

Genome sequence of *Haloarcula marismortui*: supplementary material

Evolutionary comparison of *Halobacterium sp.* NRC-1 and *H. marismortui* genomes. Using a mutual best match procedure we identified 1,708 potential orthologous gene pairs between the 4,242 predicted protein sequences (see below for proteome description) from *H. marismortui* and the 2,627 annotated protein sequences from *Halobacterium sp.* NRC-1. The vast majority of these orthologous pairs (viz. 1,475 pairs) are located in the main chromosomes (*H. marismortui* Chromosome I and *Halobacterium sp.* NRC-1 Chromosome). This is significantly greater than the 996 pairs expected assuming a random distribution of unannotated genes among all chromosomes. In contrast, there are very few orthologous pairs distributed among the remaining replicons: no clear one-to-one relationship exists between the minor *H. marismortui* replicons and the two smaller *Halobacterium sp.* NRC-1 replicons. Nevertheless, after suppressing the orthologous pairs observed in comparing the large chromosomes in each of the two halophiles, among all of the other pair-wise comparisons of replicons, some statistically significant excess of orthologous pairs is observed when comparing pNRC200 to Chromosome II, pNG600 and pNG500, as well as in the comparison of pNRC100 to Chromosome II and pNG600.

ADHoRe automatically detects genomic regions with statistically significant conserved gene content and order, paying special attention to micro-rearrangements. Following an all-against-all sequence similarity search, ADHoRe detects diagonal clusters of conserved order and orientation, then deletes statistically insignificant clusters, enriches the remaining clusters with compatible singletons, and finally merges compatible clusters in opposite orientations. The final clusters depict genomic regions of micro-colinearity that evolved from a common ancestor by rearrangement.

GRIMM calculates solutions to the pairwise genome rearrangement problem, i.e. to find an optimal scenario transforming one genome into another via rearrangement events. For circular chromosomes, the most common rearrangement event is the reversal (or inversion). The reversal distance between two genomes is the minimum number of reversals it takes to get from one genome to the other. For a given pair of genomes, the reversal distance is unique, but there are usually many possible reversal scenarios with this distance. However, it is possible that this mathematical notion of reversal distance could underestimate the actual number of steps that occurred biologically.

***H. marismortui* encodes genes that may play a role in DNA transfer between cells.** An interesting finding among the smaller replicons is an operon on pNG500 potentially involved in a DNA transfer system (conjugation). This operon encodes eight proteins including plasmid transfer complex proteins (TrwB2 and TraD), a relaxase (Rlx) for plasmid mobilization, and two CopG family proteins; CopG family proteins are involved in regulation of plasmid copy number. DNA transfer among halophiles has been observed and identification of genes that are responsible for the process may facilitate study of this process in archaea.

Construction of the Function Association Network.

1. Inference of functional associations among proteins using comparative genomics.
 - A. Domain fusion association. Two or more genes that are individually translated in one genome but translated as a single polypeptide in other genomes are predicted to be functionally related and that they may physically interact in the former (Marcotte et al. 1999). Using this strategy a total of 1,267 domain fusion associations were detected among 499 proteins encoded in *H. marismortui* genome.
 - B. Phylogenetic pattern association. This type of association predicts functional coupling of proteins on the basis of similar profiles relating to the presence or absence of pairs of orthologs in fully sequenced genomes (Eisenberg et al. 2000). We identified in *H. marismortui*, upon analyzing 90 fully sequenced genomes, 5,322 putative phylogenetic pattern associations among 671 proteins.
2. Operons. In prokaryotes genes that are functionally associated are often organized in the form of operons of closely linked genes that are co-transcribed from a single promoter. This gene arrangement enables coordinate regulation of the genes in the operon and may also facilitate appropriate stoichiometry of the translated proteins. In fact the first or the last gene in an operon often encodes a transcription regulator of all genes in that operon. These transcriptional regulators are key in deciphering the gene regulatory networks that control the individual physiological processes. We have hypothesized that 952 genes are organized into 616 operons in the *H. marismortui* genome by ascertaining the chromosomal proximity of these genes (Moreno-Hagelsieb and Collado-Vides 2002; Zheng et al. 2002). In at least 33 of

the 616 operons that we identified, the first or the last gene encodes a putative transcriptional regulator.

3. Protein families. A total of 1,448 pairwise similarities were inferred by comparing the entire *H. marismortui* predicted proteome to itself using *BLASTP*. Considering a *BLASTP* score cut-off of $10e^{-40}$, there are 218 protein families in *H. marismortui* ranging from two proteins up to 31 proteins per family.

Oxidative phosphorylation. Four subunits of succinate dehydrogenase, at least 18 genes required for biogenesis of NADH dehydrogenase and twenty-one cytochrome genes are encoded in the genome. These include three genes encoding cytochromes P450 involved in the oxidative degradation of environmental toxins and mutagens and one gene encoding a di-haem cytochrome c peroxidase which reduces hydrogen peroxide to water. At least five cytochrome biogenesis proteins were also identified. Nine genes encoding all of the subunits of an ATP synthase were also detected.

Lipid Metabolism, cell envelope components and transporters. Archaeal lipids and their metabolism differ substantially from their bacterial and eukaryotic counterparts and are thus one of the distinguishing characteristics of all known organisms in the archaeal domain of life (Koga et al. 1998). Archaeal lipids are characterized by ether linkages between isoprenoid alcohol tail and glycerol-1-phosphate, rather than ester linkages between fatty acids and glycerol-3-phosphate (Kates 1993). The synthesis of archaeal membrane lipids must therefore use different chemical pathways than those used by bacterial and eukaryotic organisms. Genes involved in the synthesis of isoprenoid precursors, isopentenyl pyrophosphate and dimethylallyl pyrophosphate, have been identified in the mevalonate pathway. However, one key enzyme in the synthesis of membrane lipids geranylgeranyl pyrophosphate (GGPP) synthase which generates the 20 carbon GGPP via the elongation of farnesyl pyrophosphate by isopentenyl pyrophosphate has not been identified. In addition, the enzymes involved in forming ether linkages between GGPP and glycerol-1-phosphate have also not been identified. This suggests that the enzymes catalyzing these steps in *H. marismortui* have either diverged significantly in their sequence such that they are no longer detectable at the level of sequence similarity. The other possibility is that an entirely different biochemical pathway exists in *H. marismortui* and the associated enzymes are

yet to be characterized. Nevertheless, phospholipid transferases PssA and PgsA are present for the formation of phospholipids. Other genes involved in lipid physiology, including the synthesis of other important apolar lipids such as beta-carotene (retinal precursor), squalene, and bacterioruberins (photoprotectants) have also been identified. Four genes encoding cell surface glycoprotein were identified including one that matched an S-layer protein in *Methanothermobacter thermautotrophicus*. These proteins as in all archaeal halophiles, such as *Halobacterium* sp. NRC-1, may assemble outside the cell membrane as a layer of sulfated-glycoproteins, which is primarily responsible for maintaining cell morphology. Finally, all enzymes of the β -oxidation pathway for the breakdown of fatty acids are present in *H. marismortui*.

Altogether at least 259 proteins with roles in the transport of small molecules including symporters, antiporters, ABC transporters, and permeases are distributed among five of the nine replicons (pNG500: 3, pNG600: 10, pNG700: 42, Chromosome I: 183, Chromosome II: 21). In the pNG600 mini-chromosome we identified ten cation transport proteins of different specificities (copper, zinc, mercury, cadmium), a mercuric reductase, and several metal-ion dependent transcription regulators suggesting that this replicon may be primarily responsible for handling stress offered by high concentrations of heavy metals in the natural environment of *H. marismortui*.

For protein translocation across the membrane eight proteins (SecY, SecF, SecD, Sec11a and b, SecE, Sec61 beta, Srp10 and Srp54) of the sec-dependent and at least three proteins (TatC1, TatC2 and TatD) of the twin-arginine protein translocation (Tat) pathway are encoded in the *H. marismortui* predicted proteome. Other proteins that may participate in protein translocation include four bacterial type II secretion proteins (GspE1-E4) and one type IV secretion protein (VirB11). Of the four *gspE* genes, one (*gspE3*) is encoded in an operon with five genes encoding flagellar proteins suggesting that it may play a role in flagellar biogenesis. The genome also encodes an ortholog (CsaA) of an export-related chaperone that also has tRNA-binding activity (Kawaguchi et al. 2001).

A total of 41 metal ion transporters were identified including active potassium uptake proteins (Trk), potassium channel proteins (Pch), and sodium-dependent symporters and antiporters. We also identified ABC transporters for a variety of solutes including spermidine/putrescine, sugars, peptides, sulfate ions and phosphate ions. All 13 proteins

mediating oligopeptide or dipeptide transport are encoded on Chromosome I.

Arginine fermentation in *Halobacterium* sp. NRC-1 and *H. marismortui*. In *Halobacterium* sp. NRC-1 arginine is fermented by the arginine deiminase (ADI) pathway into ornithine and citrulline (Ruepp et al. 1995). Ornithine accumulates in the cell and is utilized for importing additional arginine via an ornithine/arginine antiporter (Storch et al. 1999) believed to be comprised of at least one protein YhdG (Baliga et al. 2002; Storch et al. 1999). Subsequent breakdown of citrulline yields equimolar amounts of ATP.

While arginase genes have been detected in at least three other fully sequenced archaeal genomes –*Methanopyrus kandleri* AV19, *Pyrococcus abyssi* GE5, and *Pyrococcus furiosus* DSM 3638, thus far only *Sulfolobus tokodaii* and *H. marismortui* contain urease coding genes. However, *S. tokodaii* catabolizes arginine through the arginine deiminase (ADI) pathway which unlike the arginase pathway does not yield urea.

Both *Halobacterium* sp. NRC-1 and *H. marismortui* can also convert arginine to agmatine via the action of ArgDC (Pyruvoyl-dependent arginine decarboxylase). In both organisms the agmatine can be further acted upon by agmatinase (SpeB) to yield putrescine. Agmatine, putrescine and spermidine are polyamines that participate in a number of cellular processes such as chromatin condensation, maintenance of DNA structure, RNA processing, translation and protein activation (Childs et al. 2003).

Organization of arginine metabolism genes in Halobacterium sp. NRC-1. An analysis of gene organization within a single genome and across multiple genomes can provide important insights into gene function and regulation (see above). For example, the physical organization in the *Halobacterium* sp. NRC-1 genome of arginine breakdown and synthesis genes, as described below, correlates with the coordinated regulation of the two pathways with several other aspects of metabolism such as pyrimidine and glutamate metabolism and phototrophy (Baliga et al. 2002). Three genes, *argG*, *argH* and *arcB* play a central role in the synthesis of arginine from ornithine and carbamoyl phosphate. Similarly, three genes *arcA*, *arcB* and *arcC* encode enzymes for fermentation of arginine by the arginine deiminase (ADI) pathway back to ornithine and carbamoyl phosphate. The two arginine synthesis genes *argG* and *argH* in *Halobacterium* sp. NRC-1 are organized as an operon on the large chromosome; in contrast, the third gene *arcB*,

which encodes a function central to both the synthesis and the fermentation (ADI) pathways, is in an operon on the mini-chromosome pNRC200 with the two arginine fermentation genes *arcA* and *arcC*. Furthermore, all arginine fermentation genes including *arcB* are segregated on pNRC200 in a gene cluster along with a putative repressor of arginine fermentation *arcR*, an arginyl-tRNA synthetase gene and two genes of pyrimidine synthesis. Finally, the coordinated regulation of arginine metabolism with isoprenoid biosynthesis and phototrophy in *Halobacterium sp.* NRC-1 (Baliga et al. 2002) is reflected in the operon-like organization of the arginine metabolism gene *argB* with *mvk* which encodes mevalonate kinase –an isoprenoid biosynthesis enzyme. This coordinate regulation may be mediated by a common transcription regulator especially in cases where the genes are co-transcribed in the form of operons (Baliga et al. 2002).

Further Analysis of Unique Rhodopsin Xop2

Yet another potentially interesting feature of this protein is the double change to F and W, respectively, at positions Y83 and F189, two residues highly conserved in all archaeal opsins (Figure E in supplement). Although it is not clear whether or not this has any functional consequences, the side chains of these two residues again contribute, on the extracellular side of the protein, key hydrogen bonds that are thought to be functionally significant in the structural transitions that occur during the late portion of the bacteriorhodopsin photocycle. Indeed, enough uncertainty exists about the function of this protein that biochemical and physiological tests will have to be conducted to clarify its function.

Retinal Biosynthesis

The multiple homologous carotenoid biosynthesis enzymes in *Halobacterium sp.* NRC-1 has been correlated to presence of two parallel biochemical pathways, of which only one pathway is under the regulatory control of Bat –the transcriptional regulator of purple membrane biogenesis (Baliga et al. 2001; Peck et al. 2001). In *Halobacterium sp.* NRC-1 the gene encoding Bat is co-transcribed with *brp* which encodes beta-carotene lyase and located in a gene cluster along with *bop* (bacterioopsin), *crtB1* (phytoene synthase) and *blp* (function unknown). All of the genes in this cluster are under the control of Bat (Baliga et al. 2001). Although the *H. marismortui* genome encodes multiple Bat-like transcription regulators capable of sensing redox-potential and

light, intriguingly, in the *H. marismortui* genome we did not detect a single ortholog of Bat co-localizing with any of the bacterioopsin or carotenoid biosynthesis genes.

Additional Photoreceptors

For example, we find that *rrnAC3205* encodes a PRC-barrel domain containing protein and *rrnAC3204* (*hcp1*, halocyanin precursor-like) co-localized to the same regions of the Chromosome I, which as described for the genes of denitrification and arginine metabolism, often indicates functional coupling and coordinate regulation. Although we cannot determine the precise role of these photosynthesis proteins the presence of the antenna-complex and halocyanin proteins as well as their chromosomal organization clearly points to interesting photobiology.

A comparison of signaling proteins in *H. marismortui* and *Halobacterium sp.* NRC-1

In comparing the sensory proteins in *H. marismortui* with that of *Halobacterium sp.* NRC-1 it is evident that *H. marismortui* has more than twice the expected complement of proteins containing PAS, PAC, and GAF domains. Indeed, the number of such domains is 3-4 folds greater than in *Halobacterium sp.* NRC-1 suggesting that *H. marismortui* may have the ability to discriminate among a larger complement of conditions with respect to quality and quantity of light and redox conditions. The number of chemotaxis-like receptor proteins seems to be roughly similar to those found in *Halobacterium sp.* NRC-1. In concert with the abundance of light and redox sensors, *H. marismortui* has also evolved a comparatively large number of both response regulator proteins and histidine kinases to communicate the sensory information to the gene regulatory components. Therefore, it is not surprising that many of these “extra” response regulatory domains and histidine kinases are associated directly with PAS, PAC, or GAF domains.

Motility. *Halobacterium sp.* NRC-1 can physically relocate, in search of favorable environments, using the environment sensors that can, through common intermediate transducers, communicate changes in light (Luecke et al. 2001; Perazzona et al. 1996; Perazzona and Spudich 1999), oxygen (HtrVIII) (Brooun et al. 1998), and nutrient concentrations (Kokoeva and Oesterhelt 2000; Storch et al. 1999) to the flagellar apparatus. *Halobacterium sp.* NRC-1 can also synthesize buoyant gas-filled vesicles (Halladay et al. 1992) to facilitate its vertical mobility. Given the presence of the large number of sensors, transducers, and response regulators it seems

that *H. marismortui* is equally capable of relocating in response to changes in environmental factors. Like in *Halobacterium sp.* NRC-1, nearly a full complement of chemotaxis genes (minus *cheZ*) has also been identified in *H. marismortui*. In addition, all flagellar genes including two copies of flagellin precursor A (*flaA1* and *A2*) are present in *H. marismortui*. It is interesting to note that, in contrast to their *Halobacterium sp.* counterparts, laboratory cultures of *H. marismortui* used in this study did not exhibit motility suggesting that the expression of the motility genes may be restricted to specific environmental conditions as reported for *Geobacter metallireducens* (Childers et al. 2002). All the chemotaxis and flagellar genes with the exception of *flaA1*, which is located on pNG100, are encoded on Chromosome I. Finally, we did not detect any gas vesicle biogenesis genes in *H. marismortui*.

DNA replication, repair and recombination.

Replication. Subsequent to binding of Mcm and Cdc6 proteins to origin of replication, the DNA helix is unwound, presumably through the helicase activity of Mcm (Chong et al. 2000), and DNA replication initiates. The resulting ssDNA molecules are stabilized during replication by the single strand binding protein Rpa (Kelly et al. 1998). Lastly, the sliding clamp PcnA (proliferating cell nuclear antigen) (De Felice et al. 1999) is recruited by the clamp loader replication factor C protein (RfcC) (Pisani et al. 2000). At least one copy each of the ssDNA stabilizing replication protein A homolog (RpaA) and a related protein (Rpa) are encoded on Chromosome I. One large subunit (RfcB) and two small subunits (RfcC1 and RfcC2) of the replication factor C have also been identified along with a single copy of *pcnA*. The small (Pri1) and large (Pri2) subunits of the DNA primase (Desogus et al. 1999) are encoded on Chromosome I. For DNA polymerization two subunits each for two DNA polymerases PolA (PolA1 and PolA2) and PolB (PolB1 and PolB2) have been identified.

The autonomous replication in *Halobacterium sp.* NRC-1 of the pNRC100 mini-chromosome harboring the replication protein H (*repH*) gene has suggested that this gene is important in the replication and perhaps the maintenance of this mini-replicon (Ng and DasSarma 1993). At least three *repH* orthologs were identified on three of the nine replicons in *H. marismortui*: pNG200 (*repH1*), pNG300 (*repH2*), pNG400 (*repH3*). Interestingly, all replicons in *H. marismortui*, with exception of pNG300, encode either one or more copies of *cdc6* or a single copy of *repH*. pNG300 on the other hand encodes one copy each of *cdc6* and *repH*. These

observations suggest that in halophilic archaea the presence on each replicon of at least one copy of either *cdc6* or *repH* is necessary for DNA replication and/or replicon maintenance.

Repair and recombination. Halophiles thrive in an environment that exposes them to unusually high doses of a variety of DNA damaging agents such as ultraviolet radiation, dessication/rehydration cycles, and chemical mutagens (primarily due to their concentration by evaporation). Consequently, they have evolved robust DNA repair and recombination mechanisms to counter the high incidence of DNA damage (Baliga et al. 2004). The *H. marismortui* genome sequence analysis has identified genes for several DNA repair and recombination pathways such as nucleotide excision repair (NER), photoreactivation, mismatch repair (MMR), and base excision repair.

In addition to the four bacterial NER proteins (UvrA-D) a second UvrB-like protein and a UV DNA damage endonuclease (UvsE) are also present. Photoreactivation of pyrimidine dimers may be catalyzed by two putative photolyases –Phr1 and Phr2. However, in *Halobacterium sp.* NRC-1 only one of these two proteins (Phr2) is functional as a photolyase (Baliga et al. 2004); Phr1, on the other hand, may function as a cryptochrome and mediate cellular responses to blue light as has been reported for some organisms (Hitomi et al. 2000). The *H. marismortui* genome also encodes eukaryotic NER proteins Rad2, Rad3, Rad24, and Rad25.

With respect to MMR, *H. marismortui*, like *Halobacterium sp.* NRC-1, does not encode a d(GATC)-specific methylase or a MutH endonuclease. However, it encodes a d(CTAG) methylase and six RecJ homologs which in *Halobacterium sp.* NRC-1 have been implicated in a novel MMR pathway (Baliga et al. 2004). All other MMR pathway genes such as MutL, MutS, MutT are present. Among the base excision repair proteins uracil DNA glycosylase, DNA-3-methyladenine glycosylase, A/G specific adenine glycosylase (MutY), 8-oxoguanine DNA glycosylase, and an AP-endonuclease/AP-lyase have also been detected. Other putative repair and recombination proteins identified include RadA, RadB, Holliday junction DNA helicase, Holliday junction resolvase, endonuclease III, endonuclease IV, endonuclease V, exonuclease VII and a staphylococcus nuclease homolog.

Transcription.

RNA polymerase. Altogether 13 genes encoding RNA polymerase subunits were detected in *H. marismortui* including two RpoM proteins. These genes are organized as three operons: operon

1: [*rpoH*, *rpoC*, *rpoA*, *rpoB*, *rpoB1*]; operon 2: [*rpoD*, *rpoK*, *rpoN*] and operon 3: [*rpoE*', *rpoE*"]. The other RNA polymerase genes *rpoD* (*rpb3* in NRC-1), *rpoK* and *rpoN* are located in the large ribosomal protein gene cluster. These chromosomal organization features of the RNA polymerase genes are conserved between the two halophiles.

Regulators and other transcription factors. We searched for transcriptional regulators using two primary methods 1) *HMMER* searches for similarities to Pfam families of transcription factors and 2) Rosetta-predicted structural similarities to transcription factors and/or DNA-binding proteins in the PDB. Overall 192 domains matched Pfam families involved in transcriptional regulation, while 61 proteins had Rosetta-predicted three dimensional structures with similarities to characterized transcription factor or DNA-binding folds (Table F in supplement). Many of the three-dimensional folds and Pfam families identified are multifunctional with some representing non-regulatory DNA binding functions and thus this number may be an overestimate of proteins that are true transcriptional regulators in *H. marismortui*.

The majority of the 61 DNA-binding folds identified by Rosetta are helix-turn-helix motifs and slight variants of the basic HTH fold, the most common being CATH fold class 1.10.10.10 (closely followed in abundance by other small helical folds such as 1.10.10.60). [CATH is a database of classification of protein domain structures where each of the four numbers represent in order Class(C), Architecture(A), Topology(T) and Homologous superfamily (H) (Orengo et al. 1997). For example, 1.10.10.10 is a classification for "winged helix" repressor DNA binding domain and 1.10.10.60 is Homeodomain-like DNA-binding protein]. Likewise, the majority of transcriptional regulators predicted by Pfam are also small helical domains, predominantly HTH folds. This abundance of HTH transcriptional regulators is also a ubiquitous feature of the *Halobacterium sp.* NRC-1 proteome with PF04937 being the most common HTH-type transcription factor family in both genomes. It is interesting to note that with the completion of *H. marismortui* genome sequence we have added 30 new members to the PF04937 domain family which prior to this genome contained only 39 members, suggesting that several uncharacterized families of proteins await discovery in archaeal genomes extant and yet to be sequenced.

