27.4%
Folic acid	6.10	(11.1.1	23.00/	Aq2188	coxC	cytochrome c oxidase subunit II	28.6% ****
Aq2045 Aq1898	folC folD	folylpolyglutamate synthetase methylenetetrahydrofolate dehydrogenase	31.8% ···· 53.2% ····	Aq153	ctaA	heme O oxygenase	28.1% ****
Aq239	folE	GTP cyclohydrolase I	57.1% ••••	Aq042 Aq792	cyc cycB1	cytochrome c cytochrome c552	25.8% • • • 29.9% • •
Aq162	folK	folate biosynthesis 7,8-dihydro-6-	42.704	Aq1550	cycB1 cycB2	cytochrome C552	38.7% ****
Aq1468	folP	hydroxymethylpterin-pyrophosphokinase dihydropteroate synthase	43.7% 45.8%	Aq1357	cydA	cytochrome oxidase d subunit I	38.8% ****
Aq1144	pabB	p-aminobenzoate synthetase	41.5% •••	Aq1358 Aq067	cydB dmsB	cytochrome oxidase d subunit II dimethylsulfoxide reductase chain B	31.2% •••• 40.2% ••••
Aq1606	pabC	aminodeoxychorismate lyase	29.0% ••••	Aq235	fccB'	sulfide dehydrogenase, flavoprotein subunit	38.0% ***
Heme	h A	and the second s	F2 10/	Aq919a	fdx1	ferredoxin	37.1% ***
Aq207 Aq1237	cobA cysG	uroporphyrin-III c-methyltransferase siroheme synthase	52.1% ···· 36.9% ····	Aq1171a Aq1192a	fdx2 fdx3	ferredoxin ferredoxin	43.9% • • 35.0% • • •
Aq334	dcuP	uroporphyrinogen decarboxylase	41.4%	Aq108a	fdx4	ferredoxin	56.6% •••
Aq816	gsa	glutamate-1-semialdehyde aminotransferase	56.5% ••••	Aq211	fhp	flavohemoprotein	43.4% ****
Aq1279	hemA	glutamyl tRNA reductase (delta-aminolevulinate synthase)	38.7%	Aq2096	floX petA	flavodoxin Piecke Liron culfur protein	32.5%
Aq2109	hemB	porphobilinogen synthase	64.5%	Aq045 Aq044	petA petB	Rieske-I iron sulfur protein cytochrome b	38.3% •••
Aq263	hemC	porphobilinogen deaminase	53.1%	Aq234	soxF	Rieske-I iron sulfur protein	29.0% ****
Aq1424	hemF	oxygen-independent coproporphyrinogen III		Aq2186	sqr	sulfide-quinone reductase	41.0% ••••
Aq2015	hemG	oxidase protoporphyrinogen oxidase	33.1% ···· 30.3% ···	Glycolysis and	d gluconeogene	sis	
Aq948	hemH	ferrochelatase	46.4% ••••	Aq484 Aq1390	eno fba	enolase fructose-1,6-bisphosphate aldolase class II	65.0% •••• 39.9% ••••
Aq099	hemK	protoporphyrinogen oxidase	32.2% ••••	Aq1065	gap	glyceraldehyde-3-phosphate dehydrogenase	59.5% ****
Aq2124	hemN	oxygen-independent coproporphyrinogen II	50.2% ••••	Aq434	glpK	glycerol kinase	51.0% ****
Molybdopterin Aq2183	moaA2	molybdenum cofactor biosynthesis protein A	47.0%	Aq1744 Aq1634	gpmA gspA	phosphoglycerate mutase glycerol-3-phosphate dehydrogenase (NAD+)	27.9% ···· 40.5% ····
		, seriam concess stosynthesis protein A		- MIOOT	b'r.	gr) or o pricoprime derivatiogenase (1911) T)	10.070 ****

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% ••••
		triose phophate isomerase	32.270 ****	Aq2163	uraP	uracil phosphoribosyltransferase	42.0%
Hydrogenas Aq665	hoxZ	Ni/Fe hydrogenase B-type cytochrome subunit	40.4%	Regulation			
Aq667	hupD	HupD hydrogenase related function	40.9%	Aq1058	acrR1 acrR2	transcriptional regulator (TetR/AcrR family)	34.1% 31.0%