Since the function of many DNA-binding proteins is to regulate gene expression via protein-DNA interactions the precise biological function of all predicted transcription factors and transcriptional regulators identified in this manner remains unknown until the cognate binding

sites in the genome of the transcriptional factors and regulators is discovered and the correlation between regulator binding and gene expression is understood. Therefore, we await experimental data such as genome-wide transcription factor localization and genome-wide gene expression analysis to provide detailed functional information concerning these putative transcriptional regulators.

RNA processing in archaea. Subsequent to their transcription from DNA both protein-coding mRNAs and non-coding tRNAs and rRNAs undergo maturation through one or more processing steps. RNA processing in archaea occurs through processes catalyzed by proteins analogous to those in eukaryotes. In fact, the extent of rRNA modification in archaea, for example, is on a par with that observed in eukaryotic rRNAs (Omer et al. 2003). We provide below an account of several proteins encoded in the *H. marismortui* genome that are implicated, based on their functional annotations, in processing of rRNAs, tRNAs and mRNAs.

Translation.

Ribosomal proteins. Fifty nine ribosomal protein encoding genes were identified. Except for 14 genes which are distributed as singletons throughout the genome, the remainder 45 genes are arranged in operons with other genes.

tRNAs and translation factors. Altogether forty-eight of the fifty tRNA genes predicted by *tRNA*Scan program were present on Chromosome I. One copy each of tRNA^{Lys} and tRNA^{Glu} were identified on Chromosome II and pNG600, respectively. All eighteen amino acid-tRNA-synthetase genes and the aspartyl and glutamyl amidotransferase are encoded in Chromosome I. Eighteen translation factor-encoding genes were identified; these include eleven translation initiation factor subunits (*eif1A1*, *eif1A2*, *eif2A*, *eif2B2*, *eif2B1*, *eif2BA*, *eif2BD1*, *eif2BD2*, *eif2G*, *eif5A*, and *infB*), three translation elongation factor subunits (*eef1a*, *eef1b*, and *fusA*), one translation initiation inhibition factor (*tii*), and three translation termination factors (*nusA1*, *nusA2*, and *nusG*). With the exception of *tii*, which is encoded on pNG700, all of the other translation factors are encoded on Chromosome I.

Protein folding, unfolding, and degradation. At least seven chaperones were identified, viz. four DnaJ proteins as well as the DnaK and TorD proteins. These chaperone proteins along with four Cdc48 proteins may function in protein folding and unfolding. Protein degradation in *H.*

marismortui may be processed through a proteasome comprised of the four proteasome subunit proteins (PsmA1-4) encoded on Chromosome I. Two subunits of a proteasome activating nucleotidase are also encoded on Chromosome I. Seven heat-shock proteins Hsp5, HspC, Hsp20a and b, HtpX3 and 4, and GrpE, also presumed to be involved in degradation of unfolded proteins were identified.

FIGURES (in supplement)

- A. **The linear maps for the nine replicons in *H. marismortui* (not drawn to scale).** In the linear map forward encoded genes are indicated in red, orange and yellow indicating, in order, proteins with *BLASTP* matches to characterized proteins, uncharacterized proteins and no proteins in public databases. Likewise, reverse coding genes are indicated in navy blue, green and sky blue. The location of the genes in the six reading frames is indicated by their proximity to the navy blue line. Location of *ISH* elements are indicated on the aqua blue line above each line of the map.
- B. **Frequency distribution of distances between consecutive genes in the main chromosomes of *H. marismortui* (N=2788) and *Halobacterium* sp. NRC-1 (N=1794).** Distances between overlapping genes were excluded from this analysis. X axis: intergenic distance in bp; Y axis: fraction of gene pairs separated by such distance.
- C. **Analysis of nucleotide skews on the largest chromosome of (A) *Halobacterium* sp. NRC-1 and (B) *H. marismortui*.** G/C skew (blue, thick lines) and A/T skew (red, thin lines) are plotted along the chromosomes and expressed as Z-scores, i.e. standard deviations from the mean skew observed in shuffled sequences. Some relevant genes relevant to DNA replication are positioned. Large font indicates genes orthologous between the two graphed chromosomes.
- D. ***H. marismortui* function association network.** (A) The complete network of *H. marismortui*. The circular nodes represent protein-coding genes encoded in the *H. marismortui* genome. The lines (edges) connecting the nodes represent among those genes functional associations deciphered through comparative genomics approaches as described in the text. The nodes shaded blue have some associated domain information, while those shaded yellow have weak or no domain information. (B) All genes with no obvious orthologs in public databases linked to at least one gene with some domain

information. (See Table B for list of associations; this visualization is also available as a Cytoscape webstart on <http://halo.systemsbiology.net>).

- E. **Structural re-arrangements of key residues in the extracellular side of bacteriorhodopsin during the transition between the O-intermediate and ground-state.** The structures shown are the halide-free (blue) and bromide-bound (purple) structures of the D85S mutant of bacteriorhodopsin. The halide-free structure of the D85S mutant is analogous to the O-intermediate structure of the wild-type protein (Rouhani et al. 2001). Conversely, the bromide-bound state is analogous to the wild-type ground state in this mutant (Facciotti et al. 2003). The relative amino acid side-chain positions of the corresponding residues are nearly identical in the two states. Note that in Xop2, residues homologous to Y83 and F189 in bacteriorhodopsin have been replaced by F and W, respectively.

TABLES (in supplement)

- A. **List of functional associations among *H. marismortui* proteins** (see text for details).
[Note to reviewers: This table is over 200 pages long and has not been included in this submission; it can be downloaded from the *H. marismortui* genome website
[<http://halo.systemsbiology.net>]
- B. **Function Annotations.**
- C. **Proteins in *H. marismortui* implicated in the denitrification process** (see text for details).
- D. **Proteins in *H. marismortui* implicated in arginine metabolism** (see text for details).
- E. **Sensory and response domains in *H. marismortui* proteins.** Start and end refer to the amino acid residues over which a domain match was identified. Note that some proteins may have multiple unique identifications by different methods for the same domain type.
- F. **Putative transcription regulators in *H. marismortui*.** A. Transcriptional regulators deciphered from Rosetta structure prediction. Predicted transcription factor and DNA binding proteins derived from Rosetta ab initio 3-dimensional structure predictions are shown. For each protein, the Rosetta predicted structure (within the top five ranked predictions) match to a DNA binding fold is shown. Note that each protein may have more than one Rosetta prediction. For each prediction we give the fold class (CATH

code), the Z-score (strength of structure-structure match between predicted structure and the PDB), and the probability that the fold identification is correct (based on Bonneau et al, JMB, 2002). **B.** Transcriptional regulators deciphered from Pfam matches. We present the matches to DNA binding proteins and transcription regulators by the corresponding Pfam families, show the start and stop for each match with respect to the *H. marismortui* query sequence, and the e-value associated with each match.

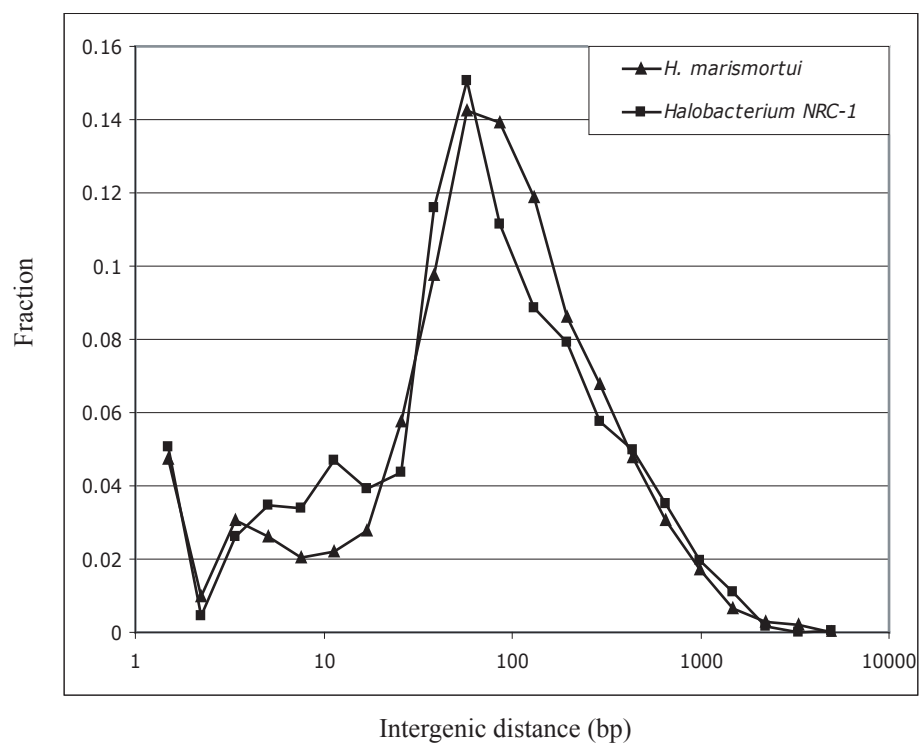
REFERENCES (in supplement)

- Baliga, N.S., S. Bjork, R. Bonneau, M. Pan, C. Iloanusi, M. Kottmann, L. Hood, and J. DiRuggiero. 2004. Systems level insights into the stress response to UV radiation in the halophilic archaeon *Halobacterium* NRC-1. *Genome Res* **in press**.
- Baliga, N.S., S.P. Kennedy, W.V. Ng, L. Hood, and S. DasSarma. 2001. Genomic and genetic dissection of an archaeal regulon. *Proc Natl Acad Sci U S A* **98**: 2521-2525.
- Baliga, N.S., M. Pan, Y.A. Goo, E.C. Yi, D.R. Goodlett, K. Dimitrov, P. Shannon, R. Aebersold, W.V. Ng, and L. Hood. 2002. Coordinate regulation of energy transduction modules in *Halobacterium* sp. analyzed by a global systems approach. *Proc Natl Acad Sci U S A* **99**: 14913-14918.
- Brooun, A., J. Bell, T. Freitas, R.W. Larsen, and M. Alam. 1998. An archaeal aerotaxis transducer combines subunit I core structures of eukaryotic cytochrome c oxidase and eubacterial methyl-accepting chemotaxis proteins. *J Bacteriol* **180**: 1642-1646.
- Childers, S.E., S. Ciufo, and D.R. Lovley. 2002. *Geobacter metallireducens* accesses insoluble Fe(III) oxide by chemotaxis. *Nature* **416**: 767-769.
- Childs, A.C., D.J. Mehta, and E.W. Gerner. 2003. Polyamine-dependent gene expression. *Cell Mol Life Sci* **60**: 1394-1406.
- Chong, J.P., M.K. Hayashi, M.N. Simon, R.M. Xu, and B. Stillman. 2000. A double-hexamer archaeal minichromosome maintenance protein is an ATP-dependent DNA helicase. *Proc Natl Acad Sci U S A* **97**: 1530-1535.
- De Felice, M., C.W. Sensen, R.L. Charlebois, M. Rossi, and F.M. Pisani. 1999. Two DNA polymerase sliding clamps from the thermophilic archaeon *Sulfolobus solfataricus*. *J Mol Biol* **291**: 47-57.
- Desogus, G., S. Onesti, P. Brick, M. Rossi, and F.M. Pisani. 1999. Identification and characterization of a DNA primase from the hyperthermophilic archaeon *Methanococcus jannaschii*. *Nucleic Acids Res* **27**: 4444-4450.
- Eisenberg, D., E.M. Marcotte, I. Xenarios, and T.O. Yeates. 2000. Protein function in the post-genomic era. *Nature* **405**: 823-826.
- Facciotti, M.T., V.S. Cheung, D. Nguyen, S. Rouhani, and R.M. Glaeser. 2003. Crystal structure of the bromide-bound D85S mutant of bacteriorhodopsin: principles of ion pumping. *Biophys J* **85**: 451-458.
- Halladay, J.T., W.L. Ng, and S. DasSarma. 1992. Genetic transformation of a halophilic archaeobacterium with a gas vesicle gene cluster restores its ability to float. *Gene* **119**: 131-136.
- Hitomi, K., K. Okamoto, H. Daiyasu, H. Miyashita, S. Iwai, H. Toh, M. Ishiura, and T. Todo.

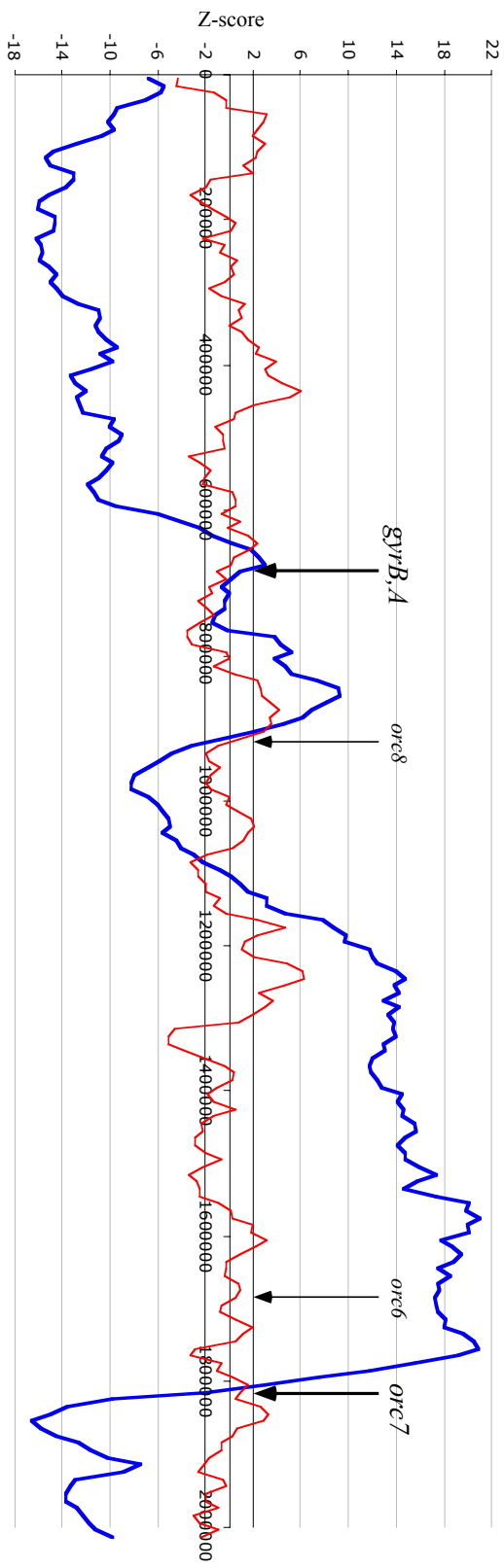
2000. Bacterial cryptochrome and photolyase: characterization of two photolyase-like genes of *Synechocystis* sp. PCC6803. *Nucleic Acids Res* **28**: 2353-2362.
- Kates, M. 1993. Biology of halophilic bacteria, Part II. Membrane lipids of extreme halophiles: biosynthesis, function and evolutionary significance. *Experientia* **49**: 1027-1036.
- Kawaguchi, S., J. Muller, D. Linde, S. Kuramitsu, T. Shibata, Y. Inoue, D.G. Vassilyev, and S. Yokoyama. 2001. The crystal structure of the ttCsaA protein: an export-related chaperone from *Thermus thermophilus*. *Embo J* **20**: 562-569.
- Kelly, T.J., P. Simancek, and G.S. Brush. 1998. Identification and characterization of a single-stranded DNA-binding protein from the archaeon *Methanococcus jannaschii*. *Proc Natl Acad Sci U S A* **95**: 14634-14639.
- Koga, Y., T. Kyuragi, M. Nishihara, and N. Sone. 1998. Did archaeal and bacterial cells arise independently from noncellular Precursors? A hypothesis stating that the advent of membrane phospholipid with enantiomeric glycerophosphate backbones caused the separation of the two lines of descent. *J Mol Evol* **47**: 631.
- Kokoeva, M.V. and D. Oesterheld. 2000. BasT, a membrane-bound transducer protein for amino acid detection in *Halobacterium salinarum*. *Mol Microbiol* **35**: 647-656.
- Luecke, H., B. Schobert, J.K. Lanyi, E.N. Spudich, and J.L. Spudich. 2001. Crystal structure of sensory rhodopsin II at 2.4 angstroms: insights into color tuning and transducer interaction. *Science* **293**: 1499-1503.
- Marcotte, E.M., M. Pellegrini, H.L. Ng, D.W. Rice, T.O. Yeates, and D. Eisenberg. 1999. Detecting protein function and protein-protein interactions from genome sequences. *Science* **285**: 751-753.
- Moreno-Hagelsieb, G. and J. Collado-Vides. 2002. A powerful non-homology method for the prediction of operons in prokaryotes. *Bioinformatics* **18 Suppl 1**: S329-336.
- Ng, W.L. and S. DasSarma. 1993. Minimal replication origin of the 200-kilobase *Halobacterium* plasmid pNRC100. *J Bacteriol* **175**: 4584-4596.
- Omer, A.D., S. Ziesche, W.A. Decatur, M.J. Fournier, and P.P. Dennis. 2003. RNA-modifying machines in archaea. *Mol Microbiol* **48**: 617-629.
- Orengo, C.A., A.D. Michie, S. Jones, D.T. Jones, M.B. Swindells, and J.M. Thornton. 1997. CATH--a hierarchic classification of protein domain structures. *Structure* **5**: 1093-1108.
- Peck, R.F., C. Echavarri-Erasun, E.A. Johnson, W.V. Ng, S.P. Kennedy, L. Hood, S. DasSarma, and M.P. Krebs. 2001. brp and blh Are Required for Synthesis of the Retinal Cofactor of Bacteriorhodopsin in *Halobacterium salinarum*. *J Biol Chem* **276**: 5739-5744.
- Perazzona, B., E.N. Spudich, and J.L. Spudich. 1996. Deletion mapping of the sites on the HtrI transducer for sensory rhodopsin I interaction. *J Bacteriol* **178**: 6475-6478.
- Perazzona, B. and J.L. Spudich. 1999. Identification of methylation sites and effects of phototaxis stimuli on transducer methylation in *Halobacterium salinarum*. *J Bacteriol* **181**: 5676-5683.
- Pisani, F.M., M. De Felice, F. Carpentieri, and M. Rossi. 2000. Biochemical characterization of a clamp-loader complex homologous to eukaryotic replication factor C from the hyperthermophilic archaeon *Sulfolobus solfataricus*. *J Mol Biol* **301**: 61-73.
- Rouhani, S., J.P. Cartailier, M.T. Facciotti, P. Walian, R. Needleman, J.K. Lanyi, R.M. Glaeser, and H. Luecke. 2001. Crystal structure of the D85S mutant of bacteriorhodopsin: model of an O-like photocycle intermediate. *J Mol Biol* **313**: 615-628.
- Ruepp, A., H.N. Muller, F. Lottspeich, and J. Soppa. 1995. Catabolic ornithine transcarbamylase of *Halobacterium halobium* (*salinarum*): purification, characterization, sequence

- determination, and evolution. *J Bacteriol* **177**: 1129-1136.
- Storch, K.F., J. Rudolph, and D. Oesterhelt. 1999. Car: a cytoplasmic sensor responsible for arginine chemotaxis in the archaeon *Halobacterium salinarum*. *Embo J* **18**: 1146-1158.
- Zheng, Y., J.D. Szustakowski, L. Fortnow, R.J. Roberts, and S. Kasif. 2002. Computational identification of operons in microbial genomes. *Genome Res* **12**: 1221-1230.

Figure B



A. *Halobacterium* NRC-1



B. *Halorarcula marismortui*

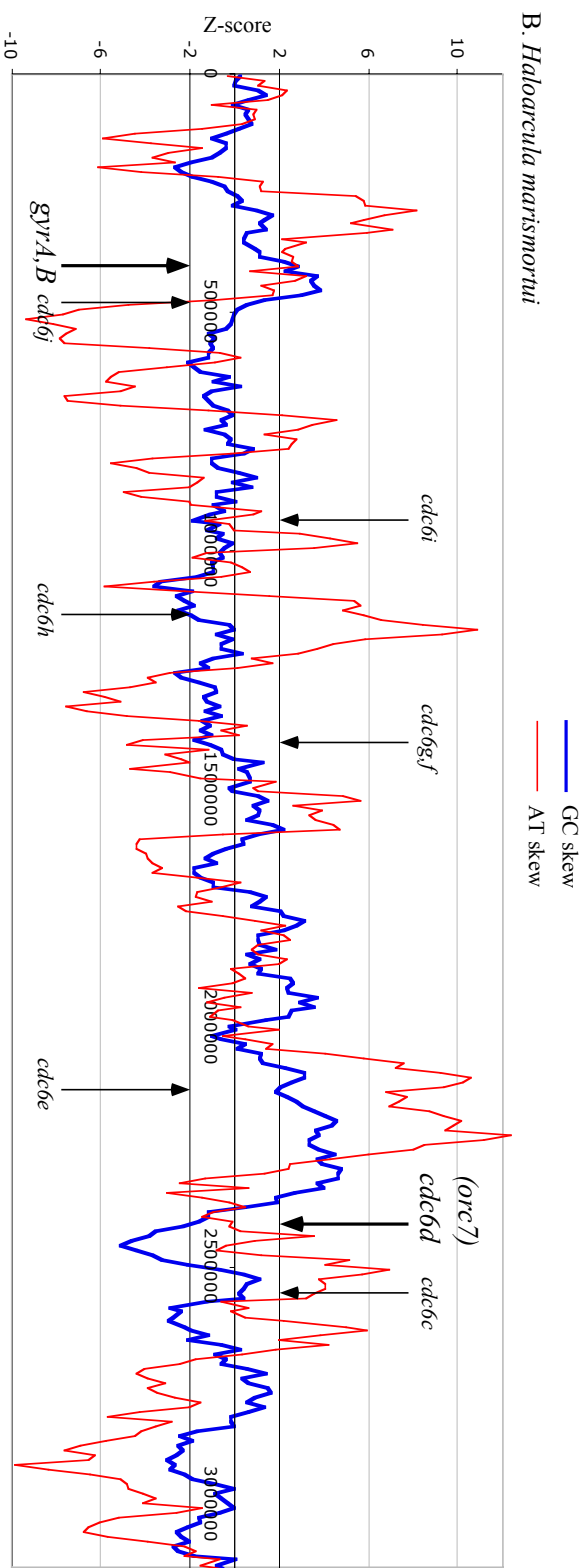
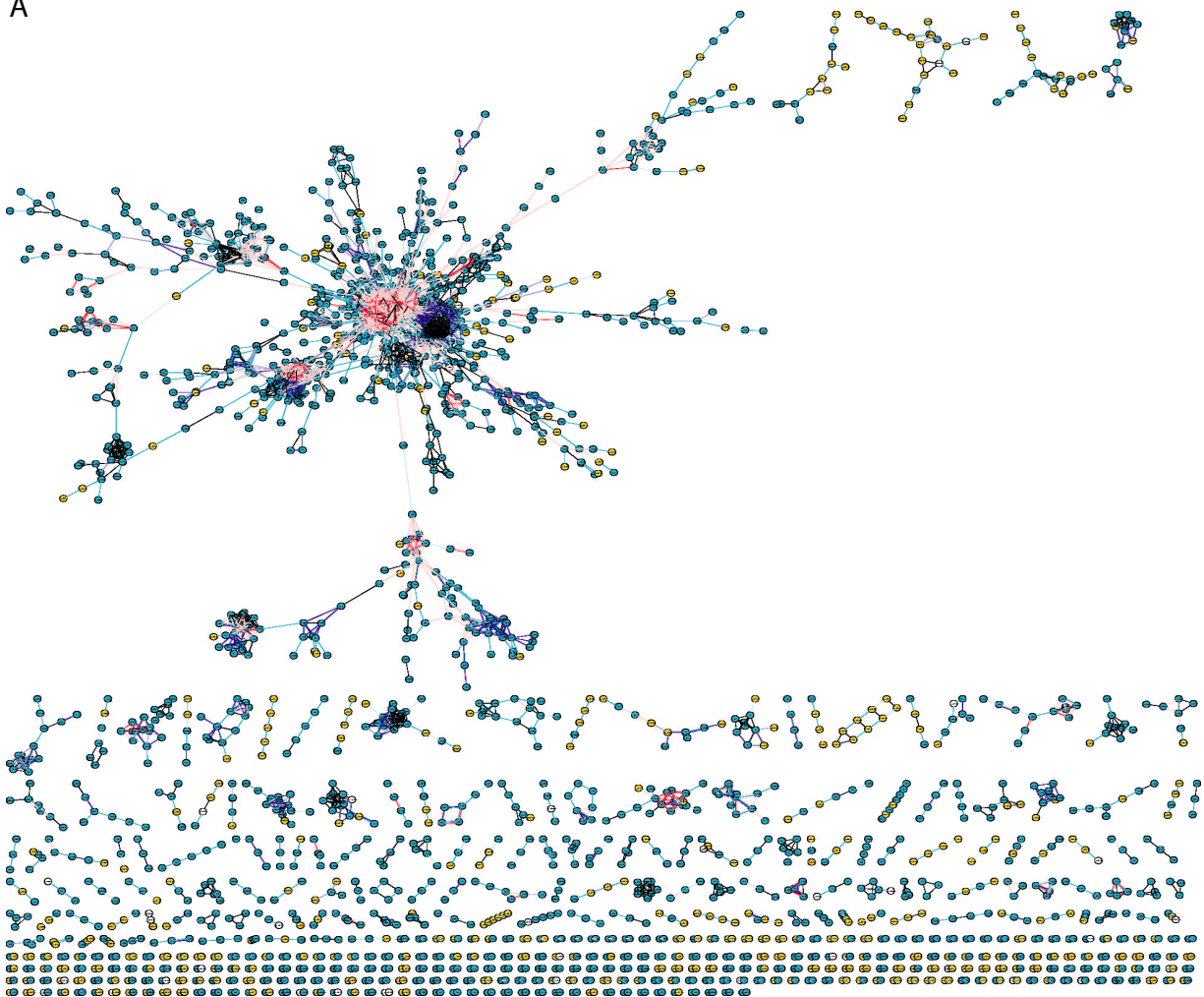


Figure C

Figure D

A



B

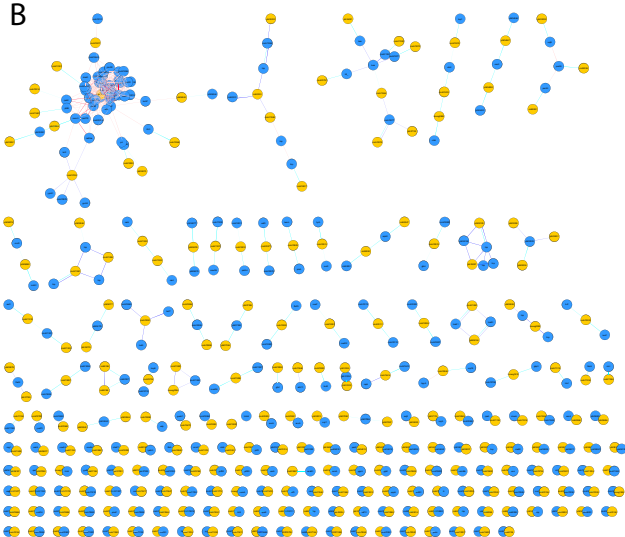


Figure E

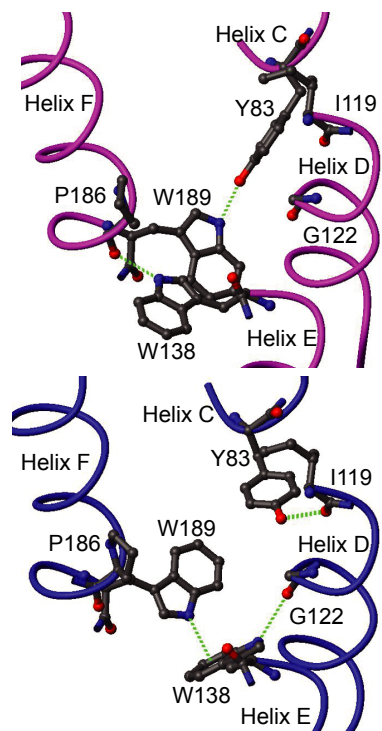


Table B

ORF	Gene name	EC number(s)	Putative function
pNG1015			transcription regulator
pNG1020	tnp		phage integrase
pNG1024	cdc6q		Cell division control protein 6 homolog 6 (CDC6 homolog 6)
pNG1026	flaA2		Flagellin A protein
pNG1040			Putative helicase
pNG2003	boa		Bacterio-opsin activator-like protein
pNG2006	padR		transcription regulator
pNG2014	sojC		Chromosome partitioning protein, membrane-associated ATPase
pNG2016	parB		ParB-like nuclease
pNG2018	rpL36		Similar to H. sapiens and R.norvegicus 60S ribosomal protein L3
pNG2022	repH1		pNRC100 replication protein H homolog
pNG2033			putative membrane-bound metal-dependent hydrolase
pNG2034	yprA1		ATP-dependant helicase
pNG2036	papSR	1.8.99.4	Phosphoadenosine phosphosulfate reductase
pNG2039			Ribbon-helix-helix protein, copG family
pNG2042			transcription regulator
pNG3007			transcription regulator
pNG3010			putative Helix-hairpin-helix motif DNA-binding protein
pNG3013	cdc6p		Cell division control protein 6 homolog
pNG3029	repH2		pNRC100 replication protein H homolog
pNG3034	tnp		Transposase and inactivated derivatives
pNG3037	sojB		Putative plasmid partitioning protein So
pNG3053	mcm3		MCM / cell division control protein 2'
pNG4001	tnp		Putative ISH4 transposase (VNG0918H)
pNG4003	tnp		Putative transposase (VNG6486H) (VNG6040H)
pNG4012	parA1		Chromosome partitioning protein ParA
pNG4017	cpcE1		Phycocyanin alpha phycocyanobilin lyase-like
pNG4019	htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
pNG4020	boa		Bacterio-opsin activator-like protein
pNG4025			transcription regulator
pNG4032	tnp		Putative ISH8 transposase
pNG4036	repH3		pNRC100 replication protein H homolog
pNG4042			DNA binding protein, putative transcriptional regulator
pNG4043			transcription regulator
pNG4049	cas3		CRISPR-associated protein, TM1801 family
pNG4051			putative helicase
pNG4052	cas4		CRISPR-associated protein Cas4
pNG4053	cas1		CRISPR-associated protein Cas1
pNG4054	cas2		CRISPR-associated protein Cas2
pNG5001	abcP-1		ABC transporter, permease protein
pNG5003	yvrO-1		ABC transporter, ATP-binding protein
pNG5007	tnp		Putative transposase
pNG5012	tnp		Probable transposase for insertion sequence element ISH1
pNG5013			Sugar-specific transcriptional regulator
pNG5019	sojE		Similar to BACILLUS SUBTILIS SOJ (SPO0A activation inhibitor)
pNG5022	tnp		Transposase
pNG5027	cdc6o		Cell division control protein 6
pNG5042	tnp		Transposase
pNG5043	tnp		Putative ISH8 transposase
pNG5045	tnp		Putative transposase (VNG6486H) (VNG6040H)
pNG5047	doxD3		terminal quinol oxidase subunit
pNG5052	usp8		Universal stress protein
pNG5054	tnp		Probable transposase for insertion sequence element ISH1
pNG5056	tnp		Putative transposase
pNG5058	tnp		Putative ISH8 transposase (VNG6331H)
pNG5061			putative collagenase
pNG5064	htl		Htr-like protein
pNG5065			Putative lipid/cholesterol transporter
pNG5066		3.2.1.18	putative exo-alpha-sialidase
pNG5067			DNA binding protein tetR family
pNG5071			transcription regulator
pNG5072	tnp		Putative transposase (VNG6486H) (VNG6040H)
pNG5075	tnp		Transposase
pNG5076	tnp		Putative transposase (VNG6486H) (VNG6040H)
pNG5087	trwB2		bacterial conjugation protein
pNG5088			Ribbon-helix-helix protein, copG family
pNG5089			Ribbon-helix-helix protein, copG family
pNG5090	rlx		Relaxase/mobilization nuclease domain
pNG5091	traD		TraD protein
pNG5113	abrB		transcriptional regulator, AbrB family
pNG5119			Putative transcriptional regulator
pNG5121	sojD		Similar to BACILLUS SUBTILIS SOJ (SPO0A activation inhibitor)
pNG5122	cdc6n		Cell division control protein 6
pNG5123	tnp		Transposase
pNG5124	tnp		Probable transposase for insertion sequence element ISH1
pNG5127	tnp		Transposase
pNG5128	tnp		Transposase
pNG5130	tnp		putative transposase
pNG5131			transcription regulator
pNG5132	tnp		Probable transposase for insertion sequence element ISH1
pNG5133			Putative transcriptional regulator
pNG5137	tnp		Transposase
pNG5138	csg1		Cell surface glycoprotein
pNG5139	tnp		putative transposase
pNG5140			Putative transcriptional regulator
pNG5142	tnp		Putative transposase
pNG5143	tnp		Putative ISH8 transposase (VNG6331H)
pNG6011			sigma-70 like region 4 HTH domain
pNG6012	parA2		Partition protein, ParA homolog
pNG6016	xerD		Site-Specific Recombinase, XerD
pNG6019	cadA		Cadmium transporting P-type ATPase
pNG6021			Putative transcriptional regulator
pNG6022	trzA5		N-ethylmaleimide chlorohydrolase
pNG6023			putative metal ion permease
pNG6029	trxA6		Thioredoxin
pNG6030			Putative Copper Binding Protein
pNG6033			ABC transporter, ATP-binding protein
pNG6034			transcription regulator
pNG6036	mitN	2.1.1.41	Sterol 24-C-methyltransferase
pNG6039	usp32		putative Universal stress protein family
pNG6044			
pNG6046	copA3	3.6.3.4	Copper-transporting ATPase
pNG6047			putative metal-binding transcription regulator
pNG6048	merP		Mercuric Transport Protein
pNG6049	acnA	4.2.1.3	Aconitate hydratase I
pNG6055			Putative cation binding protein

pNG6056	copA2		Copper transporting ATPase CopA
pNG6059	copA1		Copper-transporting ATPase copA
pNG6063	hcp4		Halocyanin precursor -like
pNG6067	pan1b		Membrane protein Pan1
pNG6069	dsbB2		Disulfide bond formation protein DsbE
pNG6070	Trx		DSBA-like thioredoxin
pNG6072	tfbG		Transcription initiation factor IIB (TFIIB
pNG6074			transcription regulator
pNG6079	czcD		Cation efflux system protein
pNG6081	zntA1		Zinc-transporting ATPase
pNG6091			transcription regulator
pNG6092			transcription regulator
pNG6094	xseA1	3.1.11.6	Probable exodeoxyribonuclease VII large subunit
pNG6095	exoVIIA	3.1.11.6	Exonuclease VII small subunit
pNG6105	trwB3		Transfer complex protein
pNG6107	traG/traD		bacterial conjugation protein
pNG6123	tfbE		Transcription initiation factor IIB 5 (TFIIB 5
pNG6134			transcription regulator
pNG6135	ctpC		Cation-transporting ATPase
pNG6143	mrr		Mrr restriction system protein homolog
pNG6154	hyrA1		Monoxygenase
pNG6155			Transcriptional regulator
pNG6156	merA	1.16.1.1	Mercuric reductase
pNG6157	copG2		Transcriptional regulator, CopG family
pNG6161	copA5		Copper-transporting ATPase CopA
pNG6165	ltrC		LtrC-like protein
pNG6174	cdc6m		Cell division control protein 6 homolog 6 (CDC6 homolog 6
pNG6176	polB2	2.7.7.7	DNA polymerase B2, exonuclease domain
pNG6184	cdc6l		Cell division control protein 6
pNG6185			putative DEAD/H helicase
pNG7003			Sulfatase
pNG7005			glycosyl transferase
pNG7006			chitin-binding protein
pNG7008	gtr-1	2.4.1.-	Glycosyl transferase
pNG7009	ypjH-1		Glycosyl transferase, group 1
pNG7011	wecB	5.1.3.14	UDP-N-acetylglucosamine 2-epimerase
pNG7012	ugd1		UDP-glucose 6-dehydrogenase
pNG7013	dpm3		Dolichyl-phosphate beta-D-mannosyltransferase
pNG7014	galE3	5.1.3.2	UDP-glucose 4-epimerase
pNG7015	ttuD	1.1.1.81	Putative hydroxypyruvate reductase
pNG7017			4Fe-S protein
pNG7021	kdgR1		Transcriptional regulator
pNG7022	adh1	1.1.1.1;1.6.5.5	Zinc-binding dehydrogenase
pNG7023	rbsB-1		Putative ABC transporter, substrate-binding protein
pNG7024	sugA		Sugar ABC transporter, permease protein (Y4OQ
pNG7025	malFG-1		Sugar ABC transporter, permease protein
pNG7026	msmX-1		Multiple sugar ABC transporter ATP-binding protein
pNG7027	fucA	4.1.2.17	L-fucose phosphate aldolase
pNG7029	rhaB	2.7.1.5	Rhamnulokinase
pNG7030	fabG3	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase
pNG7031	dgoA1		Mandelate racemase / muconate lactonizing enzyme family
pNG7032	adh10	1.1.1.1;1.6.5.5	Zinc-binding dehydrogenase
pNG7033	yvbT	1.14.14.3	Alkanal monooxygenase homolog
pNG7037	ndhF	1.6.99.5	Potential NADH-quinone oxidoreductase subunit 1
pNG7038	trh2		Transcription regulator
pNG7039			putative iron transport protein
pNG7043	csbC		Probable metabolite transport protein CsbC
pNG7044			Fructosamine kinase
pNG7045			putative DNA binding domain
pNG7046			transcription regulator
pNG7050	drdA-1		ABC transporter, ATP-binding protein
pNG7052	rdxA		Nitroreductase family protein
pNG7057	dsbD		Cytochrome C biogenesis protein
pNG7059	prrC		Regulatory protein PrrC
pNG7060	fmdA		Formamidase
pNG7061	cctA1		Thermosome alpha subunit (Thermosome subunit 1) (Chaperonin alpha subunit
pNG7062	usp12		Universal stress protein
pNG7063	cat1		Cationic amino acid transporter
pNG7065	putP-1		Probable sodium:solute symporter
pNG7066	prp2		Phosphate regulatory protein homolog
pNG7067	speB2	3.5.3.11	Agmatinase
pNG7071	fabG		Oxidoreductase
pNG7072	fabG7	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase 1
pNG7073	qgd	1.1.99.17	Quinoprotein Glucose Dehydrogenase
pNG7077	rnH	3.1.26.4	RNaseH
pNG7078	trxB1	1.8.1.9	Thioredoxin reductase
pNG7082		3.1.6.-	Sulfatase
pNG7083	usp23		putative Universal stress protein family
pNG7084	htr8		MCP domain signal transducer (membrane
pNG7085			Heavy-metal-associated protein
pNG7088	qad	1.1.99.-	Quinolomycin Alcohol Dehydrogenase
pNG7096	camH1	3.5.2.10	Creatinine amidohydrolase
pNG7098			putative membrane-bound metal-dependent hydrolase
pNG7099	cpt	2.7.8.-	CDP-alcohol phosphatidyltransferase
pNG7101	adh8	1.1.1.1;1.1.1.2	Alcohol dehydrogenase
pNG7103	adh7	1.1.1.1	putative Zinc-binding dehydrogenase
pNG7105			Glycosyl transferase group 1
pNG7110			putative permease
pNG7116	nthC	4.2.99.18	Endonuclease III
pNG7117	sdt		Sodium-dependent transporter
pNG7118	livF-1		Branched-chain amino acid ABC transporter, ATP-binding protein
pNG7119	livG-1		Branched-chain amino acid ABC transporter, ATP binding protein
pNG7120	livM-1		Branched-chain amino acid transport system / permease component
pNG7121	livH-1		Branched-chain amino acid ABC transporter, permease protein
pNG7122	livJ		Putative ABC transporter substrate-binding protein
pNG7123	ureB	3.5.1.5	Urease beta subunit
pNG7124	ureC	3.5.1.5	Urease alpha subunit
pNG7125	ureA	3.5.1.5	Urease gamma subunit
pNG7126	ureG		Urease accessory protein UreC
pNG7127	ureD		Urease accessory protein UreC
pNG7128	ureE		Urease accessory protein UreE
pNG7129	ureF	3.5.1.5	Urease accessory protein F, UreF
pNG7134	trxA2		Thioredoxin
pNG7136	noxA1		NADH oxidase
pNG7137	ctpA		Cation-transporting ATPase
pNG7139	usp13		Universal stress protein
pNG7142	usp31		Universal stress protein