Aq666 Aq1021	hupE hypA	HupE hydrogenase related function hydrogenase accessory protein HypA	39.8% ••••	Aq2179 Aq281	acrR3	transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family)	29.7%
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	34.6% • • • • 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	44.3%
Aq1765	tktA	transketolase	52.4% ••••	Aq764	iclR	transcriptional regulator (IclR family)	30.4%
NADH dehy Aq1385	ydrogenase nuoA1	NADU debuduogeness I shain A	42.0%	Aq638 Aq1038	lysR1 lysR2	transcriptional regulator (LysR family)	32.8% ···· 28.9% ····
Aq1310	nuoA2	NADH dehydrogenase I chain A NADH dehydrogenase I chain A	44.9%	Aq702	merR	transcriptional regulator (LysR family) transcriptional regulator (MerR family)	32.8% ****
Aq1312	nuoB	NADH dehydrogenase I chain B	60.1% •••	Aq218	nifA	transcriptional regulator (NifA family)	42.8%
Aq551 Aq1314	nuoD1 nuoD2	NADH dehydrogenase I chain D NADH dehydrogenase I chain D	37.7% ···· 42.2% ····	Aq1117 Aq1792	ntrC1 ntrC2	transcriptional regulator (NtrC family) transcriptional regulator (NtrC family)	40.2%
Aq574	nuoE	NADH dehydrogenase I chain E	36.8% ••••	Aq230	ntrC3	transcriptional regulator (NtrC family)	40.0% ****
Aq573 Aq437	nuoF nuoG	NADH dehydrogenase I chain F NADH dehydrogenase I chain G	20.5% • • 35.4% • •	Aq164 Aq2069	ntrC4 obg	transcriptional regulator (NtrC family) GTP-binding protein	38.3% •••• 54.9% ••
Aq1315	nuoH1	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	nuoI1	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	29.2% 35.4%	DNA Replica	tion and Repair	:	
Aq1377	nuoJ2	NADH dehydrogenase I chain J NADH dehydrogenase I chain J	30.6%	Aq358 Aq322	dinG dnaA	ATP-dependent helicase (DinG family)	27.9%
Aq1319	nuoK1	NADH dehydrogenase I chain K	51.1%	Aq1472	dnaB	chromosome replication initiator protein DnaA replicative DNA helicase	40.3%
Aq1378 Aq1320	nuoK2 nuoL1	NADH dehydrogenase I chain K NADH dehydrogenase I chain L	48.4%	Aq910	dnaC	DNA replication protein DnaC	26.4%
Aq866	nuoL2	NADH dehydrogenase I chain L	30.2% •••	Aq1008 Aq1493	dnaE dnaG	DNA polymerase III alpha subunit DNA primase	41.9%
Aq1379 Aq1321	nuoL3 nuoM1	NADH dehydrogenase I chain L NADH dehydrogenase I chain M	43.1%	Aq1882	dnaN	DNA polymerase III beta chain	32.1%
Aq1382	nuoM2	NADH dehydrogenase I chain M	36.9% ••••	Aq932 Aq1855	dnaQ dnaX	DNA polymerase III epsilon subunit DNA polymerase III gamma subunit	40.0%
Aq1322 Aq1383	nuoN1 nuoN2	NADH dehydrogenase I chain N NADH dehydrogenase I chain N	34.1%	Aq1422	dpbF	DNA polymerase beta family	39.1% ****
Lipid metabo		1011911 denydrogenase i enam 14	32.070	Aq1693 Aq980	dplF gyrA	N-terminus of phage SPO1 DNA polymerase DNA gyrase A subunit	37.3% •••• 43.6% ••••
Aq2058	aas	2-acylglycerophosphoethanolamine		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	acpP	acyl carrier protein	71.2% ••••	Aq308	mutS1	DNA mismatch repair protein MutS	77.5% ••••