pNG7145	nosL	NosL protein
pNG7146		transcription regulator
pNG7149	drvA-2	ABC transporter, ATP-binding protein
pNG7150	nosD1	copper-binding protein
pNG7151	fdhA	Formate dehydrogenase alpha subunit
pNG7153	guaB1	1.1.1.205 Inosine-5'-monophosphate dehydrogenase
pNG7155	htlD	Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
pNG7156	oye2	11-domain light and oxygen sensing histidine kinase
pNG7157	gudB	1.4.1.3 NAD(P)-specific glutamate dehydrogenase
pNG7159	boa	Bacterio-opsin activator-like protein
pNG7160		CopG family ribbon-helix-helix transcription regulator
pNG7161	mntH	Putative Mn transporter, NRAMR family
pNG7164	hyuA	3.5.2.9 N-methylhydantoinase I
pNG7165	hyuB	3.5.2.9 N-methylhydantoinase E
pNG7167		Sensor histidine kinase
pNG7169	rhaC4	Na+/H+ antiporter
pNG7171	arcR3	Transcription regulator
pNG7173	tnp	Transposase
pNG7175	sojA	Putative plasmid partitioning protein Soj
pNG7176	tnp	phage integrase
pNG7178	sdt-2	Sodium-dependent transporter
pNG7180		transcription regulator, tetR family
pNG7182		sialidase
pNG7183		transcription regulator, tetR family
pNG7187	cdc6k	Cell division control protein 6 homolog 1 (CDC6 homolog 1)
pNG7188		HTH DNA binding domain protein
pNG7189	ndhG1	NADH dehydrogenase/oxidoreductase
pNG7190		Ferrichrome-Binding protein
pNG7191	gfo2	Putative glucose-fructose oxidoreductase
pNG7192	phnM	Phosphonate metabolism protein
pNG7194		transcription regulator
pNG7196	dpm4	Dolichyl-phosphate beta-D-mannosyltransferase
pNG7198	wlaE	Glycosyl transferase, group 1
pNG7199	lbp1	LPS biosynthesis protein
pNG7200	ypjH-2	Glycosyltransferase
pNG7203		3.1.6.- Sulfatase
pNG7204		putative sulfatase
pNG7205		2.4.1.- Glycosyl transferase
pNG7206		N-acetylgalactosamine-4-sulfatase
pNG7210		putative carbohydrate binding module (family 6) protein
pNG7214	rfbX	Probable export protein
pNG7215	gfo3	glucose fructose oxidoreductase
pNG7218	rffH4	Glucose-1-phosphate thymidyltransferase
pNG7223	boa	Bacterio-opsin activator-like protein
pNG7227	nadE2	6.3.5.1 NH(3)-dependent NAD(+) synthetase
pNG7228	rps17E	Ribosomal protein S17e
pNG7229		Cytosine Deaminase
pNG7231	phnD1	Phosphonates ABC transporter, permease protein
pNG7233	phnC1	Phosphonate transporter, ATP binding protein
pNG7234	phnD2	Phosphate ABC transporter, phosphate-binding protein
pNG7235	ern1	Endoribonuclease L-PSP (ssRNase)
pNG7236	glmU	2.7.7.23 UDP-N-acetylglucosamine pyrophosphorylase
pNG7239	selD	Putative selenophosphate synthase
pNG7242	dsrE/dsrF_2	intracellular sulfur reduction protein
pNG7243	dsrE/dsrF_1	intracellular sulfur reduction protein
pNG7244	xdhD1	1.-.-.- Possible hypoxanthine oxidase XdhC
pNG7245	iorA	Isoquinoline 1-oxidoreductase, alpha subunit
pNG7246	xdhD2	1.-.-.- Possible hypoxanthine oxidase XdhC
pNG7247	cutC	Carbon monoxide dehydrogenase, small subunit
pNG7248	amaB	3.5.1.- N-carbamoyl-L-amino acid amidohydrolase
pNG7249	ureX	3.5.1.5 urease subunit
pNG7250	bmp-1	Basic membrane protein
pNG7251	bmp-2	Basic membrane protein
pNG7252	rbsA	Ribose ABC transporter ATP-binding protein
pNG7253	rbsC-1	Sugar ABC transporter permease protein
pNG7254	rbsC-2	Sugar ABC transporter, permease protein
pNG7255	mer4	F420-dependent N5,N10-methylene-tetrahydromethanopterin reductase
pNG7256	pbuX	Xanthine permease
pNG7257	thrC2	4.2.3.1 Threonine synthase
pNG7258	pyrC	3.5.2.3 Dihydroorotase
pNG7259	trxA1	N-ethylmaleimide chlorohydrolase
pNG7265	fadD2	Putative long-chain-fatty-acid-CoA ligase
pNG7272		Retinal pigment epithelial membrane protein
pNG7273	trxB5	Thioredoxin reductase
pNG7275	thuD1	Ferrichrome ABC transporter permease protein
pNG7276	thuD2	Ferrichrome ABC transporter ATP-binding protein
pNG7278	adh12	1.1.1.1 Alcohol dehydrogenase
pNG7279		Putative pyridine nucleotide-disulphide oxidoreductase
pNG7283	lctP	L-lactate permease
pNG7284	glcD3	Putative oxidoreductase
pNG7288		putative phosphoesterase
pNG7289	adh6	1.1.1.1;1.6.5.5 Zinc-binding dehydrogenase
pNG7291	htpX2	3.4.24.- Probable protease HtpX homolog
pNG7293	yafB	Aldehyde reductase
pNG7295		3-beta hydroxysteroid dehydrogenase/isomerase family
pNG7296	mox	1.14.14.3 Alkanal monooxygenase (luciferase-like)
pNG7297	tehB	Tellurite resistance protein
pNG7301	pphA	3.1.3.16 Serine/threonine protein phosphatase
pNG7302	ppk	2.7.4.1 Polyphosphate kinase
pNG7305	matE1	Multi Antimicrobial Extrusion family drug/sodium antiporter
pNG7307		putative tetR family regulator
pNG7308	tetR	transcription regulator
pNG7310		PRC-barrel domain, possible photosystem reaction centre subunit I
pNG7313		putative protease
pNG7314	adhC	1.1.1.1 Formaldehyde dehydrogenase
pNG7316	cobW/P47K_2	Cobalamin synthesis protein/P47K
pNG7318	fdhG	Formate dehydrogenase alpha subunit
pNG7319	nuoF	Putative NADH dehydrogenase I, F subunit
pNG7321	ern2	Endoribonuclease L-PSP (ssRNase)
pNG7323	pch1	Potassium channel homolog
pNG7324	betL1	Glycine betaine transporter BetL
pNG7325	trpG2	4.1.3.27 Anthranilate synthase component II
pNG7327	trpE3	4.1.3.27 Anthranilate synthase component I
pNG7328	folD2	1.5.1.5;3.5.4.9 Methylene-tetrahydrofolate dehydrogenase
pNG7330	cysE1	2.3.1.30 Serine acetyltransferase
pNG7331	gltP	Proton/sodium-glutamate symport protein
pNG7333	serB2	Phosphoserine phosphatase

pNG7334	tii		Translation initiation inhibitor
pNG7335	fabG5	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase
pNG7336	pcaB		N-acylamino acid racemase
pNG7338	malFG-2		ABC transporter, permease protein
pNG7339	malFG-3		Sugar ABC transport system, permease protein
pNG7340			putative extracellular solute binding protein
pNG7341	camH2	3.5.2.10	Creatinine amidohydrolase
pNG7342	msmK		Multiple sugar ABC transporter ATP-binding protein
pNG7343	arcR2		Transcription regulator
pNG7344	arcR4		Transcription regulator
pNG7346	potD1		Spermidine/putrescine transporter, substrate binding protein
pNG7347	potA1		Putrescine ABC transporter, ATP-binding protein
pNG7349	potB1		Spermidine/putrescine ABC transporter, permease protein
pNG7350	potC1		Spermidine/putrescine ABC transporter, permease protein (PotC)
pNG7351	adh13	1.1.1.1;1.6.5.5	Zinc-binding dehydrogenase
pNG7352	aldA	1.2.1.3	Aldehyde dehydrogenase
pNG7353			sugar transporter
pNG7354	nitB	3.5.5.1	Nitrilase
pNG7357			Putative transcriptional regulator
pNG7359	folA2	1.5.1.3	Dihydrofolate reductase
pNG7361	gcvT5	2.1.2.10	Probable aminomethyltransferase
pNG7363	metF	1.7.99.5	5,10-methylenetetrahydrofolate reductase
pNG7365	htrA2		serine protease
pNG7366	gcvT3	1.5.3.1;2.1.2.1	Sarcosine dehydrogenase/glycine cleavage T-protein
pNG7367	yeaW	1.14.1.-	Putative dioxygenase alpha subunit YeaW
pNG7370	gcvT1	1.5.3.1;2.1.2.1	Sarcosine dehydrogenase/glycine cleavage T-protein
pNG7371	ilvA3	4.2.1.16	Threonine dehydratase
pNG7373	usp25		Universal stress protein
pNG7375	betL2		Glycine betaine transporter
pNG7379	folP2	2.5.1.15	Dihydropterolate synthase
pNG7380	fhs	6.3.4.3	Formyltetrahydrofolate synthetase
pNG7381	ftc	4.3.1.4	Formimidoyltetrahydrofolate cyclodeaminase
pNG7382	folE	3.5.4.16	GTP cyclohydrolase I
pNG7387	ptsC	2.7.1.69	sugar Phosphotransferase system, IIC component
pNG7388	ptsA	2.7.1.69	Sugar Phosphotransferase system, IIA component
pNG7389	hpr		Phosphocarrier protein Hpr
pNG7391	ptsI	2.7.3.9	Phosphoenolpyruvate-protein phosphotransferase
pNG7392	ptsB	2.7.1.69	Phosphotransferase system, IIB component
pNG7395	gtr-6	2.4.1.-	Glycosyltransferase
pNG7397	tnp		Putative transposase (VNG6486H) (VNG6040H)
rmAC0001	birA		Biotin-(acetyl-CoA carboxylase) ligase
rmAC0002	accC2	6.3.4.16	Carbamoyl phosphate synthase L chain
rmAC0004	accA		Acetyl-CoA carboxylase alpha subunit
rmAC0006			Putative DNA binding
rmAC0010	nac		Sodium-and chloride-dependent transporter
rmAC0011	ywfD1	1.1.1.47	Glucose 1-dehydrogenase
rmAC0012	adh11	1.1.1.1;1.6.5.5	Zinc-binding dehydrogenase
rmAC0013	htr		MCP domain signal transducer (membrane)
rmAC0014	sop2		Sensory rhodopsin 1
rmAC0016	tfbA		Transcription initiation factor IIB (TFIIB)
rmAC0018	trmH		RNA methyltransferase, TrmH family, group
rmAC0019	boa		Bacterio-opsin activator-like protein
rmAC0023	gatE	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit E
rmAC0026	hat7		Putative Acetyltransferase (GNAT)
rmAC0028	fumC	4.2.1.2	Fumarate hydratase, class-II
rmAC0029			Sugar ABC transporter, permease protein
rmAC0030	yurM		ABC transporter, permease protein
rmAC0031	ugpC3		Sugar ABC transporter, ATP-binding protein (UGPC)
rmAC0032	rad2		DNA repair protein Rad2
rmAC0038	ocd1	4.3.1.12	Ornithine cyclodeaminase
rmAC0041	srp19		Signal recognition particle 19 kDa protein (Srp19)
rmAC0043	coxB1	1.9.3.1	Cytochrome c oxidase subunit II
rmAC0044	ctaB		Heme synthase
rmAC0045	trp4		ABC transporter, ATP-binding protein homolog
rmAC0048			ABC transporter, ATP-binding protein
rmAC0049			ABC transporter ATP-binding domain
rmAC0051		2.7.8.-	sugar transferase
rmAC0052	dpg	1.3.1.2	Dihydropyrimidine Dehydrogenase
rmAC0053	citG		CitG family protein
rmAC0054			
rmAC0055	rps17E		30S ribosomal protein S17e
rmAC0056	mrp1		Mrp protein homolog
rmAC0058	rps13P		30S ribosomal protein S13P
rmAC0059	rps4P		30S ribosomal protein S4P
rmAC0061	rps11P		30S ribosomal protein S11P
rmAC0062	rpoD		DNA-directed RNA polymerase, subunit C
rmAC0064	rpl18E		50S ribosomal protein L18e
rmAC0065	rpl13P		50S ribosomal protein L13F
rmAC0066	rps9P		30S ribosomal protein S9P
rmAC0067	rpoN	2.7.7.6	DNA-directed RNA polymerase subunit N
rmAC0068	rpoK	2.7.7.6	DNA-directed RNA polymerase subunit K
rmAC0069	eno	4.2.1.11	Enolase
rmAC0070	rps2P		30S ribosomal protein S2P
rmAC0073	cyc	1.14.14.1;1.6.2	Cytochrome P450
rmAC0075	htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0077	mvk	2.7.1.36	Mevalonate kinase
rmAC0078	argB1	2.7.2.8	Acetylglutamate kinase
rmAC0080			predicted hydrolase (COG0595)
rmAC0081	idsA	2.5.1.1;2.5.1.1	Geranylgeranyl diphosphate synthase
rmAC0083	arsA1	3.6.3.16	arsenical pump-driving ATPase
rmAC0085	gltX	6.1.1.18	Glutamyl-tRNA synthetase
rmAC0086	htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0087	hsp5		Heat shock protease protein
rmAC0088	lipC		Lipase/esterase
rmAC0089	ferB		Ferredoxin
rmAC0090	etfB2		Electron transfer flavoprotein beta subunit
rmAC0091	etfA1		Electron transfer flavoprotein alpha-subunit
rmAC0094	ydiS		Flavoprotein, probably electron transporter
rmAC0096	hat-1		Acetyl transferase, GNAT family
rmAC0097	mer3		N5,N10-methylenetetrahydromethanopterin reductase
rmAC0098	alkK1		Medium-chain acyl-CoA ligase
rmAC0102	npd		2-nitropropane dioxygenase-related protein
rmAC0103	rpl7AE		50S ribosomal protein L7Ae
rmAC0104	rpl24E		50S ribosomal protein L24e
rmAC0106	ndk	2.7.4.6	Nucleoside diphosphate kinase
rmAC0107			Glutaredoxin like
rmAC0109	msrB	1.8.4.6	Peptide methionine sulfoxide reductase msrB

rmAC0110 betA		Oxidoreductase, GMC family
rmAC0113 pai1		Sporulation regulator homolog
rmAC0114 guaB5		Inosine-5'-monophosphate dehydrogenase related protein
rmAC0123 udg2	3.2.2.-	uracil DNA glycosylase superfamily protein
rmAC0124 aroC	4.2.3.5	Chorismate synthase
rmAC0127 aroA	2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase
rmAC0128 sdr		short chain dehydrogenase
rmAC0129 zip		Zinc transporter
rmAC0130 htl		Signal-transducing histidine kinase homolog
rmAC0131		RecA/helicase homology
rmAC0132	1.5.1.7;1.5.1.11	lysine-ketoglutarate reductase/saccharopine dehydrogenase
rmAC0134 iivB1	4.1.3.18	Acetolactate synthase large subunit
rmAC0137 cysK2	2.5.1.47	Cysteine synthase
rmAC0138 eif2B1		Probable translation initiation factor 2 beta subunit (eIF-2-beta)
rmAC0141 sdhA2	1.3.99.1	Succinate dehydrogenase flavoprotein subunit
rmAC0143 nhaC2		Na ⁺ /H ⁺ antiporter
rmAC0145 potA3		Spermidine/putrescine ABC transporter, ATP-binding protein
rmAC0146 cysT2		Sulfate transport system permease protein
rmAC0147 tppA		Thiamin-binding periplasmic protein precursor homolog
rmAC0149 pdhA1	1.2.4.1;1.2.4.4	Pyruvate dehydrogenase E1 component, alpha subunit
rmAC0155 epf2b		mRNA 3'-end processing factor homolog
rmAC0161		Putative transcriptional regulator
rmAC0166 proS	6.1.1.15	Proline-tRNA synthetase
rmAC0167		putative Patatin-like phospholipase
rmAC0169 gltB	1.4.1.13	Glutamate synthase large subunit
rmAC0172		transcription regulator
rmAC0173 bglX-1		Beta-glucosidase
rmAC0175 glcA	1.1.1.6;1.1.1.2	Glycerol-1-phosphate dehydrogenase [NAD(P)]
rmAC0178 pop		Prolyl oligopeptidase family protein
rmAC0179 rfbU		LPS biosynthesis
rmAC0180 nhaC5		Na ⁺ /H ⁺ antiporter
rmAC0181 rad25-1		DNA repair helicase
rmAC0182 ubiE2		Ubiquinone/menaquinone biosynthesis methyltransferase Ubi
rmAC0183 htr		Heme-based aerotactic transducer HemAT
rmAC0184 folP	2.5.1.15	Dihydropteroate synthase
rmAC0187		Transporter, putative
		Bifunctional purine biosynthesis protein PurH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase
rmAC0189 purH	3.5.4.10;2.1.2.3; (EC 2.1.2.3) (AICAR transformylase); IMP cyclohydrolase	
rmAC0191 adh3	1.1.1.1;1.6.5.5	Zinc-binding dehydrogenase
rmAC0192 purB	4.3.2.2	Adenylosuccinate lyase
rmAC0194 yfmO2		Multidrug resistance protein homolog
rmAC0196 argE	3.5.1.16	Acetylornithine deacetylase
rmAC0198 odc	4.1.1.17;4.1.1.1	Ornithine Decarboxylase
rmAC0199		Sigma-70, region 4 like DNA binding protein
rmAC0201 aldY2	1.2.1.3	Aldehyde dehydrogenase
rmAC0204 dapD	2.3.1.117	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
rmAC0205 aglA2		Alpha-glucosidase
rmAC0206 dapB	1.3.1.26	Dihydrodipicolinate reductase
rmAC0207 dapA1	4.2.1.52	Dihydrodipicolinate synthase
rmAC0210		putative RNA binding protein
rmAC0215 pimT		L-isoadipyl protein carboxyl methyltransferase
rmAC0218 rpoM		DNA-directed RNA-polymerase subunit M
rmAC0223 camH3	3.5.2.10	Creatinine amidohydrolase
rmAC0224 aglA1	3.2.1.20	Alpha-glucosidase
rmAC0226 iutH2	3.2.2.1	Inosine-uridine preferring nucleoside hydrolase
rmAC0227 ocd3	4.3.1.12	Ornithine cyclodeaminase
rmAC0229 nhaC1		Na ⁺ /H ⁺ antiporter
rmAC0230 arcR		Transcription regulator
rmAC0231		transcription regulator
rmAC0233 ykfB2		Chloromuconate cycloisomerase
rmAC0237 otsA		Trehalose-6-phosphate synthase
rmAC0239 mer2		N5,N10-methylenetetrahydromethanopterin reductase
rmAC0240 qacE		Quaternary ammonium compound-resistance protein
rmAC0241 hadL	3.8.1.2	2-haloalkanoic acid dehalogenase
rmAC0243 trkA7		TRK potassium uptake system protein
rmAC0244 cat		Cationic amino acid transporter
rmAC0245 trkA4		Trk potassium uptake system protein
rmAC0246 folP3	2.5.1.15	Dihydropteroate synthase
rmAC0247		putative light-sensing histidine kinase
rmAC0248		phosphotransferase
rmAC0249 pfk3	2.7.1.11	phosphofructokinase
rmAC0251 yvrO-2		ABC transporter, ATP-binding protein
rmAC0252 abcS-2		ABC transporter, permease protein
rmAC0254 metE	2.1.1.14	5-methyltetrahydropteroyltrimethylglutamate-homocysteine methyltransferase
rmAC0255	2.1.1.14	Methionine synthase, vitamin-B12 independent
rmAC0256 hemK		Protoporphyrinogen oxidase
rmAC0257 ksgA	2.1.1.-	Dimethyladenosine transferase
rmAC0259 rpb4		RNA polymerase Rpb4 (RNAP sub F)
rmAC0260 rpl21E		50S ribosomal protein L21e
rmAC0261 eef1b		Elongation factor 1-beta (EF-1-beta) (aEF-1beta)
rmAC0264 hbd-1	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase
rmAC0265 apl	3.1.21.2; 4.2.9	AP-endonuclease/AP-lyase
rmAC0267 imd1	1.1.1.205	Inosine Monophosphate Dehydrogenase
rmAC0268 yrbE		Oxidoreductase
rmAC0269 gbp1		GTP-binding protein
rmAC0272 hisD	1.1.1.23	Histidinol dehydrogenase
rmAC0273 phoD	3.1.3.1	Alkaline phosphatase D
rmAC0274		putative HesB-like protein
rmAC0275 ddeA		Dodecin
rmAC0278		membrane-bound metal-dependent hydrolase
rmAC0282 cpdB3	3.1.4.16	2',3'-cyclic-nucleotide 2'-phosphodiesterase
rmAC0286		
rmAC0289 eif2BD1		Translation initiation factor eIF-2B subunit delta
rmAC0292 pri1	2.7.7.-	Eukaryotic-type DNA primase small subunit
rmAC0296 htrA1		Serine protease HtrA
rmAC0298 zntA3		Zinc-transporting ATPase
rmAC0301		signal transducing histidine kinase
rmAC0302 iivD	4.2.1.9;4.2.1.1	Dihydroxy-acid dehydratase
rmAC0303 ghmP		GHMP kinases putative ATP-binding protein
rmAC0304 yqjM1		NADH-dependent flavin oxidoreductase
rmAC0307 purD1	6.3.4.13	Phosphoribosylamine-glycine ligase
rmAC0313 rpoM	2.7.7.6	DNA-directed RNA-polymerase subunit M
rmAC0317 htlC		Htr-like protein
rmAC0318		putative carotenoid biosynthesis protein
rmAC0320 ubiA		prenyltransferase
rmAC0321 crtI2	1.3.99.-	Phytoene dehydrogenase
rmAC0322 pepQ	3.4.11.9	Xaa-Pro aminopeptidase

rmAC0326 fofB		Fosfomycin resistance protein FofE
rmAC0329 leuA2	2.3.3.13	2-isopropylmalate synthase 2
rmAC0330 iivB2		Acetolactate synthase, large subunit
rmAC0331 iivN	2.2.1.6	Acetolactate synthase small subunit
rmAC0332 iivC	1.1.1.86	Ketol-acid reductoisomerase
rmAC0334 leuC	4.2.1.33	3-isopropylmalate dehydratase large subunit
rmAC0336 leuD	4.2.1.33	3-isopropylmalate dehydratase small subunit
rmAC0339 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0340 ipmD	1.1.1.85	3- Isopropylmalate Dehydrogenase
rmAC0341 deoR2		Transcriptional regulator, DeoR family
rmAC0342 pfk4	2.7.1.11	1-phosphofructokinase
rmAC0345 fba	4.1.2.13	Fructose-bisphosphate aldolase
rmAC0351 ubiA		putative UbiA prenyltransferase
rmAC0353 dnaJ3		Chaperone protein DnaJ
rmAC0356 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0357 dcuC		C4-dicarboxylate anaerobic carrier
rmAC0358 imp-1		immunogenic protein
rmAC0359	□1.14.13.2	4-hydroxybenzoate 3-monoxygenase
rmAC0361 hlx7		HoxA-like transcriptional regulator
rmAC0362 serA4	1.1.1.95	Phosphoglycerate dehydrogenase
rmAC0365 asd	1.2.1.11	Aspartate-semialdehyde dehydrogenase
rmAC0367 dbp		DNA binding protein eukaryotic-like
rmAC0369 tnp		Transposase
rmAC0370 lbp		leucine-binding protein
rmAC0371 htr		MCP domain signal transducer (membrane)
rmAC0375 ssrA		Integrase/recombinase
rmAC0376		transcription regulator
rmAC0377 yckA-1		Amino acid ABC transporter, permease protein
rmAC0379 glnQ2		Glutamine ABC transporter (ATP-binding protein)
rmAC0380 glnP		Glutamine-binding periplasmic protein of glutamine ABC transporter
rmAC0381 glnH1		Glutamine ABC transporter, permease protein
rmAC0382 gabT		4-aminobutyrate aminotransferase
rmAC0383 arg2	3.5.3.1	Arginase
rmAC0384 gdhA1	1.4.1.3	NADP-specific glutamate dehydrogenase
rmAC0385 arcR1		Transcription regulator
rmAC0389 pcy		copper-binding plastocyanin like protein
rmAC0390 nosZ	1.7.99.6	Nitrous-oxide reductase
rmAC0392 nosD2		copper binding protein
rmAC0394 nosF-1		ABC transporter, ATP-binding protein
rmAC0396 nosY1		ABC-type transport system involved in multi-copper enzyme maturation, permease component
rmAC0402 usp15		universal stress protein
rmAC0404 htr12		MCP domain signal transducer (soluble)
rmAC0407 fbr3		Cytochrome-like protein
rmAC0409 lemA		LemA protein
rmAC0410 ark-4		Sensory transduction histidine kinase
rmAC0411 rre-1		Response regulator receiver
rmAC0412 kinA6		Signal-transducing histidine kinase
rmAC0413 oye		gaf-pac Signal-transducing histidine kinase homolog
rmAC0414		putative RNA methylase
rmAC0415 rhoM		putative intramembrane serine protease
rmAC0416 doxD4		terminal quinol oxidase subunit
rmAC0417		transcription regulator
rmAC0419 gtl		Glycosyl transferase-like
rmAC0420 TrmB2		Sugar-specific transcriptional regulator
rmAC0421 gtr-2		Predicted glycosyltransferase
rmAC0423		Arylsulfatase
rmAC0426		putative sulfatase
rmAC0427		putative polysaccharide biosynthesis protein
rmAC0428 yidJ		Putative sulfatase
rmAC0429 lpg3		LPS glycosyltransferase
rmAC0430 exoM		Succinoglycan biosynthesis protein
rmAC0431 tot		Transmembrane oligosaccharyl transferase
rmAC0434 act		Acyl-CoA thioester hydrolase
rmAC0435		transcription regulator
rmAC0436 traB		putative plasmid transfer protein
rmAC0437		metallopeptidase
rmAC0438 purM	6.3.3.1	Phosphoribosylformylglycinamide cyclo-ligase
rmAC0440		transcription regulator
rmAC0442 psmA3		Proteasome, subunit alpha
rmAC0444 manB2	5.4.2.2;5.4.2.8	Phosphoglucomutase/Phosphomannomutase
rmAC0446 cdd	3.5.4.5	Cytidine deaminase
rmAC0448 udp2	2.4.2.3	Uridine phosphorylase
rmAC0450 yjID1		NADH dehydrogenase
rmAC0452 galE	5.1.3.2	UDP-glucose 4-epimerase
rmAC0453 arg1	3.5.3.1	Arginase
rmAC0455 gyrA	5.99.1.3	DNA gyrase subunit A
rmAC0456 gyrB	5.99.1.3	DNA gyrase subunit B
rmAC0457 top6B	5.99.1.3	Type II DNA topoisomerase VI subunit B
rmAC0459 top6A	5.99.1.3	Type II DNA topoisomerase VI subunit A
rmAC0460 pknA2		Serine/threonine protein kinase related protein
rmAC0463 ligA	6.5.1.1	DNA ligase
rmAC0466 gspE4		Type II secretion system protein
rmAC0470 sir2		Transcriptional regulator, Sir2 family
rmAC0472 sucC	6.2.1.5	Succinyl-CoA synthetase beta chain
rmAC0474 sucD	6.2.1.5	Succinyl-CoA synthetase alpha chain
rmAC0475		signal transducing histidine kinase
rmAC0476		transcription regulator/DNA-binding protein
rmAC0477		membrane associated histidine kinase
rmAC0479 trp5		ABC transporter, ATP-binding protein
rmAC0482 yajO		Putative NAD(P)H-dependent xylose reductase
rmAC0485 yqjF		Hypothetical protein yqjF
rmAC0487 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0488 araL1		Arabinose operon protein araL
rmAC0489 pip	3.2.-.-	putative intracellular protease
rmAC0496 sirR		Transcription repressor
rmAC0500 zurM		ABC transporter, permease protein
rmAC0501 zurA		Zinc uptake system ATP-binding protein Zur
rmAC0502 ycdH		Adhesion protein
rmAC0503		transcription regulator
rmAC0504 copA4		Copper-transporting ATPase CopA
rmAC0506 phr2		cryptochrome/photolyase
rmAC0508 hcp2		Halocyanin precursor-like protein
rmAC0510 hcp9		Halocyanin precursor-like
rmAC0511 hpcEa		2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
rmAC0512 tyrA	1.3.1.12	Prephenate dehydrogenase
rmAC0514 surE	3.1.3.2	Acid phosphatase SurE
rmAC0517 alaS2	6.1.1.7	Alanyl-tRNA synthetase

rmAC0522 bcp-1		Peroxisedoxir
rmAC0524		Putative sec-independent translocation prc
rmAC0525		Glucose-methanol-choline family oxidoreductas
rmAC0526		putative membrane-bound metal-dependent hydrolase
rmAC0528 cheC1		Chemotaxis protein CheC
rmAC0529 hisC2	2.6.1.9	Histidinol-phosphate aminotransferase
rmAC0532 pgsA	2.7.8.5	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
rmAC0534 tnp		Transposase
rmAC0535		HTH DNA-binding protein
rmAC0536 hlx4		HoxA-like transcriptional regulator
rmAC0537 tpiA	5.3.1.1	Triosephosphate isomerase
rmAC0538		
rmAC0540 dinB	2.7.7.7	DNA polymerase IV
rmAC0542	2.1.1.-	methyltransferase
rmAC0543 tyrS		Tyrosyl-tRNA synthetase
rmAC0544 tnp		Transposase
rmAC0545 pfk1	2.7.1.11	phosphofructokinase
rmAC0546 pykA	2.7.1.40	Pyruvate kinase
rmAC0547 glcK	2.7.1.2	Glucokinase
rmAC0548 cdc6j		Cell division control protein 6 homolog 6 (CDC6 homolog 6)
rmAC0550 glpK	2.7.1.30	Glycerol kinase
rmAC0552 htr		MCP domain signal transducer (soluble)
rmAC0554 gpdA	1.1.99.5	Glycerol-3-phosphate dehydrogenase
rmAC0555 gpdB		Glycerol-3-phosphate dehydrogenase chain I
rmAC0556 gpdC		Glycerol-3-phosphate dehydrogenase chain C
rmAC0558		HAMP domain protein (signal transducer)
rmAC0559 xop2		opsin of unknown function
rmAC0561 usp14		universal stress protein
rmAC0562 pepC	4.1.1.31	Phosphoenolpyruvate carboxylase
rmAC0566 livK-1		Branched-chain amino acid ABC transporter, branched chain amino acid-binding protein
rmAC0567 livG-2		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0568 livF-2		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0569 livH-2		Branched-chain amino acid ABC transporter, permease protein
rmAC0570 livM-2		Branched-chain amino acid ABC transporter, permease protein
rmAC0572 catD	3.1.1.24	3-oxoadipate enol-lactone hydrolase
rmAC0573 fadD1		Long-chain fatty-acid-CoA ligase
rmAC0574 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0575 dgoA4		Mandelate racemase/muconate lactonizing enzyme family
rmAC0578		Putative DNA binding
rmAC0581 tnp		phage integrase/site-specific recombinase
rmAC0583		Ribbon-helix-helix protein, copG family
rmAC0584 phrH1		PhiH1 repressor homolog
rmAC0589		putative Phage integrase
rmAC0616 pecE	3.1.1.11	Pectinesterase
rmAC0617 rad25		DNA repair protein Rad25
rmAC0626 msbA-1		ABC transporter, ATP-binding protein
rmAC0628 sun		tRNA and rRNA cytosine-C5-methylase
rmAC0630 sppA	3.4.21.-	Putative signal peptide peptidase SppA
rmAC0633 rffH2	2.7.7.24	Glucose-1-phosphate thymidyltransferase
rmAC0634 nudB		NTP pyrophosphohydrolase
rmAC0635 gloA2		Lactoylglutathione lyase and related lyase
rmAC0637 mcmA1		Methylmalonyl-CoA mutase, subunit alpha
rmAC0638 ppiB2	5.2.1.8	Peptidylprolyl isomerase
rmAC0639		Acetyltransferase (GNAT) family
rmAC0640		transcription regulator
rmAC0641 livF-3		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0642 livG-3		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0645 livM-3		Branched-chain amino acid ABC transporter, permease protein
rmAC0646 livH-3		Branched-chain amino acid ABC transporter, permease protein
rmAC0647 abcS-1		ABC transporter substrate-binding protein
rmAC0648 bdhA		D-beta-hydroxybutyrate dehydrogenase
rmAC0650 acs1	6.2.1.1	Acyl-coenzyme A synthetase
rmAC0651		sugar transporter
rmAC0653 cysH	1.8.99.4;1.8.4.1	Phospho-Adenylyl-Sulfate Reductase
rmAC0656 ferA3		Ferredoxin
rmAC0657	1.14.13.2	P-Hydroxybenzoate Hydroxylase
rmAC0659 ama		N-acyl-L-amino acid amidohydrolase
rmAC0660 rps10p		Ribosomal protein S10p
rmAC0661 apa		Diadenosine tetraphosphate pyrophosphohydrolase
rmAC0665 abcP-2		ABC transporter, permease protein
rmAC0666		ABC transporter, ATP-binding protein
rmAC0669 polX		DNA polymerase IV (Family X)
rmAC0674 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0676 rfi	3.1.21.7	Endonuclease V
rmAC0677 yusZ4		Short-chain dehydrogenase/oxidoreductase
rmAC0678 arsA2		Arsenical pump-driving ATPase
rmAC0680 Rad3a		Helicase
rmAC0681 tbpE		TATA-box binding protein E (TATA-box factor E) (TATA sequence-binding protein E) (TBP E) (Box A binding protein E)
rmAC0684 mamA1	5.4.99.1	Methylaspartate mutase S chain
rmAC0685 mamB		Methylaspartate mutase
rmAC0687 mal	4.3.1.2	Methylaspartate ammonia-lyase
rmAC0690 citE1	4.1.3.6	Citrate lyase beta chain
rmAC0691 aspC4	2.6.1.1	Aspartate aminotransferase
rmAC0693 cinA		Competence/damage-inducible protein CinA
rmAC0695		putative membrane-bound metal-dependent hydrolase
rmAC0698 nusG		Transcription antitermination protein NusG
rmAC0700 secE		Protein translocase SecE
rmAC0701 htr18		MCP domain signal transducer (membrane)
rmAC0702		Leucine/Isoleucine/Valine-Binding Protein
rmAC0703 ftsZ1		Cell division protein FtsZ
rmAC0706 nce1		Na+/Ca2+-exchanging protein
rmAC0707 aroE	1.1.1.25	Shikimate 5-dehydrogenase
rmAC0709 trpE1	4.1.3.27	Anthranyl synthase component I
rmAC0710 trpD2	4.1.3.27	Anthranyl synthase, component II
rmAC0711 ilvE2		Branched-chain amino acid aminotransferase
rmAC0713		Rieske [2Fe-2S] domain containing oxidoreductase
rmAC0716 usp6		Universal stress protein
rmAC0717	1.18.1.3	FAD/NAD binding oxidoreductase
rmAC0718 porA	1.2.7.3;1.2.7.1	Pyruvate ferredoxin oxidoreductase, subunit alpha
rmAC0719 porB	1.2.7.3;1.2.7.1	Pyruvate ferredoxin oxidoreductase, subunit beta
rmAC0720 ubiE3		ubiE/COQ5 methyltransferase family protein
rmAC0721 phr1		Photolyase/cryptochrome
rmAC0722 mop		Molybdenum-pterin binding protein
rmAC0723		putative membrane-bound metal-dependent hydrolase
rmAC0727	EC:2.7.1.23	ATP-NAD kinase
rmAC0731		Cytochrome b(C-terminal)/bC

rmAC0732 petB1		Cytochrome b6
rmAC0733		Rieske [2Fe-2S] domain protein
rmAC0735 hcp8		Halocyanin precursor-like
rmAC0738 usp29		Universal stress protein
rmAC0739 nthA	4.2.99.18	Endonuclease III
rmAC0740 hat1		Acetyltransferase
rmAC0741 hat2		Probable acetyltransferase
rmAC0742 top2		Topoisomerase DNA binding C4 zinc finger
rmAC0743		putative PRC-barrel domain
rmAC0745 yyaI		Acetyltransferase, GNAT family
rmAC0748 guaB3	1.1.1.205	Inosine-5'-monophosphate dehydrogenase
rmAC0751 icfA1		Carbonic anhydrase
rmAC0753 aroK	2.7.1.71	Shikimate kinase
rmAC0754 trkA1		Trk potassium uptake system protein
rmAC0755 trkH3		TRK potassium uptake system protein
rmAC0757 trkH2		Potassium uptake protein TrkI-
rmAC0758 usp17		universal stress protein
rmAC0759 cat		Cationic amino acid transport
rmAC0764 csg3		Cell surface protein
rmAC0766		putative cell surface protein
rmAC0768		DNA binding, putative transcriptional regulat
rmAC0770 acdB	1.3.99.-	Acyl-CoA dehydrogenase
rmAC0771 paaH	1.1.1.35	3-hydroxybutyryl-CoA dehydrogenase
rmAC0772 fbp2	3.1.3.11	Fructose-1,6-bisphosphatase
rmAC0775 gdhA2	1.4.1.3	NAD(P)-specific Glutamate dehydrogenase
rmAC0779 acdE	1.3.99.-	Acyl-CoA dehydrogenase
rmAC0780 acdF	1.3.99.-	Acyl-CoA dehydrogenase
rmAC0781 usp30		universal stress protein
rmAC0784 dox1		terminal quinol oxidase
rmAC0788 psaA		CDP-diacylglycerol-serine O phosphatidyltransferase
rmAC0789		putative PAS/PAC sensing histidine kinase
rmAC0790 est		Carboxylesterase
rmAC0792 cdc48b		Cell division control protein 48
rmAC0794 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0796 hat4		Putative acetyltransferase
rmAC0797 purF	2.4.2.14	Amidophosphoribosyl transferase
rmAC0798 snp		snRNP homolog
rmAC0799 cdlM		Endoglucanase
rmAC0806		putative C2H2 Zinc finger DNA-binding protein
rmAC0807 cdc48c		Cell division control protein 48
rmAC0810 nitA		Nitrilase
rmAC0814 nosY		Membrane protein NosY precursor
rmAC0815 tnp		Probable transposase
rmAC0816 tnp		Transposase
rmAC0819		2-domain regulatory protein
rmAC0821	2.7.1.23	ATP-NAD kinase
rmAC0822 mogA		Molybdenum Cofactor Biosynthesis Protein
rmAC0824 livH-4		Branched-chain amino acid ABC transporter, permease protein
rmAC0825 livM		High-affinity branched-chain amino acid transport (High-affinity branched-chain amino acid transport protein)
rmAC0827 livG-4		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0829 livF-4		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC0831 sodA	1.15.1.1	Superoxide dismutase [Mn] 2
rmAC0832 phrB1	4.1.99.3	Deoxyribodipyrimidine photolyase
rmAC0833 ech2	4.2.1.17	Enoyl-CoA hydratase
rmAC0836 csg2		Surface glycoprotein precursor
rmAC0837 menF	5.4.99.6	Menaquinone-specific isochorismate synthase
rmAC0838 menD		2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase
rmAC0839 dnaJ		Chaperone protein DnaJ
rmAC0841 ech1	4.2.1.17	Enoyl-CoA hydratase
rmAC0842 cinR		Transcription repressor CinF
rmAC0843 menE	6.2.1.26	O-succinylbenzoate-CoA ligase
rmAC0844 ykfB1		Chloromuconate cycloisomerase
rmAC0845 menA		1,4-dihydroxy-2-naphthoate octaprenyltransferase
rmAC0847 alkK3		Medium-chain acyl-CoA ligase
rmAC0848 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC0854 pebP		Phosphatidylethanolamine-binding protein
rmAC0855 galE4	5.1.3.2	UDP-glucose 4-epimerase
rmAC0858	3.1.6.8	Arylsulfatase
rmAC0859 folA1	1.5.1.3	Dihydrofolate reductase
rmAC0861 tfeA		Transcription initiation factor IIE alpha subunit
rmAC0864 nop56/58		Archaeal nucleolar protein homolog
rmAC0865 fib		Fibrillar-like pre-rRNA processing protein
rmAC0866 gcs2	6.3.2.2	gamma-glutamylcysteine synthetase
rmAC0867		transcription regulator
rmAC0868 coaD2	2.7.7.3	Phosphopantetheine adenylyltransferase
rmAC0869		putative Transcription factor TFIIB repeat
rmAC0872		putative DNA binding domain
rmAC0874 acdA	1.3.99.-	Acyl-CoA dehydrogenase
rmAC0875		putative haloacid dehalogenase-like hydrolase
rmAC0878 panB	2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyltransferase
rmAC0879 coxB3		Cytochrome c oxidase subunit I
rmAC0880 coxA4	1.9.3.1	Cytochrome C oxidase subunit I
rmAC0882 coxC		Cytochrome c oxidase subunit II
rmAC0883 bioB	2.8.1.6	Biotin synthase
rmAC0884 gdhA3	1.4.1.2	NAD-specific Glutamate Dehydrogenase
rmAC0885 bioF	2.3.1.47	8-amino-7-oxononanoate synthase
rmAC0887 cbiA1		Cobyrinic acid a,c-diamide synthase
rmAC0888 scs	6.2.1.5	Succinyl-CoA Synthetase
rmAC0890 frt		ferritin
rmAC0894 cpdB2	3.1.4.16	2',3'-cyclic-nucleotide 2'-phosphodiesterase
rmAC0896 acaB3	2.3.1.9	3-ketoacyl-CoA thiolase
rmAC0903 accA		Acetyl-CoA carboxylase alpha subunit
rmAC0904 fabG1	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase
rmAC0906 ibp		Iron-binding protein
rmAC0907 sfuB		Iron ABC transporter, permease protein
rmAC0908 potA4		Spermidine/putrescine ABC transporter, ATP-binding protein
rmAC0912 gtr-3		Glycosyltransferase
rmAC0913		
rmAC0914 TrmB1		Sugar-specific transcriptional regulator TrmB
rmAC0917 sorD	1.1.1.140	sorbitol dehydrogenase
rmAC0918 gfo4		oxidoreductase
rmAC0920 msmX-2		Sugar ABC transporter, ATP-binding protein
rmAC0921 malFG-4		Putative sugar ABC transporter permease protein
rmAC0922 malFG-5		Putative ABC transporter permease protein
rmAC0923 rbsB-2		Sugar ABC transporter, substrate binding protein
rmAC0925 yajO2		Oxidoreductase, aldo/keto reductase family
rmAC0927 pyrE2	2.4.2.10	Orotate phosphoribosyltransferase

rmAC0929 acaB4	2.3.1.16	3-ketoacyl-CoA thiolase
rmAC0933 argK		ArgK protein
rmAC0934 mcmA3		Putative methylmalonyl-CoA mutase
rmAC0935 gtr-8	3.5.1.-	Putative glycosyltransferase
rmAC0937 ybaN		Polysaccharide deacetylase
rmAC0939 dpm6		Dolichyl-phosphate-mannose-protein mannosyltransferase
rmAC0940	2.4.1.-	Glycosyl transferase
rmAC0942 htr		MCP domain signal transducer (membrane
rmAC0944		Putative sugar transport
rmAC0951		glycosyl transferase
rmAC0952 moxR1		Methanol dehydrogenase regulatory protei
rmAC0954 hel		DNA helicase
rmAC0958 icfA2		Carbonic anhydrase
rmAC0959 yprA3		ATP-dependent DNA helicase
rmAC0960 dapA2	4.2.1.52	Dihydrodipicolinate synthase
rmAC0962 pcm3	2.1.1.77	Protein-L-Isoaspartate O-Methyltransferase
rmAC0964 (kinA)		Signal-transducing histidine kinase homolo
rmAC0965 pelA		Cell division protein pelot
rmAC0967 hypE		Hydrogenase expression/formation protei
rmAC0970 aor3		Flavin-containing amine-oxidoreductas
rmAC0971 csg4		Cell surface glycoprotein (S-layer protein) related protei
rmAC0972 tnp		Putative ISH4 transposase (VNG0918H
rmAC0976 htr8		MCP domain signal transducer (membrane
rmAC0979		putative nuclease
rmAC0982 ssuE1	1.5.1.29	NADPH-dependent FMN reductase
rmAC0984 mamA2	5.4.99.1	Methylaspartate mutase S chain
rmAC0986 nce2		Na ⁺ /Ca ²⁺ -exchanging proteir
rmAC0987 mutY	3.2.2.1	A/G-specific adenine glycosylase
rmAC0988 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein
rmAC0990 mgtC1		Magnesium transporter accessory protei
rmAC0991 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein
rmAC0992		DNA binding domain, similar to hmvng186
rmAC0995 mutT6		Mut/nudix family proteir
rmAC0996 folD1	1.5.1.5;3.5.4.9	Methylenetetrahydrofolate dehydrogenas
rmAC0999 glyA	2.1.2.1	Serine hydroxymethyltransferase
rmAC1004 suhB1	3.1.3.25	Inositol-1-monophosphatase
rmAC1010 rfbB1	4.2.1.46	dTDP-glucose 4-6-dehydratase
rmAC1011 rffG	4.2.1.46	dTDP-glucose dehydratase
rmAC1015 gtr-7	2.4.1.-	Glycosyltransferase
rmAC1017 lpg2		LPS glycosyltransferase
rmAC1018	2.4.1.-	glycosyltransferase
rmAC1019 dpm1		Dolichyl-phosphate beta-D-mannosyltransferas
rmAC1020 dpm2		Dolichyl-P-glucose synthetasi
rmAC1022		
rmAC1025 moxR6		Methanol dehydrogenase regulatory protei
rmAC1028 lolC		putative permease
rmAC1029		ABC transporter, ATP-binding proteir
rmAC1030 nps		putative sodium/phosphate symporte
rmAC1039 yafB-2		Oxidoreductase, aldo/keto reductase famil
rmAC1042 msbA-2		ABC transporter, ATP-binding proteir
rmAC1043 lgtD		Glycosyl transferase
rmAC1044	3.5.1.-	putative Acetamidase/Formamidase
rmAC1047		putative membrane-bound metal-dependent hydrolase
rmAC1049		transcription regulato
rmAC1053 odc6i		Cell division control protein 6 homolog 6 (CDC6 homolog 6
rmAC1054 tnp		Putative transposase (VNG6486H) (VNG6040H
rmAC1057 stbB		Plasmid stability protein StbE
rmAC1061 twbB1		Transfer complex proteir
rmAC1067 prk1		Protein kinase
rmAC1068 prkA		Kinase anchor proteir
rmAC1070 spoVR		Stage V sporulation protein R homolog
rmAC1072 cyp2		Cytochrome P450
rmAC1074 fadD3		Long-chain fatty-acid-CoA ligase
rmAC1076 capB		Mur ligase family CapB proteir
rmAC1081 rffH1		Glucose-1-phosphate thymidyltransferas
rmAC1083 hbd1	1.1.1.35;4.2.1.	3-hydroxyacyl-CoA dehydrogenase
rmAC1084 acdG	1.3.99.-	Acyl-CoA dehydrogenase
rmAC1085 tnp		Transposase
rmAC1087 cysE2	2.3.1.30	Serine acetyltransferase
rmAC1088 alkA		DNA-3-methyladenine glycosylas
rmAC1091 sdhC		Succinate dehydrogenase subunit C
rmAC1093 sdhB	1.3.99.1	Succinate dehydrogenase iron-sulfur protein subuni
rmAC1096 kinA4		Signal-transducing histidine kinase homolo
rmAC1097 sdhA1	1.3.99.1	Succinate dehydrogenase flavoprotein subuni
rmAC1102 cbiA2		Cobyrinic acid a, c-diamide synthas
rmAC1107 trkH1		Potassium uptake protein, TrkH famil
rmAC1109 purD2	6.3.4.13	Phosphoribosylamine-glycine ligase
rmAC1111		Highly conserved protein containing a thioredoxin domai
rmAC1113 bglX-2		Beta-D-glucosidase
rmAC1114 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein
rmAC1118 hlx1		HoxA-like transcriptional regulato
rmAC1121 thyX	2.1.1.-	Thymidylate synthase ThyX
rmAC1124 eif2B2		Probable translation initiation factor 2 beta subunit (eIF-2-beta
rmAC1126 tfbH		Transcription initiation factor IIB (TFIIB
rmAC1129 trxB3	1.6.4.5	Thioredoxin reductase
rmAC1131 ribG	1.1.1.-	2,5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductas
rmAC1133 rpaA		Replication Protein A
rmAC1137 yhcR1		Phosphoesterase
rmAC1138 fbp1	3.1.3.11	Fructose-b1,6-isphosphatase
rmAC1139 yprA4		ATP-dependent helicase
rmAC1144 mutS3		DNA mismatch repair proteir
rmAC1145 blp		Bacterio-opsin linked produc
rmAC1149 ctpB		Cation transporting ATPase
rmAC1152 hcp5		Halocyanin precursor-like
rmAC1153 coxB2	1.9.3.1	Cytochrome c oxidase subunit II
rmAC1154 coxA3	1.9.3.1	Cytochrome c oxidase polypeptide I
rmAC1157		putative DNA-binding protein with a phosphopeptide binding mol
rmAC1158		Protein phosphatase 2C like phosphatas
rmAC1159 pknA1	2.7.1.37	Serine/threonine-protein kinase pknA
rmAC1160		von Willebrand factor type A like metal binding protei
rmAC1163 estA		Phospholipase/carboxylesteras
rmAC1166 ogg	3.2.2.-	8-oxoguanine DNA glycosylase
rmAC1167 acyP	3.6.1.7	Acyolphosphatase
rmAC1169 hflX		GTP-binding protein HflX
rmAC1171 katG2	1.11.1.6	Peroxidase/catalase HPI
rmAC1174 psmA4	3.4.25.1	Proteasome alpha subunit
rmAC1175 rpp14		RNaseP_Subunit14