Aq813 Aq2104	acpS acs	holo-[acyl-carrier protein] synthase acetyl-coenzyme A synthetase	30.8% ···· 54.0% ····	Aq1242 Aq1449	mutS2 mutT	DNA mismatch repair protein MutS 8-OXO-dGTPase domain (mutT domain)	37.0% •••• 46.3% ••••
Aq2103	acs'	acetyl-coenzyme A synthetase		Aq282	mutYl	endonuclease III	53.6% ••••
Aq1249	cds	c-terminal fragment phosphatidate cytidylyltransferase	61.2% ···· 29.2% ····	Aq172 Aq496	mutY2 mutY3	endonuclease III endonuclease III	51.8%
Aq1737	cfa	cyclopropane-fatty-acyl-phospholipid synthase	37.5% ••••	Aq1629	nfo	deoxyribonuclease IV	39.0% ••••
Aq892 Aq1717	fabD fabF	malonyl-CoA:Acyl carrier protein transacylase 3-oxoacyl-[acyl-carrier-protein] synthase II	42.1% 58.4%	Aq710 Aq1495	nucI ogt	thermococcal nuclease homolog O-6-methylguanine-DNA-alkyltransferase	36.4% ••••
Aq1716	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	52.9% ••••	Aq1628	pol	DNA polymerase I 3'-5' exo domain	43.2%
Aq1099 Aq1552	fabH fabI	3-oxoacyl-[acyl-carrier-protein] synthase III enoyl-[acyl-carrier-protein] reductase (NADH)	47.0% •••• 49.6% ••••	Aq1967 Aq1610	polA radC	DNA polymerase I (PolI) DNA repair protein RadC	30.5%
Aq056	fabZ	(3R)-hydroxymyristoyl-(acyl carrier protein)		Aq2150	recA	recombination protein RecA	88.5%
Aq999	fadD	dehydratase long-chain-fatty-acid CoA ligase	58.7% ···· 30.0% ···	Aq2053 Aq2155	recG recJ	ATP-dependent DNA helicase RecG single-strand-DNA-specific exonuclease RecJ	38.9%
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% • • · · · · · · · · · · · · · · · · ·	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% ••••
		otides and Nucleosides		Aq064 Aq657	ssb topA	single stranded DNA-binding protein topoisomerase I	39.4% ••• 39.6% ••••
Aq094 Aq1505	nrdA nrdF	ribonucleotide reductase alpha chain ribonucleotide reductase beta chain	35.0% • • • • 36.2% •	Aq1159	topG1	reverse gyrase	41.6% ••••
Purines		Thomas of the chairman	30.270	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%
Aq236 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	n arasa and transca	wintion factors	
Aq078	kad ndk	adenylate kinase	50.0% 48.2%	Aq613	erase and transc deaD	ATP-dependent RNA helicase DeaD	42.3%
Aq1590 Aq1636	prs	nucleoside diphosphate kinase phosphoribosylpyrophosphate synthetase	55.2% ••••	Aq357a	flgM	anti sigma factor FlgM	20.6%
Aq1290	purA	adenylosuccinate synthetase adenylosuccinate lyase	49.2% 52.4%	Aq1218 Aq259	fliA nusA	RNA polymerase sigma factorFliA transcription termination NusA	37.2% · · · · 45.4% · · ·
Aq597 Aq2117	purB purC	phosphoribosylaminoimidazole-		Aq133	nusB	transcription termination NusB	32.3% ••••
		succinocarboxamide synthase	52.5% ••••	Aq1931 Aq873	nusG rho	transcription antitermination protein NusG transcriptional terminator Rho	46.3% •• 59.6% ••••
Aq742 Aq1178	purD purE	phosphoribosylamine-glycine ligase phosphoribosylaminoimidazole carboxylase	54.2% ···· 64.6% ····	Aq070	rpoA	RNA polymerase alpha subunit	40.4% ****
Aq1175	purF	amidophosphoribosyltransferase	42.7% ••••	Aq1939 Aq1945	rpoB rpoC	RNA polymerase beta subunit RNA polymerase beta prime subunit	44.0%
Aq1963	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	48.2%	Aq1490	rpoD	RNA polymerase sigma factor RpoD	41.6%
Aq245	purK	phosphoribosyl aminoimidazole carboxylase	35.6% ••••	Aq599 Aq1452	rpoN rpoS	RNA polymerase sigma factor RpoN RNA polymerase sigma factor RpoS	30.6% ···· 40.5% ····
Aq1836 Aq769	purL purM	phosphoribosylformylglycinamidine synthase II phosphoribosylformylglycinamidine cyclo-ligase	49.3% 50.0%	RNA modifi			10.2 /U ****
Aq857	purN	phosphoribosylglycinamide formyltransferase	48.3% ••••	Aq1816	ksgA	dimethyladenosine transferase	36.1%
Aq1105	purQ	phosphoribosyl formylglycinamidine synthase I formyltetrahydrofolate deformylase	51.1%	Aq1067	miaA	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase	38.2% ****
Aq1818 Pyrimidines	purU	o.mytectanyerototate deformytase	50.5 /0 ****	Aq411	pcnB1	poly A polymerase	28.5% ****
Aq410	carA	carbamoyl phosphate synthetase small subunit	52.2% ••••	Aq2158	pcnB2	poly A polymerase polyribonucleotide nucleotidyltransferase	33.9% •• 45.0% •••
Aq1172	carB	carbamovl-phosphate synthase large subunit	60.7% ••••	Aq221 Aq894	phpA queA	polyribonucleotide nucleotidyltransferase queuosine biosynthesis protein	45.0%
Aq2101 Aq2153	carB cmk	carbamoyl-phosphate synthase, large subunit cytidylate kinase	63.1% 38.5%	Aq946	rnc	RNase III	35.8% ****
Aq1607	dcd	deoxycytidine triphosphate deaminase	39.5% ••••	Aq1955 Aq924	rnhB rnpH	RNase HII RNase PH	48.4% 64.0%
Aq220 Aq409	dut pyrB	deoxyuridine 5'triphosphate nucleotidohydrolase aspartate carbamoyltransferase catalytic chain	42.0%	Aq1661	spoU	rRNA methylase SpoU	44.0%
Aq806	pyrC	dihydroorotase	37.3% •••	Aq1308 Aq841	tgt trm1	queuine tRNA-ribosyltransferase N2,N2-dimethylguanosine tRNA	52.6%

Aq1489	trmD	methyltransferase tRNA guanine-N1 methyltransferase	34.6% • • • • 42.9% • • • •	Aq1671 Aq1450	hslV htrA	heat shock protein HsLV periplasmic serine protease	57.6% ···· 38.3% ····
Aq749	truA	pseudouridine synthase I	33.1% ••••	Aq242	lon	Lon protease	50.6% ****
Aq705 Aq1890	truB tsnR	tRNA pseudouridine 55 synthase rRNA methylase	38.2% ···· 36.4% ····	Aq076 Aq1459	map npr	methionyl aminopeptidase neutral protease	44.1% •••• 27.7% ••
Aq2046	vacB	VacB protein (ribonuclease II family)	37.9% • • • • 28.8% • • • •	Aq2099 Aq1535	pepA	leucine aminopeptidase	39.5%
Aq257 Translation	ygcA	RNA methyltransferase (TrmA-family)	20.070 ****	Aq618	pepQ pfpI	xaa-pro dipeptidase protease I	41.8% ****
Aq2131	fmt	methionyl-tRNA formyltransferase	45.7% ••••	Aq797 Aq552	prc sms	carboxyl-terminal protease ATP-dependent protease sms	41.8%