rmAC1177 mp30		ribonuclease P, subunit p3l
rmAC1180 mutT1	3.6.1.-	Mut/nudix family protein
rmAC1182 thiC		Thiamine biosynthesis protein ThiI
rmAC1184 cysT1		Sulfate transport system permease protein
rmAC1186 moaE		Molybdenum cofactor biosynthesis protein
rmAC1187 moaC		Molybdenum cofactor biosynthesis protein C
rmAC1188 moaB1		Molybdenum cofactor biosynthesis protein B
rmAC1191		metal-dependent phosphohydrolase
rmAC1193 boa		Bacterio-opsin activator-like protein
rmAC1195 petA		Putative Rieske iron-sulfur protein
rmAC1196 petB2		Cytochrome B6
rmAC1199 narG	1.7.99.4	Nitrate reductase, alpha chain
rmAC1200 narH	1.7.99.4	Nitrate reductase, beta chain
rmAC1204 narJ		Chaperone protein
rmAC1205		putative ABC-type phosphate transport system, permease component
rmAC1206 prp		protein phosphatase
rmAC1208 mrp2		Mrp protein
rmAC1210 rbnBN1		Ribonuclease BN-like
rmAC1213 moz		Molybdopterin oxidoreductase
rmAC1214 hmoA		Molybdopterin oxidoreductase
rmAC1215 dmsA		Dimethylsulfide reductase
rmAC1217		transcription regulator
rmAC1222 moxR4		Methanol dehydrogenase regulatory protein
rmAC1224 pyrI	2.1.3.2	Aspartate carbamoyltransferase regulatory chain
rmAC1225 pyrB	2.1.3.2	Aspartate carbamoyltransferase
rmAC1227 minD2		Cell division inhibitor MinD homolog
rmAC1230 slyD	5.2.1.8	Peptidyl-prolyl cis-trans isomerase
rmAC1231 ilvA1	4.2.1.16	Threonine dehydratase
rmAC1232 cytH	4.6.1.1	Adenylate cyclase
rmAC1233 metK	2.5.1.6	S-adenosylmethionine synthetase
rmAC1234 thil		Probable thiamine biosynthesis protein ThiH
rmAC1236 cysK1	4.2.99.8	Cysteine synthase
rmAC1238 nikR		Putative nickel responsive regulator
rmAC1241 eif1A2		Translation initiation factor 1A (aIF-1A)
rmAC1250 gspE2		Type II secretion system protein
rmAC1251 aspB1	2.6.1.1	Aspartate aminotransferase
rmAC1252 lrp		Leucine responsive regulatory protein
rmAC1257		Caffeoyl-CoA O-methyltransferase
rmAC1258 cheC2		Chemotaxis protein CheC
rmAC1259 alkK2		Medium-chain-fatty-acid--CoA ligase
rmAC1261 acdD	1.3.99.-	Acyl-coA dehydrogenase
rmAC1262 cdc6h		Cell division control protein 6 homolog 2 (CDC6 homolog 2)
rmAC1267 korA	1.2.7.3;1.2.7.1	2-oxoglutarate ferredoxin oxidoreductase, subunit alpha
rmAC1268 korB	1.2.7.3;1.2.7.1	Putative 2-ketoglutarate ferredoxin oxidoreductase (Beta)
rmAC1269 asnC2		Transcription regulator, AsnC family
rmAC1274 guaB2	1.1.1.205	Inosine Monophosphate Dehydrogenase/GMP reductase
rmAC1275 mcmA2		Methylmalonyl-CoA mutase, subunit alpha
rmAC1278 coxA1	1.9.3.1	Cytochrome c oxidase polypeptide I
rmAC1283 purA	6.3.4.4	Adenylosuccinate synthetase
rmAC1287 htpX5	3.4.24.-	Probable protease HtpX homolog 2
rmAC1289		chelatase
rmAC1292 cysS	6.1.1.16	CysteinyI-tRNA synthetase
rmAC1296 corA		Magnesium Mg(2+)-cobalt Co(2+) transport protein
rmAC1298 moeA2		Molybdopterin biosynthesis protein moeA
rmAC1299 moeA3		Molybdopterin biosynthesis protein moeA
rmAC1300 adh9	1.1.1.1	Alcohol dehydrogenase
rmAC1301 yjID2		NADH dehydrogenase
rmAC1302 thuA		Trehalose utilization-related protein
rmAC1303		transcription regulator
rmAC1307		Putative transcriptional regulator
rmAC1308		Glutaredoxin
rmAC1310 epf2a		mRNA 3'-end processing factor homolog
rmAC1311 recJ1		RecJ Exonuclease
rmAC1312 cysT3		Sulfate transporter family, permease
rmAC1314 moaA		Molybdenum cofactor biosynthesis protein A
rmAC1317 mobA		Molybdopterin-guanine dinucleotide biosynthesis protein
rmAC1318 aor2		Aldehyde ferredoxin oxidoreductase
rmAC1330 torD		Cytoplasmic chaperone TorD
rmAC1331 fixX		Putative ferredoxin protein
rmAC1332 fdhF		Formate dehydrogenase alpha subunit
rmAC1333 fdhH		Formate dehydrogenase-O, iron-sulfur subunit
rmAC1338 arcR-6		Transcription regulator
rmAC1339		Fumarylacetoacetate (FAA) hydrolase family protein
rmAC1346 kinA1		Signal-transducing histidine kinase homolog
rmAC1347		putative Mechanosensitive ion channel
rmAC1349 Rnp		RNAse P Rpr2/Rpp21 subunit
rmAC1350 gtr-4		Putative sugar transferase
rmAC1351		putative sugar transporter
rmAC1352 gtr-5		Glycosyltransferase
rmAC1354 htpX6	3.4.24.-	Probable protease HtpX homolog 2
rmAC1355 gatA1	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit A
rmAC1356 gatC	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit C
rmAC1357 tfbB		Transcription initiation factor IIB (TFIIB)
rmAC1358 mutT5		Mut/nudix family protein
rmAC1359 asnB	6.3.5.4	Asparagine synthetase
rmAC1363 nirJ		Heme biosynthesis protein
rmAC1367 ccdA		Cytochrome c-type biogenesis protein CcdA
rmAC1368 trp-6		ABC transporter, ATP-binding protein
rmAC1369 ccmB		Cytochrome C-type biogenesis protein, heme exporter protein I
rmAC1370 ccmF		Cytochrome c-type biogenesis protein CcmF
rmAC1371 trxA7		Thioredoxin
rmAC1372 ccpA		Cytochrome c551 peroxidase
rmAC1373 ccmC		Heme exporter protein C
rmAC1375 soxA2		Putative sulfite oxidase
rmAC1376 ccmE		Cytochrome c-type biogenesis protein CcmE
rmAC1377 hcp6		Halocyanin precursor like
rmAC1378 pan1a		Membrane protein Pan1
rmAC1384 gluTR	1.2.1.-	Glutamyl-tRNA-Glu reductase
rmAC1390 purL	6.3.5.3	Phosphoribosylformylglycinamide synthase I
rmAC1391		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC1394 hisF	4.1.3.-	Imidazole glycerol phosphate synthase subunit hisF
rmAC1396 rpoL	2.7.7.6	DNA-directed RNA polymerase subunit L
rmAC1397		Putative DNA binding
rmAC1399 cyoC	1.9.3.1	Cytochrome c oxidase polypeptide III
rmAC1402 adh4	1.1.1.1	Alcohol dehydrogenase
rmAC1404 usp28		universal stress protein
rmAC1405		predicted methyltransferase

rmAC1406 dph5	2.1.1.98	Diphthine synthase
rmAC1407 cyo		Cytochrome oxidase subunit I homoloq
rmAC1409 gloA1	4.4.1.5	Lactoylglutathione lyase
rmAC1411 drg		GTP-binding protein Drg
rmAC1414 rpl11P		50S ribosomal protein L11F
rmAC1415 rpl1P		50S ribosomal protein L1F
rmAC1417 rpl10E		50S ribosomal protein L10E
rmAC1418 rpl12P		50S ribosomal protein L12P ('A' type)
rmAC1426 rps15P		30S ribosomal protein S15P
rmAC1427 recJ2		putative Exonuclease RecJ
rmAC1429 rps3AE		30S ribosomal protein S3Ae
rmAC1430 fbr2		Cytochrome-like protein
rmAC1431 purK	4.1.1.21	Phosphoribosylaminoimidazole carboxylase ATP binding subur
rmAC1432 dpm5	2.4.1.-; 2.4.1.1c	Dolichyl-phosphate-mannose-protein mannosyltransferase
rmAC1433 ribE	2.5.1.9	6,7-dimethyl-8-ribityllumazine synthase
rmAC1434 aspC3	2.6.1.1	Aspartate aminotransferase
rmAC1435 atpC2	3.6.3.14	ATP synthase subunit C
rmAC1438 taqD		Glycerol-3-phosphate cytidyltransferase
rmAC1441 recJ3		putative exonuclease, recJ like
rmAC1442 pld		Phospholipase D
rmAC1444 xup		Xanthine/uracil permease family protein
rmAC1446 purE	4.1.1.21	Phosphoribosylaminoimidazole carboxylase, catalytic subun
rmAC1447 nolB	1.6.5.-	NAD(P)H-quinone oxidoreductase chain 3
rmAC1448 nuoB		NADH dehydrogenase I, B subuni
rmAC1449 ndhG5		NADH dehydrogenase/oxidoreductase
rmAC1450 ndhG4		NADH dehydrogenase/oxidoreductase-like protei
rmAC1451 nolD		NADH dehydrogenase/oxidoreductase-like protei
rmAC1452 ndhG6	1.6.5.-	NAD(P)H-quinone oxidoreductase chain 6
rmAC1454 nolC		NADH dehydrogenase/oxidoreductase-like protei
rmAC1455 nuoL2		NADH dehydrogenase I, L subuni
rmAC1456 ndhD		NADH dehydrogenase subunit 4
rmAC1458 ndhG3		NADH dehydrogenase/oxidoreductase
rmAC1459		Metallo-beta-lactamase superfamily protein
rmAC1468 tnp		Phage integrase
rmAC1470 trxB2	1.8.1.9	Thioredoxin Reductase
rmAC1471 doxD5		terminal quinol oxidase subun
rmAC1472 acrR		transcription regulator, acrR family
rmAC1477 fdtT	2.5.1.21	Farnesyl-diphosphate farnesyltransferase
rmAC1478 sacB	2.4.1.10	Levansucrase
rmAC1479 scrB		Sucrose-6-phosphate hydrolase
rmAC1482 fapE2		Flagella-related protein E
rmAC1483 parA4		Chromosome partitioning protein parA
rmAC1484 cheW2		Chemotaxis signal transduction protein CheV
rmAC1485 yjiD4	1.6.99.3	NADH dehydrogenase
rmAC1486 (kinA)		Signal-transducing histidine kinase homolo
rmAC1489 dmd	4.1.1.33	Diphosphomevalonate decarboxylase
rmAC1490 cadT		Cobalamin adenosyltransferase
rmAC1491 msrA2	1.8.4.6	Peptide methionine sulfoxide reductase msrA 1
rmAC1494 htlD		Similar to Escherichia coli protein kinase GP:GI-606149 (Htr-like protei
rmAC1495 oye3		putative light- and oxygen-sensing transcription regulat
rmAC1497 nifS	4.4.1.16	Selenocysteine lyase
rmAC1498 gcvP1	1.4.4.2	Glycine dehydrogenase subunit
rmAC1499 gcvH		Probable glycine cleavage system H protein
rmAC1500 gcvT2	2.1.2.10	Probable aminomethyltransferase
rmAC1501		pas-pac-pac sensing his kinase
rmAC1504 tatD	3.5.1.-; 3.5.2.5	TatD related DNase
rmAC1505 pstB1		Phosphate ABC transporter, ATP-binding protein
rmAC1507 pstA2		Phosphate ABC transporter, permease protein
rmAC1508 pstC1		Phosphate ABC transporter, permease protein
rmAC1509 phoX		Phosphate ABC transporter phosphate-binding protei
rmAC1510 prp3		Phosphate regulatory protein homoloq
rmAC1511 rps8E		30S ribosomal protein S8e
rmAC1515 pyrF	4.1.1.23	Orotidine 5'-phosphate decarboxylase
rmAC1517 trpG1	4.1.3.27	Anthranelate synthase, component II
rmAC1518 trpE2	4.1.3.27	Anthranelate synthase component I
rmAC1519 trpF	5.3.1.24	N-(5'-phosphoribosyl)anthranilate isomerase
rmAC1520 trpD3	2.4.2.18	Anthranelate phosphoribosyltransferase
rmAC1526 yfmJ2	1.6.5.5	Quinone oxidoreductase
rmAC1527 cdc48d		Cell division control protein 4t
rmAC1532 radB		DNA repair and recombination protein RadE
rmAC1533 phoU2		Phosphate transport system regulatory protein Phol
rmAC1536 trkA2		Potassium uptake protein TrkA
rmAC1541		putative DNA binding domain
rmAC1544 spoVT/abrB		transcription regulato
rmAC1546 tnp		Transposase
rmAC1559 tnp		Transposase
rmAC1560 tnp		Putative transposase (VNG6486H) (VNG6040H
rmAC1565 tnp		transposase
rmAC1568 cdc6g		Cell division control protein 6
rmAC1569 cdc6f		Cell division control protein 6 homolog 2 (CDC6 homolog 2
rmAC1570 trp-7		ABC transporter, ATP-binding protein
rmAC1571 wcaH	3.6.1.-	GDP-mannose mannosyl hydrolase
rmAC1572 rfbB2	4.2.1.46	DTDP-glucose-4,6-dehydratase
rmAC1573 galE8		UDP-glucose 4-epimerase
rmAC1577 tnp		Putative transposase
rmAC1580 tnp		Putative transposase (VNG6486H) (VNG6040H
rmAC1583 icsA		LPS glycosyltransferase
rmAC1584 lpb2		LPS biosynthesis protein
rmAC1585 graD4a		Glucose-1-phosphate thymidyltransferase
rmAC1587 glmS1	2.6.1.16	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing
rmAC1589 secY		Protein translocase subunit SecY
rmAC1590 rpl15P		50S ribosomal protein L15F
rmAC1591 rpl30P		50S ribosomal protein L30F
rmAC1592 rps5P		30S ribosomal protein S5P
rmAC1593 rpl18P		50S ribosomal protein L18P (Hsa118)
rmAC1594 rpl19E		50S ribosomal protein L19e
rmAC1595 rpl32E		50S ribosomal protein L32E
rmAC1596 rpl6P		50S ribosomal protein L6F
rmAC1597 rps8P		30S ribosomal protein S8P
rmAC1598 rpl5P		50S ribosomal protein L5P (Hsa15)
rmAC1600 rps4E		30S ribosomal protein S4e
rmAC1601 rpl24P		50S ribosomal protein L24F
rmAC1602 rpl14P		50S ribosomal protein L14F
rmAC1603 rps17P		Ribosomal protein S17f
rmAC1604 rpl29P		50S ribosomal protein L29F
rmAC1605 rps3P		30S ribosomal protein S3P (Hsa4) (HHAS3)
rmAC1606 rpl22P		50S ribosomal protein L22F

rmAC1607 rps19P		30S ribosomal protein S19P
rmAC1608 rpl2P		50S ribosomal protein L2F
rmAC1609 rpl23P		50S ribosomal protein L23F
rmAC1610 rpl4		50S ribosomal protein L4
rmAC1611 rpl3		50S Ribosomal protein L3
rmAC1612		nucleic acid methylase
rmAC1616 mch	3.5.4.27	N(5),N(10)-methyltetrahydromethanopterin cyclohydrolase
rmAC1619 gbp2		GTP-binding protein homolog
rmAC1620		haloacid dehalogenase-like hydrolase
rmAC1622 nrdA	1.17.4.1	Ribonucleoside-diphosphate reductase alpha chain
rmAC1624 soxA3		Probable sulfite oxidase
rmAC1626 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC1630 hlx6		HoxA-like transcriptional regulator
rmAC1639 smc2		Chromosome segregation protein
rmAC1642 gatB	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit B
rmAC1645 topA	5.99.1.2	DNA topoisomerase I
rmAC1650 pcrB		PcrB protein
rmAC1651 yhdG		Amino acid transporter
rmAC1652 trkA5		Trk potassium uptake system protein
rmAC1653 asnC3		Transcription regulator, Asn family
rmAC1655 nosF-2		ABC transporter, ATP-binding protein
rmAC1656		Nitrite/nitrate reduction protein
rmAC1657 aspS	6.1.1.12	Aspartyl-tRNA synthetase
rmAC1659 hop		Halorhodopsin precursor (HR)
rmAC1660 yafB-3		Oxidoreductase, aldo/keto reductase family
rmAC1663 boa		Bacterio-opsin activator-like protein
rmAC1668 rpoP	2.7.7.6	DNA-directed RNA polymerase subunit P
rmAC1669 rpl37AE		50S ribosomal protein L37ae
rmAC1676 tnp		Transposase and inactivated derivatives
rmAC1680 pfdB		Prefoldin beta subunit (GimC beta subunit)
rmAC1687 boa		Bacterio-opsin activator-like protein
rmAC1690 leuA1	2.3.3.13	2-isopropylmalate synthase 2
rmAC1693		membrane bound histidine kinase
rmAC1694 guaA2	6.3.5.2	GMP synthase [glutamine-hydrolyzing]
rmAC1698 moxR2		Methanol dehydrogenase regulatory protein
rmAC1700	3.1.6.-	sulfatase
rmAC1701 hat6		Putative Acetyltransferase (GNAT)
rmAC1703		Hsp20
rmAC1705 moeA1		Molybdenum cofactor biosynthesis protein
rmAC1706 pgp		3-phosphoglycerate kinase
rmAC1707 cad	4.2.1.96	Pterin-4-alpha-carbinolamine dehydratase
rmAC1708 hemA	2.3.1.37	Glutamyl-tRNA reductase
rmAC1709 hemX		Uroporphyrin-III C-methyltransferase
rmAC1711 NirH		Heme biosynthesis protein NirH
rmAC1714 cspD5		Cold shock protein
rmAC1715 cspD1		Cold shock protein
rmAC1716 uppS	2.5.1.31	Undecaprenyl pyrophosphate synthetase
rmAC1719 rimI		Pab N-terminal acetyltransferase
rmAC1720 dnaG		dnaG
rmAC1722 csaA		Protein secretion chaperonin CsaA
rmAC1726 panF		Pantothenate permease
rmAC1729 valS	6.1.1.9	Valyl-tRNA synthetase
rmAC1732		SOR/SNZ family
rmAC1740 mvaS	4.1.3.5	Hydroxymethylglutaryl-CoA synthase
rmAC1744 rfcB		Replication factor C large subunit
rmAC1745 yckA-2		Amino acid ABC transporter, permease protein
rmAC1747 glnQ1		Glutamine ABC transporter (ATP-binding protein)
rmAC1749 glnH2		Glutamine ABC transporter, permease protein
rmAC1750 argT		Amino acid ABC transporter, amino acid-binding protein
rmAC1751 ccp		Cytochrome aa3 controlling protein
rmAC1752 htl5		MCP domain signal transducer (soluble)
rmAC1754 maeB	1.1.1.40	NAD-dependent malate dehydrogenase
rmAC1757 gptA		Purine phosphoribosyltransferase
rmAC1760		transporter, possibly hexose
rmAC1761 atoE		Short chain fatty acid transporter
rmAC1762 serA2	1.1.1.95	D-3-phosphoglycerate dehydrogenase
rmAC1764		HTH DNA-binding protein
rmAC1765 tenA		Transcriptional activator tenA
rmAC1767 tenA-2		Transcriptional regulator, putative
rmAC1769 putP-2		Sodium-solute symporter, putative
rmAC1772 psmA1	3.4.25.1	Proteasome, subunit alpha
rmAC1773 psmA2		Proteasome alpha subunit
rmAC1776 dcd2	3.5.4.13	Deoxycytidine triphosphate deaminase
rmAC1777		DNA binding protein
rmAC1779 aknG		Alkanonic acid methyltransferase
rmAC1782 thi1		Putative thiazole biosynthetic enzyme
rmAC1786		HTH DNA-binding protein
rmAC1787 hutU	4.2.1.49	Urocanate hydratase
rmAC1789 hutG	3.5.3.8	Probable formimidoylglutamate
rmAC1790 hutI	3.5.2.7	Imidazolonepropionase
rmAC1791 hutH	4.3.1.3	Histidine ammonia-lyase
rmAC1792 ruvB		Holliday junction DNA helicase
rmAC1794 dapF	5.1.1.7	Diaminopimelate epimerase
rmAC1795 ppsA	2.7.9.2	Phosphoenolpyruvate synthase
rmAC1797 htlC		Htr-like protein
rmAC1798 gadD		Glutamate decarboxylase
rmAC1800 metS	6.1.1.10	Methionyl-tRNA synthetase
rmAC1805 gntR		transcription regulator
rmAC1806 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC1812 pnm		N-methyltransferase homolog
rmAC1813	2.4.1.-	glycosyl transferase
rmAC1815 cctA3		Thermosome alpha subunit (Thermosome subunit 1) (Chaperonin alpha subunit)
rmAC1818		Putative hydrolase
rmAC1821 lysE		L-lysine exporter
rmAC1824		Acetyltransferase (GNAT) family
rmAC1825 idr		Iron-dependent repressor
rmAC1830 yurF		ABC transporter, ATP-binding protein
rmAC1831 polB1	2.7.7.7	DNA polymerase B, elongation subunit
rmAC1836 tnp		Phage integrase/site-specific recombinase
rmAC1840 smc1		structural maintenance of chromosome
rmAC1841 yhcR2		Phosphoesterase
rmAC1848 virB11		Type IV secretion system protein
rmAC1856		putative RNA binding protein
rmAC1858		Aldo/keto reductase
rmAC1860		sugar transporter
rmAC1863 mutT4		Mut/nudix family protein
rmAC1865 soxB		Sarcosine oxidase