Aq247 Aq461	gatA gatB	glutamyl-tRNA(Gln) amidotransferase subunit A glutamyl-tRNA(Gln) amidotransferase subunit B	53.6% 48.8%	Aq2204	ymxG	processing protease	28.3%
Aq2147a	gatC	glutamyl-tRNA(Gln) amidotransferase subunit C	41.1% •••• 48.8% ••••	Transport Aq1222	abcT1	ABC transporter	34.7%
Aq346 Aminoacyl tR1	pth VA conthetness	peptidyl-tRNA hydrolase	40.070 ****	Aq620	abcT2	ABC transporter 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 lysyl-tRNA synthetase (genX) homolog	45.0% • • • • 38.6% • • • •	Aq417 Aq413	abcT6 abcT7	ABC transporter ABC transporter	51.8%
Aq763 Aq1221	genX gltX	glutamyl-tRNA synthetase	48.5% ••••	Aq297 Aq2160	abcT8 abcT9	ABC transporter	49.3% ···· 45.3% ····
Aq945 Aq2141	glyQ glyS	glycyl-tRNA synthetase alpha subunit glycyl-tRNA synthetase beta subunit	61.9%	Aq1531	abcT10	ABC transporter ABC transporter	36.4% ****
Aq122	hisS1	histidyl-tRNA synthetase	43.3% ••••	Aq2122 Aq2137	abcT11 abcT12	ABC transporter ABC transporter	42.5%
Aq1155 Aq305	hisS2 ileS	histidyl-tRNA synthetase isoleucyl-tRNA synthetase	34.9% • • • • 82.1% • •	Aq1563	abcT13	ABC transporter (MsbA subfamily)	30.5% ****
Aq351	leuS	leucyl-tRNA synthetase alpha subunit	50.7% • • • • • 47.2% • • • •	Aq695 Aq1122	acrD1 acrD2	cation efflux system (AcrB/AcrD/AcrF family) cation efflux system (AcrB/AcrD/AcrF family)	22.7%
Aq1770 Aq1202	leuS' lysU	leucyl-tRNA synthetase beta subunit lysyl-tRNA synthetase	53.2% •••	Aq469	acrD3	cation efflux system (AcrB/AcrD/AcrF family)	34.2% ···· 27.7% ····
Aq1257 Aq422	metG'	methionyl-tRNA synthetase alpha subunit methionyl-tRNA synthetase beta subunit	45.0%	Aq786 Aq112	acrD4 amtB	cation efflux (AcrB/AcrD/AcrF family) ammonium transporter	49.0% ****
Aq953	pheS	phenylalanyl-tRNÁ synthetase alpha subunit	51.9% ••••	Aq682 Aq343	arsA1 arsA2	anion transporting ATPase	41.5%
Aq1730 Aq365	pheT proS	phenylalanyl-tRNA synthetase beta subunit proline-tRNA synthetase	35.4% 44.1%	Aq851	corA	anion transporting ATPase 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	rplA	ribosomal protein L01	57.9% ••••	Aq1073 Aq911	czcD ebs	cation efflux system (CzcD-like) erythrocyte band 7 homolog	43.4%
Aq013 Aq009	rplB rplC	ribosomal protein L02 ribosomal protein L03	46.9% 53.8%	Aq1062 Aq1255	emrB feoB	major facilitator family transporter ferrous iron transport protein B	28.3%
Aq011	rplD	ribosomal protein L04	51.3%	Aq1330	gltP	proton/sodium-glutamate symport protein	35.6% ****
Aq1652 Aq1649	rplE rplF	ribosomal protein L05 ribosomal protein L06	67.0% 46.2%	Aq1268 Aq1863	hvsT kch	high affinity sulfate transporter potassium channel protein	29.4% •••• 30.1% •••
Aq2042	rplI	ribosomal protein L09	35.6%	Aq1725	lepA	G-protein LepA	59.8% ••••
Aq1936 Aq1933	rplJ rplK	ribosomal protein L10 ribosomal protein L11	36.5% 71.4%	Aq1229 Aq447	mffT mgtC	transporter (major facilitator family) Mg(2+) transport ATPase	37.2%
Aq1937	rplL	ribosomal protein L7/L12	75.4%	Aq1609	modA	molybdate periplasmic binding protein	38.2% ****
Aq1877 Aq1654	rplM rplN	ribosomal protein L13 ribosomal protein L14	60.6% 59.5%	Aq086 Aq415	modC napA1	Molybdenum transport system permease Na(+)/H(+) antiporter	44.8% ···· 27.6% ····
Aq1642 Aq018	rplO rplP	ribosomal protein L15 ribosomal protein L16	57.4% • • • • 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%
Aq1653	rplX	ribosomal protein L24	50.8% ••••	Aq1055	pstB	phosphate transport ATP binding protein	68.1% 45.2%
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	52.4% ••••
Aq792a Aq1485	rpmI rpsA	ribosomal protein L35 ribosomal protein S01	48.3% ···· 32.6% ····	Aq2129 Aq098	sbf secG	Na(+) dependent transporter (Sbf family) protein export membrane protein SecG	34.9% ···· 35.7% ····
Aq2007	rpsB	ribosomal protein S02	60.3% ••••	Aq2077	snf	Na(+):neurotransmitter symporter (Snf family)	25.7% ****
Aq017 Aq072	rpsC rpsD	ribosomal protein S03 ribosomal protein S04	54.0% ···· 51.9% ····	Aq2106 Aq1988	ssf tolQ	Na(+):solute symporter (Ssf family) TolQ homolog	47.4% • 32.5% •
Aq1645	rpsE	ribosomal protein S05	60.6% •••	Aq1504	trkl	K+ transport protein homolog	40.6% ****
Aq063 Aq1832	rpsF rpsG1	ribosomal protein S06 ribosomal protein S07	32.7% ···· 52.5% ····	Aq031	trnS	transporter (Pho87 family)	46.8% ••••
Aq734	rpsG2 rpsH	ribosomal protein S07 ribosomal protein S08	51.9%	Uncategorized Aq1023	acuC1	acetoin utilization protein	36.9% ••••
Aq1651 Aq1878	rpsI	ribosomal protein S09	50.5% •••	Aq2110 Aq158	acuC2 apfA	acetoin utilization protein AP4A hydrolase	38.6%
Aq008 Aq073	rpsJ rpsK	ribosomal protein S10 ribosomal protein S11	55.9%	Aq458	bcp	bacterioferritin comigratory protein	40.6% ****
Aq735	rpsL1	ribosomal protein S12	78.9% ••••	Aq542 Aq147	bcpC cobW	phosphonopyruvate decarboxylase cobalamin synthesis related protein CobW	37.4% ···· 29.5% ···
Aq1834 Aq074	rpsL2 rpsM	ribosomal protein S12 ribosomal protein S13	78.9% •••• 61.9% ••••	Aq1303a Aq1265	cspC cstA	cold shock protein carbon starvation protein A	67.2% ···· 33.0% ····
Aq1651a	rpsN rpsO	ribosomal protein S14 ribosomal protein S15	51.6%	Aq348	ctc	general stress protein Ctc	34.7% ••••
Aq226a 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% 38.2%	Aq1994 Aq1919	era1 era2	GTP-binding protein Era	49.7% ···· 43.0% ····
Translation fac				Aq1540	gcpE	GTP binding protein Era GcpE protein	50.1%
Aq1364 Aq2114	efp eif	elongation factor P initiation factor eIF-2B alpha subunit	48.6% 58.4%	Aq1052 Aq1657	gcsH1 gcsH2	glycine cleavage system protein H	28.6%
Aq2114 Aq712	frr	ribosome recycling factor	43.0% ••••	Aq944	gcsH3	glycine cleavage system protein H glycine cleavage system protein H	36.7% •••
Aq001 Aq075a	fusA infA	elongation factor EF-G initiation factor IF-1	91.9% •••• 69.1% ••••	Aq1108 Aq1458	gcsH4 gcvT	glycine cleavage system protein H aminomethyltransferase	44.8% •••