rmAC1867		putative hsp20
rmAC1869 trp1		ABC transporter, ATP-binding protein
rmAC1870 nhaC3		Na ⁺ /H ⁺ antiporter
rmAC1872		radical HHH
rmAC1873 dpG		Dolichol-P-glucose synthetase
rmAC1875 tfbD		Transcription initiation factor IIB (TFIIB)
rmAC1876 zim		CTAG modification methylase
rmAC1877 aroD	4.2.1.10	3-dehydroquinate dehydratase
rmAC1879 aroB	4.6.1.3	3-dehydroquinate synthase
rmAC1880 minD6		Septum site-determining protein minD (Cell division inhibitor minD)
rmAC1881 deoC2		Deoxyribose-phosphate aldolase
rmAC1884 trpA	4.2.1.20	Tryptophan synthase alpha chain
rmAC1885 trpB	4.2.1.20	Tryptophan synthase beta chain
rmAC1886 trpC	4.1.1.48	Indole-3-glycerol phosphate synthase
rmAC1887 hat5		Putative Acetyltransferase (GNAT)
rmAC1888 gbp5		GTP-binding protein
rmAC1892		DSBA-like thioredoxin domain
rmAC1893 ldc		LD-carboxypeptidase
rmAC1895		Putative DNA binding
rmAC1901 brp		Bacteriorhodopsin related protein
rmAC1902 crtI	1.3.99.-	Phytoene dehydrogenase
rmAC1903 apt2	2.4.2.7	Adenine phosphoribosyltransferase
rmAC1905 dsbB1		Disulfide bond formation protein
rmAC1906 tas		Probable oxidoreductase
rmAC1907		putative sugar transporter
rmAC1908 nthD	4.2.99.18	Endonuclease III
rmAC1910 fbr1		Cytochrome-like protein Fbr
rmAC1913 nadM	2.7.7.1	Nicotinamide-nucleotide adenyltransferase
rmAC1914 lon	3.4.21.53	ATP-dependent protease LA
rmAC1915		putative protease
rmAC1916		6-O-methylguanine DNA methyltransferase, DNA binding domain
rmAC1917 glpQ2	3.1.4.46	Glycerophosphoryl diester phosphodiesterase
rmAC1918 dhs	2.5.1.46	Probable deoxyhypusine synthase 1
rmAC1920 azlC		Branched-chain amino acid transport protein AzlC
rmAC1923 nif3		NIF3 (NGG1p interacting factor 3)
rmAC1925 mhpC	3.7.1.-	2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase
rmAC1926 trzA2		N-ethylmellamine chlorohydrolase
rmAC1927 speB1	3.5.3.11	Agmatinase
rmAC1929 eIF5A		Translation initiation factor 5A (eIF-5A) (Hypusine-containing protein)
rmAC1930		putative CobD/Cib protein
rmAC1931 cobS		Cobalamin-5-phosphate synthase
rmAC1932 ispD	2.7.7.60	4-diphosphocytidyl-2C-methyl-D-erythritol synthase
rmAC1934 hisC1	2.6.1.9	Histidinol-phosphate aminotransferase
rmAC1936 cobI	2.5.1.17	Cobalamin adenosyltransferase
rmAC1938 cobQ		Cobyrinic acid synthase
rmAC1939 minD1		Cell division inhibitor
rmAC1943 phrB2	4.1.99.3	Deoxyribodipyrimidine photolyase
rmAC1951 gspE1		Type II secretion system protein
rmAC1953		DNA binding protein
rmAC1954 yusZ1		Oxidoreductase
rmAC1955 glpA		Glycerol-3-phosphate dehydrogenase subunit A (EC1.1.99.1)
rmAC1956 eIF2BD2		Translation initiation factor eIF-2B subunit delta
rmAC1957 malQ	2.4.1.25	4-alpha-glucanotransferase
rmAC1958 lpg1		LPS glycosyltransferase
rmAC1960 graD4b		Glucose-1-phosphate thymidyltransferase
rmAC1961 cga-1		Glucosylase
rmAC1962 malA		Putative alpha-D-1,4-glucosidase
rmAC1964 arcR6		Transcription regulator
rmAC1965 aceB		malate synthase
rmAC1966 gloA3	4.4.1.5	Lactoylglutathione lyase
rmAC1967 glcD1		Glycolate oxidase subunit GlcD
rmAC1971 arcR5		Transcription regulator
rmAC1972 gcdH	1.3.99.7	Glutaryl-CoA dehydrogenase
rmAC1973 aldY4	1.2.1.3	Aldehyde dehydrogenase
rmAC1974 aacC	2.3.1.81	Aminoglycoside N3'-acetyltransferase
rmAC1975 adh5	1.1.1.1	Alcohol dehydrogenase
rmAC1977 alkK4		Medium-chain fatty acid-CoA ligase
rmAC1979 ech5	4.2.1.17	Enoyl-CoA hydratase/isomerase
rmAC1980 aph		aminoglycoside phosphotransferase
rmAC1982 hbd2	1.1.1.35;4.2.1.	3-hydroxybutyryl-CoA dehydrogenase
rmAC1983 acdI	1.3.99.3	Acyl-CoA dehydrogenase
rmAC1984 fabG4	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase
rmAC1985 maoC1		Monoamine oxidase regulatory protein
rmAC1986 acdC	1.3.99.-	Acyl-CoA dehydrogenase
rmAC1987 anf		ABC transporter substrate-binding protein
rmAC1989 livH-5		Branched-chain amino acid ABC transporter, permease protein
rmAC1991 livM-4		Branched-chain amino acid ABC transporter, permease protein
rmAC1992 livG-5		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC1993 livF-5		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC1996		putative DNA binding domain
rmAC1997 rbnBN2		Ribonuclease BN
rmAC1999 spaT		Aminotransferase, class V
rmAC2000 usp9		Universal stress protein family
rmAC2004 ftsZ3		Cell division protein FtsZ
rmAC2014		methyltransferase
rmAC2015 xthA	3.1.21.2	Probable endonuclease IV
rmAC2017		transcription regulator
rmAC2018 katG1	1.11.1.6	Peroxidase/catalase
rmAC2019 lpl	6.3.4.-	Lipoate protein ligase
rmAC2022		transcription regulator
rmAC2023 nuoC		NADH dehydrogenase I chain C, C
rmAC2024 msaA1	1.8.4.6	Peptide methionine sulfoxide reductase MsrA
rmAC2027 cdc48a		Cell division cycle protein 48
rmAC2030 xop1		Bacteriorhodopsin precursor (BR)
rmAC2032		thioesterase of unknown specificity
rmAC2034 htlA		Htr-like protein
rmAC2036 pkn		Serine/threonine protein kinase
rmAC2037 troR		Iron-dependent repressor
rmAC2038 nifU2		NifU-like domain protein
rmAC2039 oppA		Oligopeptide ABC transporter, solute-binding protein
rmAC2040 oppB		Oligopeptide ABC transporter, permease protein
rmAC2041 oppC2		Oligopeptide transport system permease protein OppC
rmAC2042 oppD1		Oligopeptide ABC transporter, ATPase component
rmAC2043 oppF		Oligopeptide ABC transporter, ATP-binding protein
rmAC2044 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC2047 sppA	3.4.21.-	Protease IV homolog
rmAC2048 mocA		oxidoreductase

rmAC2051 ttfF		Transcription initiation factor IIB (TFIIB)
rmAC2052		transcription regulator
rmAC2056 serA3	1.1.1.95	D-3-phosphoglycerate dehydrogenase
rmAC2057 moaD		Molybdopterin converting factor, subunit
rmAC2064 aor1		Aldehyde ferredoxin oxidoreductase
rmAC2065 rpl15E		50S ribosomal protein L15e
rmAC2066 blh		Brp-like homolog
rmAC2067 crtY		Lycopene cyclase
rmAC2069 crtB	2.5.1.32;2.5.1.1	Phytoene synthase
rmAC2070 boa		putative light- and oxygen-sensing transcription regulator
rmAC2072 vacB	3.1.-.-	Ribonuclease R
rmAC2073 trp2		ABC transporter, ATP-binding protein
rmAC2075 nusA1		transcription anti-termination factor
rmAC2083 yadH		ABC transporter, permease protein
rmAC2084 nosF-3		ABC transporter, ATP-binding protein
rmAC2087		putative PUA domain RNA-binding protein
rmAC2090 moeB		Molybdopterin biosynthesis protein Moef
rmAC2091 htr		MCP domain signal transducer (soluble)
rmAC2092 cpx		Probable carboxypeptidase
rmAC2094		Amidase-related protein
rmAC2095 argE	3.5.1.16	Acetylornithine deacetylase
rmAC2096 uvsE	3.-.-.-	UV DNA damage endonuclease
rmAC2100 entB1	3.3.2.1	Isochorismatase
rmAC2103 rli		RNase L inhibitor
rmAC2108 npdG-1	1.6.8.-	F420-dependent NADP reductase
rmAC2109 htlD		Htr-like protein
rmAC2110 trxA3		Thioredoxin
rmAC2111 sec61beta		component of the Sec61/SecYEG protein secretory system
rmAC2116 uvrA		Excinuclease ABC, subunit A
rmAC2121		Pentapeptide repeats of unknown function
rmAC2126 bchP		Geranylgeranyl hydrogenase
rmAC2128 sseA1	2.8.1.1	Thiosulfate sulfurtransferase
rmAC2129 sseA2		Thiosulfate sulfurtransferase
rmAC2133 epf1		mRNA 3'-end processing factor
rmAC2137 tcmJ		Tetracenomycin polyketide synthesis protein
rmAC2139 imd3	1.1.1.205	Inosine Monophosphate Dehydrogenase
rmAC2140 sdr2		Oxidoreductase, short-chain dehydrogenase/reductase family
rmAC2141 trxA8		thioredoxin
rmAC2143 thiE	2.5.1.3	Thiamine-phosphate pyrophosphorylase
rmAC2144		transcription regulator
rmAC2145 phoU1		Phosphate transport system regulatory protein PhoU
rmAC2146 pstB2		Phosphate ABC transporter, ATP-binding protein
rmAC2147 pstA1		Phosphate ABC transporter, permease protein
rmAC2148 pstC2		Phosphate ABC transporter, permease protein
rmAC2149 yqgG		Phosphate ABC transporter binding
rmAC2150 prp1		Phosphate regulatory protein homolog
rmAC2152		putative Rhodanese
rmAC2153 mutT2		Mut/nudix family protein
rmAC2157 rimI		Pab N-terminal acetyltransferase
rmAC2158 acnB	4.2.1.3	Aconitate hydratase
rmAC2159 dcd3	3.6.1.23	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase
rmAC2160		Putative DNA binding
rmAC2162 mgsA	4.2.3.3	Methylglyoxal synthase
rmAC2163 exsB		Succinoglycan biosynthesis ExsB protein
rmAC2166 ptpS	4.2.3.12	6-pyruvoyl tetrahydropterin synthase
rmAC2170 pepB4		Aminopeptidase
rmAC2172 adh14	1.1.1.1	Alcohol dehydrogenase
rmAC2174 fdx		Ferredoxin
rmAC2175 seb		Selenium-binding protein
rmAC2176 galE9		UDP-glucose 4-epimerase
rmAC2178 rfbB3	4.2.1.46	Dtdp-Glucose 4,6-Dehydratase
rmAC2179 fer2		2Fe-2S iron-sulfur cluster binding domain
rmAC2180 gnd	1.1.1.44	6-phosphogluconate dehydrogenase
rmAC2181 pepB2		Aminopeptidase
rmAC2183 fapJ		Flagella accessory protein
rmAC2184 gspE3		Type II secretion system protein
rmAC2186 flpH		Flagella-related protein H
rmAC2187 flaG		Putative flagella-related protein G
rmAC2190 flaF		Archaeal flagellar protein F
rmAC2191 fapE1		Flagella-related protein E
rmAC2192 cheD		Chemotaxis protein CheC
rmAC2193 cheA1		CheA histidine kinase (Chemotaxis protein)
rmAC2194 cheY		Chemotaxis protein CheY
rmAC2198 flaB		Flagellin B precursor
rmAC2202 kaiC1		Circadian regulator
rmAC2203 cheW1		Chemotaxis protein CheW
rmAC2204 cheB	3.1.1.61	Protein-glutamate methyltransferase
rmAC2205 cheA3	2.7.3.-	Chemotaxis protein CheA
rmAC2206 cheR	2.1.1.80	Chemotaxis protein methyltransferase CheR
rmAC2207 cpcE2		Phycocyanin alpha phycocyanobilin lyase-like
rmAC2211 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC2212 rps6E		30S ribosomal protein S6e
rmAC2215 dcd1		Deoxycytidine triphosphate deaminase
rmAC2217 recJ4		RecJ-like exonuclease (DHH/DHHA1 family protein)
rmAC2219 phoR		PhoR protein homolog
rmAC2220 usp5		Universal stress protein
rmAC2222		Acetyltransferase (GNAT) family
rmAC2223 usp2		Universal stress protein family
rmAC2227 dppF		Dipeptide ABC transporter ATP-binding
rmAC2228 dppD		Dipeptide ABC transporter ATP-binding
rmAC2229 dppB1		Dipeptide ABC transporter permease
rmAC2230 oppC1		Oligopeptide transport system permease protein OppC
rmAC2232 pyrC	3.5.2.3	Dihydroorotase
rmAC2236 entB2		Isochorismatase
rmAC2241	2.4.2.19	Quinolinate phosphoribosyl transferase
rmAC2244		putative ZIP domain Zinc transporter
rmAC2245		M50 family metalloproteinase
rmAC2247 eif2BA		Translation initiation factor eIF-2B alpha subunit
rmAC2248 csd2	4.4.1.-	Probable cysteine desulfurase
rmAC2252 crcB1		integral membrane protein possibly involved in chromosome condensation
rmAC2253 crcB2		Integral membrane protein possibly involved in chromosome condensation
rmAC2256 pcm2	2.1.1.77	Protein-L-isoaspartate O-methyltransferase 2
rmAC2258 pcm1	2.1.1.77	Protein-L-isoaspartate O-methyltransferase 1
rmAC2261 pepB1		Aminopeptidase
rmAC2262 gapB	1.2.1.59	Glyceraldehyde 3-phosphate dehydrogenase
rmAC2267 uvrD		Repair helicase
rmAC2270 gvpE		Transcriptional regulator PadR-like family

rmAC2272 norB		Cytochrome B subunit of nitric oxide reductase
rmAC2277 dox		Dioxygenase
rmAC2278 coaD1	2.7.7.3	Phosphopantetheine adenylyltransferase
rmAC2280 cbiQ1		Cobalt transport protein
rmAC2282 cbiM		Cobalamin biosynthesis protein CbiM
rmAC2283 copG1		Transcriptional regulator, CopG family
rmAC2284 tnp		Phage integrase/site-specific recombinase
rmAC2285 phrH2		PhiH1 repressor homolog
rmAC2298 cca	2.7.7.25	tRNA nucleotidyltransferase
rmAC2299 aup		Acetoin utilization protein
rmAC2301 hpyA		Archaeal histone A1
rmAC2302 rpa		Replication A related protein
rmAC2310 coxB4	1.9.3.1	Cytochrome C oxidase subunit II, membrane domain
rmAC2311 coxA2	1.9.3.1	Cytochrome c oxidase, subunit I
rmAC2314 trp3		ABC transport protein
rmAC2318 mcm1		MCM / cell division control protein 2'
rmAC2321 boa		Bacterio-opsin activator-like protein
rmAC2325 repC		replication factor C
rmAC2329 tnp		phage integrase
rmAC2333 hspC		Small heat shock protein
rmAC2334 glcD2		Putative oxidoreductase
rmAC2337	2.7.3.-	Histidine Kinase
rmAC2338 cspD4		Cold shock protein
rmAC2339 cspD3		Cold shock protein
rmAC2343 rfbA		Glucose-1-phosphate thymidyltransferase
rmAC2346 malG		Maltose ABC transporter, permease protein
rmAC2347 malFG-6		ABC-type sugar transport systems, permease component
rmAC2349 malE1		Maltose ABC transporter, maltose-binding protein
rmAC2350 amy	3.2.1.-	Alpha amylase
rmAC2352 ugpC1		Sugar ABC transporter, ATP-binding protein (UGPC)
rmAC2353 cga-2	3.2.1.3	Glucan 1,4-alpha-glucosidase (Glucoamylase)
rmAC2354		transcription regulator
rmAC2356 gst1		Glutathione S-transferase
rmAC2357 rpl10E		50S ribosomal protein L10e
rmAC2359 usp16		Universal stress protein
rmAC2360 rimK		Ribosomal protein S6 modification protein
rmAC2361 hsp20b		Putative heat shock protein
rmAC2363 gapA	1.2.1.12	Glyceraldehyde 3-phosphate dehydrogenase
rmAC2364 pgk	2.7.2.3	Phosphoglycerate kinase
rmAC2367 ribC	2.5.1.9	Riboflavin synthase alpha chain
rmAC2369 hisH1		Imidazoleglycerol-phosphate synthase
rmAC2371 hisI1	3.6.1.31	Phosphoribosyl-ATP pyrophosphatase
rmAC2372 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC2374 gbp4		GTP-binding protein
rmAC2378 engB		Probable GTP-binding protein EngE
rmAC2380		putative Serine/threonine phosphatase
rmAC2382 tnp		phage integrase
rmAC2383 phrH3		PhiH1 repressor homolog
rmAC2385 cdc6e		Orc / cell division control protein I
rmAC2394 tnp		Putative ISH8 transposase
rmAC2405 rps10P		30S ribosomal protein S10P
rmAC2406 eef1a		Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu)
rmAC2408 hom	1.1.1.3	Homoserine dehydrogenase
rmAC2412		putative peptidase
rmAC2413 fusA		Elongation factor G (EF-G)
rmAC2414 metB	4.2.99.9;2.5.1.	Cystathionine gamma-synthase
rmAC2416		putative light and redox sensing histidine kinase
rmAC2417 cbiQ2		Cobalt transport protein
rmAC2418 cbiO		Cobalt transport ATP-binding protein
rmAC2420 bioY		dethiobiotin synthesis
rmAC2423 rps7P		30S ribosomal protein S7P
rmAC2424 rps12P		30S ribosomal protein S12P (HmaS12)
rmAC2425 htr18		MCP domain signal transducer (membrane)
rmAC2426 nusA2		Transcription termination factor NusA
rmAC2427 rpoC	2.7.7.6	RNA polymerase Rpb1, domain 5
rmAC2428 rpoA		DNA-directed RNA polymerase subunit A
rmAC2429 rpoB	2.7.7.6	DNA-directed RNA polymerase, beta subunit
rmAC2430 rpoB		DNA-directed RNA polymerase, subunit E
rmAC2432 rpoH	2.7.7.6	DNA-directed RNA polymerase subunit H
rmAC2435		Putative phosphoesterase
rmAC2437 mer1		F420-dependent N5,N10-methylene-tetrahydromethanopterin reductase
rmAC2439 tnaA	4.1.99.1	Tryptophanase
rmAC2440 scm		24-sterol C-methyltransferase
rmAC2442 moxR3		Methanol dehydrogenase regulatory protein
rmAC2443		
rmAC2445 sui1		Protein translation factor SUI1 homolog
rmAC2446		putative glycol aminopeptidase
rmAC2449 thiD	2.7.4.7	Phosphomethylpyrimidine kinase
rmAC2450 trxA9		thioredoxin
rmAC2451 serA5	1.1.1.95	Phosphoglycerate dehydrogenase
rmAC2455 usp10		putative Universal stress protein
rmAC2458 trxA1		Thioredoxin
rmAC2459 maa	2.3.1.79	Maltose O-acetyltransferase
rmAC2461 ark2		Adaptive-response sensory-kinase
rmAC2463 scp2		Sterol Carrier Protein
rmAC2464 livF-6		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC2465 livG-6		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC2466 livM-5		Branched-chain amino acid ABC transporter, permease protein
rmAC2468 livH-6		Branched chain amino acid transporter, permease protein
rmAC2470 prr	5.1.1.4	Proline racemase
rmAC2471 yusM		Proline dehydrogenase
rmAC2472 boa-8		Similar to Halobacterium Bat (Bacterio-opsin activator-like protein)
rmAC2473 aldY2	1.2.1.3	Aldehyde dehydrogenase
rmAC2474 eif1A1		Translation initiation factor 1A (aIF-1A)
rmAC2476 prk2		protein kinase
rmAC2477 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC2480 act		Acyl-CoA thioester hydrolase
rmAC2484 ech3	4.2.1.17	Enoyl-CoA hydratase
rmAC2486 nadE1	6.3.5.1	NH(3)-dependent NAD(+) synthetase
rmAC2487 rfcC2		Replication factor C small subunit
rmAC2488 rps24E		30S ribosomal protein S24e
rmAC2489 rps27AE		30S ribosomal protein S27ae
rmAC2490 gcp	3.4.24.57	O-sialoglycoprotein endopeptidase
rmAC2493 ham1		Ham1 protein
rmAC2494 yqjQ		Oxidoreductase, short chain dehydrogenase/reductase family
rmAC2495 htr14		MCP domain signal transducer (membrane)
rmAC2498 trkA6		TRK potassium uptake system protein