Aa2032	infB	initiation factor IF-2	48.5% ••••			(glycine cleavage system T protein)	42.2% ••••
Aq1777 Aq876	infC prfA	initiation factor IF-3 peptide chain release factor RF-1	53.6% • • • • 54.8% • • • •	Aq108b Aq101	hfq hly	host factor I hemolysin	53.5% ···· 33.7% ···
Aq1840 Aq1033	prfB selB	peptide chain release factor RF-2	49.9% ••••	Aq2120	hlyC	hemolysin homolog protein hemolysin	29.3% ••••
Aq1033 Aq715	tsf	elongation factor SelB elongation factor EF-Ts	30.4% 35.8%	Aq1091 Aq708	hylA hyuA	N-methylhydantoinase A	33.5%
Aq005 Aq1928	tufA1 tufA2	elongation factor EF-Tu elongation Factor EF-Tu	74.4% • • • • 73.9% • • • •	Aq1925 Aq1579	hyuB iagB	N-methylhydantoinase B invasion protein IagB	43.1%
Protein modifi		ciongation ractor Er-ru	75.570 ****	Aq1983	imp2	myo-inositol-1(or 4)-monophosphatase	36.0% ****
Aq731	ccdA	cytochrome c-type biogenesis protein	32.0% ••••	Aq748 Aq1739	ispA lytB	geranylgeranyl pyrophosphate synthase LytB protein	40.7% ···· 43.9% ····
Aq579 Aq2093	def dsbC	polypeptide deformylase thiol:disulfide interchange protein	41.4% • • • • 27.6% • • • •	Aq1977	masA	enolase-phosphatase E-1	42.3% ****
Aq055	hemX1	cytochrome c biogenesis protein	26.2% ••••	Aq1560 Aq1823	mglA1 mglA2	gliding motility protein gliding motility protein MglA	42.4%
Aq2043 Aq1053	hemX2 nifS1	cytochrome c biogenesis protein FeS cluster formation protein NifS	36.2% ···· 38.5% ····	Aq1789	mviB	'virulence factor' homolog MviB	29.7% ••••
Aq739	nifS2 pmbA	FeS cluster formation protein NifS	45.5% • • • • 25.6% • • • •	Aq587 Aq1820	neaC nfeD	N-ethylammeline chlorohydrolase nodulation competitiveness protein NfeD	42.8%
Aq1871 Aq2102	prmA	peptide maturation ribosomal protein L11 methyltransferase	35.1% ••••	Aq896 Aq1300	nifU omp	NifU protein outer membrane protein	48.3% ···· 25.5% ····
Aq567 Aq576	rimI stpK	ribosomal-protein-alanine acetyltransferase ser/thr protein kinase	37.9% 30.8%	Aq1507	omt	O-methyltransferase	39.5% ****
Aq152	tlpA	thiol disulfide interchange protein	37.6%	Aq967 Aq141	ostA pkcI	organic solvent tolerance protein protein kinase C inhibitor (HIT family)	22.0% ···· 59.0% ····
Proteases			26 506	Aq994	pncA	pyrazinamidase/nicotinamidase	39.1% ****
Aq1950 Aq1672	aprV clpB	serine protease ATPase subunit of ATP-dependent protease	26.5% • • • 46.8% • • • •	Aq057 Aq287	sfsA smb	sugar fermentation stimulation protein small protein B	27.3% ···· 52.0% ····
Aq1296 Aq1339	clpC	ATP-dependent Clp protease	54.9% 65.4%	Aq832	surE thdF	stationary phase survival protein SurE	44.1% 45.4%
Aq1337	clpP clpX	ATP-dependent Clp protease proteolytic subunit ATP-dependent protease ATPase subunit clpX	66.1% ••••	Aq871 Aq2021	tldD	thiophene and furan oxidation protein TldD protein	40.9% ••••
Aq1015 Aq801	col gcp	collagenase sialoglycoprotease	41.3% •••• 45.5% ••••	Aq773 Aq629	tly xcpC	hemolysin chromosome assembly protein homolog	43.8%
-1*	0-1				-r -	protein nomorog	