rmAC2500		Metallo-beta-Lactamase like
rmAC2501 gfo5		oxidoreductase
rmAC2502 phzC/phzF		Phenazine biosynthesis-like protein
rmAC2503 araC		Transcriptional regulator, AraC family
rmAC2504 lgl	4.4.1.5	Putative lactoyglutathione lyase
rmAC2505		putative polysaccharide biosynthesis protein
rmAC2508 ilvA2	4.2.1.16	Threonine dehydratase
rmAC2510 trk		trk active potassium channel
rmAC2511 citZ	2.3.3.1	Citrate synthase II
rmAC2512 pchB		potassium channel-related protein
rmAC2515 thrC4	4.2.99.2	Threonine synthase
rmAC2519		putative DNA binding protein
rmAC2520 gstN		Glutathione S-transferase, N-terminal domain
rmAC2521 pyrE1	2.4.2.10	Orotate phosphoribosyltransferase
rmAC2522 manB3	5.4.2.2;5.4.2.8	Phosphoglucosyltransferase/Phosphomannomutase
rmAC2524 hisI2	3.5.4.19	Phosphoribosyl-AMP cyclohydrolase
rmAC2526 fer1		Ferredoxin
rmAC2527 ylnA		Anion permease
rmAC2529 hisA	5.3.1.16	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase
rmAC2530		Putative methyltransferase
rmAC2532 mutS4		DNA mismatch repair protein MutS
rmAC2533 ark1		Adaptive-response sensory-kinase
rmAC2535 trp-11		ABC transporter, ATP-binding protein
rmAC2550 mutL		DNA mismatch repair protein mutL
rmAC2551 kdgK	2.7.1.45	2-keto-3-deoxygluconate kinase
rmAC2552 gcvT4	2.1.2.10	Aminomethyltransferase
rmAC2553		2Fe-2S iron-sulfur cluster binding domain
rmAC2555 hisB	4.2.1.19	Imidazoleglycerol-phosphate dehydratase
rmAC2557 pca		3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase
rmAC2558 nhaC6		Na ⁺ /H ⁺ antiporter
rmAC2561 alaS1	6.1.1.7	Alanyl-tRNA synthetase
rmAC2565 rfcC1		Replication factor C small subunit
rmAC2566		Acetyltransferase (GNAT) family
rmAC2568 pmm	5.4.2.2;5.4.2.8	Phosphoglucosyltransferase/phosphomannomutase
rmAC2569		putative nuclease
rmAC2570 purE-2		NCAIR mutase (PurE)-related protein
rmAC2572 rpiA	5.3.1.6	Ribose 5-phosphate isomerase A
rmAC2574 manB1	5.4.2.2;5.4.2.8	Phosphoglucosyltransferase/Phosphomannomutase
rmAC2577 upp	2.4.2.9	Uracil phosphoribosyltransferase
rmAC2580 imp		Immunogenic protein
rmAC2586		phosphate transporter family protein
rmAC2590 cstA		Carbon starvation protein CstA
rmAC2592 arsA3	3.6.3.16	arsenical pump-driving ATPase
rmAC2593 cobW/P47K_1		Cobalamin synthesis protein/P47K
rmAC2599 gst2		Glutathione S-transferase
rmAC2601 prxS		AhpC/TSA family peroxiredoxins (Prxs)
rmAC2602 yrdC		DNA binding protein
rmAC2605 hdrD		Heterodisulfide reductase
rmAC2606 mthK2		Potassium channel protein, putative
rmAC2608 dip3		Competence-damage protein ClnA-like
rmAC2610 hemB	4.2.1.24	Delta-aminolevulinic acid dehydratase
rmAC2616 ark3		Adaptive-response sensory-kinase
rmAC2618 htr		MCP domain signal transducer (soluble)
rmAC2619 amt		Ammonium transporter
rmAC2621 glnB		Nitrogen regulatory protein P-II
rmAC2622 asnC4		Transcription regulator, AsnC family
rmAC2623 cheA2		CHEA histidine kinase (Chemotaxis protein)
rmAC2624		ABC transporter, substrate-binding protein
rmAC2625 nirA1		Ferredoxin-nitrite reductase
rmAC2626		putative transporter
rmAC2627 narB	1.7.99.4	Nitrate reductase
rmAC2628 hemL	5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase
rmAC2630 prsA	2.7.6.1	Ribose-phosphate pyrophosphokinase
rmAC2631 aldY1	1.2.1.3	Aldehyde dehydrogenase
rmAC2632		Sodium symporter transmembrane region
rmAC2633 htr		MCP domain signal transducer (soluble)
rmAC2634 ileS	6.1.1.5	Isoleucyl-tRNA synthetase
rmAC2636 udg1	3.2.2.-	uracil DNA glycosylase superfamily protein
rmAC2638 hit2		Histidine triad protein
rmAC2639 minD5		Cell Division Inhibitor
rmAC2645 comA		Competence-like protein
rmAC2648 nthB	4.2.99.18	Endonuclease III
rmAC2650 leuS1	6.1.1.4	Leucyl-tRNA synthetase
rmAC2651 rbsC		Ribose ABC transporter permease
rmAC2653 rbsC-4		Sugar ABC transporter, permease protein
rmAC2654 rbsA-2		Sugar ABC transporter ATP binding protein
rmAC2655 rbsA		Sugar ABC transporter, ATP binding protein
rmAC2656 ynfN		ABC transporter (Lipoprotein)
rmAC2657 phoT2		Sodium-dependent phosphate transporter
rmAC2658 usp20		Universal Stress Protein
rmAC2661 rad24		DNA repair protein
rmAC2662 fer		Ferredoxin
rmAC2663 lysC	2.7.2.4	Aspartokinase
rmAC2667 thrC3		Threonine synthase
rmAC2669		Putative DNA binding
rmAC2670 ort	2.4.2.10	Orotate Phosphoribosyltransferase
rmAC2671 inb		Oxidoreductase homologue
rmAC2672 arcB	2.1.3.3	Ornithine carbamoyltransferase
rmAC2674 gltCP	3.4.17.11	Glutamate Carboxypeptidase
rmAC2675 argD	2.6.1.11	Acetylornithine aminotransferase
rmAC2676 argB2	2.7.2.8	Acetylglutamate kinase
rmAC2678 argC	1.2.1.38	N-acetyl-gamma-glutamyl-phosphate reductase
rmAC2679 rimK		Ribosomal protein S6 modification protein
rmAC2681 argH	4.3.2.1	Argininosuccinate lyase
rmAC2683 argG	6.3.4.5	Argininosuccinate synthase
rmAC2691 polA2	2.7.7.7	DNA polymerase II large subunit
rmAC2692		oxygen and light sensing histidine kinase
rmAC2696 serA1	1.1.1.95	D-3-phosphoglycerate dehydrogenase
rmAC2699	1.1.1.205	putative inosine monophosphate dehydrogenase
rmAC2701 glyS	6.1.1.14	Glycyl-tRNA synthetase
rmAC2704 eif4A		ATP-dependent RNA helicase homologue eIF-4A
rmAC2706 mdh	1.1.1.37	L-malate dehydrogenase
rmAC2710 gbp3		GTP-binding protein homologue
rmAC2711 cdc6d		Cell division control protein 6 homologue
rmAC2712 sec11a		Signal sequence peptidase
rmAC2713 sec11b		Signal sequence peptidase
rmAC2714 polA1	2.7.7.7	DNA polymerase II small subunit

rmAC2716 cysD	4.2.99.10	O-acetylhomoserine (thiol)-lyase
rmAC2717 serB1	3.1.3.3	Phosphoserine phosphatase
rmAC2719 rad3b		Helicase
rmAC2721 cat		cation efflux protein
rmAC2722 yhcR3		phosphoesterase
rmAC2723		Putative Bacterial regulatory protein, arsR family
rmAC2726 pepB3		Aminopeptidase
rmAC2728 htr		putative HAMP and MCP domain signal transduce
rmAC2737 glbN		Cyanoglobin
rmAC2740		TRAM domain protein
rmAC2741 ywFD2	1.1.1.47	glucose dehydrogenase
rmAC2742 manC		Mannose-1-phosphate guanylyltransferas
rmAC2748		Ribbon-helix-helix protein, copG family
rmAC2749		putative helicase
rmAC2753 prt	2.4.2.-	phosphoribosyltransferase
rmAC2756 rad24a		rad24a plus uvrB domain
rmAC2759 nso		Transporter, sodium/sulfate symporter fami
rmAC2760 htr6		MCP domain signal transducer (membrane
rmAC2761 tmpC		Membrane lipoprotein tmpC precursor (Membrane protein C) (35 kDa antigen) (Lipoprotein TpnN3)
rmAC2762 mcm2		Cell division control protein 2'
rmAC2768 minD4		cell division inhibito
rmAC2769 tfbI		Transcription initiation factor IIB (TFIIB
rmAC2773 ssuE2	1.5.1.29	NADPH-dependent FMN reductase
rmAC2776 matE2		Multi Antimicrobial Extrusion (MATE) drug/sodium antiporter
rmAC2777		DNA binding protein, putative transcriptional regulatc
rmAC2779 asnC1		Transcription regulator, AsnC family
rmAC2780 glnA	6.3.1.2	Glutamine synthetase
rmAC2781 pap2a	3.1.3.9	Glucose-6-phosphatase
rmAC2782 rbn		Ribonuclease BN
rmAC2783 dip2		DNA damage-inducible protein
rmAC2785		transcription regulato
rmAC2788 trm1	2.1.1.32	N(2),N(2)-dimethylguanosine tRNA methyltransferase
rmAC2789 htl_		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein
rmAC2793 yusZ3		Oxidoreductase
rmAC2794 hisH2	2.4.2.-	Imidazole glycerol phosphate synthase subunit HisH
rmAC2796 udg3	3.2.2.-	uracil DNA glycosylase superfamily protein
rmAC2797 ern3		Endoribonuclease L-PSP
rmAC2800 fprA		Flavoprotein (Hydroxyacylglutathione hydrolase-like protein
rmAC2802 rpl40E		50S ribosomal protein L40E
rmAC2805 hyrA2		Monoxygenase
rmAC2808 serS	6.1.1.11	Seryl-tRNA synthetase
rmAC2809 usp21		Universal stress protein
rmAC2811 mthK		Potassium Channel Related Protein
rmAC2814 mutT3		MutT/nudix family protein
rmAC2815 aca2	2.3.1.9	Acetyl-coA acetyltransferase
rmAC2818 ftsH	3.4.24.-	Cell division protein FtsH
rmAC2820 phnP		ATP-binding protein PhnF
rmAC2827 eIF2G		Translation initiation factor eIF-2 subunit gamm
rmAC2829 rpoE'		DNA-directed RNA polymerase subunit E
rmAC2830 rpoE''		DNA-directed RNA polymerase subunit E'
rmAC2834		Putative RNA methylase
rmAC2835 hisG	2.4.2.17	ATP phosphoribosyltransferase
rmAC2836 did		sugar (and other) transporte
rmAC2837 trzA3		N-ethylmellamine chlorohydrolase
rmAC2840 ahcY	3.3.1.1	Adenosylhomocysteinase
rmAC2844 pri2		Eukaryotic-type DNA primase, large subuni
rmAC2847 hjr		Holliday junction resolvase
rmAC2850 pcbD-1		Hydrolase, alpha/beta hydrolase fold fami
rmAC2851 pcnA		DNA polymerase sliding clamp (Proliferating cell nuclear antigen homolog) (PCN/
rmAC2853 nirK		nitrite reductase, copper containin
rmAC2854 ftsJ	2.1.1.-	Ribosomal RNA large subunit methyltransferase J
rmAC2857 tatC1		Sec-independent protein translocase protein TatC
rmAC2858 tatC2		Sec-independent protein translocase TatC
rmAC2859 gpmB	5.4.2.4; 5.4.2.1	Phosphoglycerate mutase
rmAC2860 trmU	2.1.1.61	tRNA methyl transferase
rmAC2861 mutS2		Mismatch repair protein
rmAC2862 cdc6c		Cell division control protein C
rmAC2867 dip1		DNA damage-inducible protein
rmAC2868 potD2		Spermidine/putrescine ABC transporter, spermidine/putrescine binding prote
rmAC2870 potA2		Spermidine/putrescine ABC transporter, ATP-binding protei
rmAC2872 potB2		Spermidine/putrescine ABC transporter, permease protei
rmAC2873 potC2		Spermidine/putrescine ABC transporter permease
rmAC2874 phaJ1	4.2.1.-	(R)-specific enoyl -CoA hydratase
rmAC2876 rad24-2	3.6.1.-	Putative ski2-type helicase
rmAC2880 yqjM2		NADH-dependent flavin oxidoreductase
rmAC2882 maoC1		MaoC family protein
rmAC2886 phaC		POLY(3-hydroxyalkanoate) synthas
rmAC2891 cctA2		Thermosome alpha subunit (Thermosome subunit 1) (Chaperonin alpha subun
rmAC2897 galE2	5.1.3.2	UDP-glucose 4-epimerase
rmAC2900 cspD2		Cold shock protein
rmAC2901 uvrB		putative uvrB
rmAC2902		putative methyltransferase
rmAC2903 nmd3		putative nonsense mediated mRNA decay protei
rmAC2904 galE6		UDP-glucose 4-epimerase
rmAC2906 htpX1	3.4.24.-	Probable protease htpX homolog
rmAC2910 radA		DNA repair and recombination protein RadA
rmAC2912 gsp		General stress protein 6S
rmAC2914 yvaI		Acetyltransferase homolog
rmAC2924 guaA3	6.3.5.2	GMP synthase (glutamine-hydrolyzing)
rmAC2927 yafB-4		Oxidoreductase
rmAC2929 gfo1		Glucose-fructose oxidoreductase
rmAC2936 boa		Bacterio-opsin activator-like protei
rmAC2937 mutS1		DNA mismatch repair protein MutS
rmAC2939 cctB		Thermosome beta subunit (Thermosome subunit 2) (Chaperonin beta subun
rmAC2941 ocd2	4.3.1.12	Ornithine cyclodeaminase
rmAC2945		signal-transducing histidine kinas
rmAC2947 leuS2	6.1.1.4	Leucyl-tRNA synthetase
rmAC2948 bcp3		Bacterioferritin comigratory protei
rmAC2949 hsp20a		Small heat shock protein
rmAC2950 pheA	4.2.1.51	Prephenate dehydratase
rmAC2951 yccK	1.-	Oxidoreductase
rmAC2953 lpdA2	1.8.1.4	Dihydrolipoamide dehydrogenase
rmAC2955 pdhC2	2.3.1.12	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase comple
rmAC2956 pdhB1	1.2.4.1	Pyruvate Dehydrogenase
rmAC2957 pdhA3	1.2.4.1;1.2.4.4	Pyruvate dehydrogenase E1 component, alpha subuni
rmAC2959 lipA		Lipoic acid synthetase (Lip-syn) (Lipoate synthase
rmAC2961 brr2		Pre-mRNA splicing helicase

rmAC2962		Putative haloacid dehalogenase-like hydrolase
rmAC2963 top1		Topoisomerase DNA binding C4 zinc finger
rmAC2964 endA	3.1.27.9	tRNA intron endonuclease
rmAC2965 trpS	6.1.1.2	Tryptophanyl-tRNA synthetase
rmAC2966 pheS	6.1.1.20	Phenylalanyl-tRNA synthetase alpha chain
rmAC2967 pheT	6.1.1.20	Phenylalanyl-tRNA synthetase beta chain
rmAC2969 pyrD	1.3.3.1	Dihydroorotate dehydrogenase
rmAC2992 nirA2		Ferredoxin-nitrite reductase
rmAC2996 uvrB		UvrABC system protein B
rmAC2997		membrane bound histidine kinase <i>?</i>
rmAC2998 cbiT	1.-.-.-	Precorin-8W decarboxylase
rmAC3000 cbiL		Precorin-2 C20-methyltransferase
rmAC3001 cbiF		Cobalamin biosynthesis precorrin-3 methylase
rmAC3003 cbiG		Cobalamin biosynthesis protein C
rmAC3004 fabG6	1.1.1.100	3-oxoacyl-[acyl-carrier protein] reductase
rmAC3005 cobH	2.1.1.131	Precorin-3B C17-methyltransferase
rmAC3008 cbiH	2.1.1.131	Precorin-3B C17-methyltransferase
rmAC3011 cbiK	4.99.1.-	colbalt chelase thioredoxin
rmAC3013 tup1		Tup1 like Transcriptional Repressor
rmAC3018 hmcA		Protoporphyrin IX magnesium chelatase
rmAC3019 cobN		Cobalamin biosynthesis protein
rmAC3020 cbiC	5.4.1.2	Precorin-8X methylmutase
rmAC3021 cbiJ		Precorin-3 methylase
rmAC3023 cbiX		putative cobalamin biosynthesis protein
rmAC3025 napA		Sodium/proton antiporter, putative
rmAC3026 yfmJ1	1.6.5.5	Quinone Oxidoreductase
rmAC3031 iunH1		Inosine-uridine preferring nucleoside hydrolase
rmAC3032 dgoA2		Mandelate racemase/muconate lactonizing enzyme family protein
rmAC3033		Metallo-beta-lactamase
rmAC3034 gfo6		Glucose-fructose oxidoreductase
rmAC3036 aldY3		Aldehyde dehydrogenase
rmAC3038 htpX3		Heat shock protein X
rmAC3039 hpcEb		2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
rmAC3041 uvrC		UvrABC system protein C
rmAC3046 aspC2		Aspartate aminotransferase
rmAC3049 ligB	6.5.1.2	DNA ligase
rmAC3050 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC3052 nosY2		ABC-type transport system involved in multi-copper enzyme maturation, permease component
rmAC3053		ABC transporter, ATP-binding protein
rmAC3062 moxR5		Methanol dehydrogenase regulatory protein
rmAC3063 metY		O-acetylhomoserine (thiol)-lyase
rmAC3064 metA	2.3.1.31	Homoserine O-acetyltransferase
rmAC3068 panE	1.1.1.169	2-dehydropanoate 2-reductase
rmAC3069 dgoA3		Mandelate racemase/muconate lactonizing enzyme family
rmAC3071 ilvE1		Branched-chain amino acid aminotransferase
rmAC3073 ribA	3.5.4.25	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase
rmAC3078 rub		rubredoxin
rmAC3086 hemC	4.3.1.8	Porphobilinogen deaminase
rmAC3087 cysG2	2.1.1.107	Uroporphyrin-III C-methyltransferase
rmAC3088 cysG1		Uroporphyrin-III C-methyltransferase
rmAC3089 pspA2		transcription regulator
rmAC3094 recJ5		RecJ-like exonuclease (DHH/DHHA1 family protein)
rmAC3099 edp		Proteinase IV homolog
rmAC3101	2.1.1.-	methyltransferase
rmAC3102 nifU1		NifU-like protein
rmAC3104 csd1	4.4.1.-	Probable cysteine desulfurase
rmAC3108 tpr		tetratricopeptide repeat (TPR) protein
rmAC3109		2'-5' RNA ligase
rmAC3110 gufA		Metal transporter family GufA protein
rmAC3112 rpl39E		50S ribosomal protein L39e
rmAC3113 rpl31E		50S ribosomal protein L31e
rmAC3118 dpa		Signal recognition particle receptor
rmAC3119		LPXTG-motif cell wall anchor domain protein
rmAC3121 eda	4.1.2.14	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
rmAC3122 mdcM		Malonate transporter
rmAC3124 srp54		Signal recognition 54 kDa protein (SRP54)
rmAC3125 usp33		universal stress protein
rmAC3126 trxA4		Thioredoxin
rmAC3127 livF-7		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC3128 livG-9		Branched-chain amino acid ABC transporter, ATP-binding protein
rmAC3129 livM-6		Branched-chain amino acid ABC transporter, permease protein
rmAC3130 livH-7		Branched-chain amino acid ABC transporter, permease protein
rmAC3132 livK-2		Branched-chain amino acid ABC transporter, amino acid-binding protein
rmAC3135 cat		Divalent cation transporter
rmAC3138 hat3		putative GNAT-family histone acetyltransferase
rmAC3139 maoC2		MaoC family protein
rmAC3140 nuc		endonuclease, Staphylococcal nuclease homolog
rmAC3141 soxA1		Sulfite Oxidase
rmAC3143		putative haloacid dehalogenase-like hydrolase
rmAC3145 adk		Adenylate kinase
rmAC3146 fps		farnesyl-pyrophosphate synthase
rmAC3147 etfA2		Electron transfer flavoprotein alpha-subunit
rmAC3148 etfB1		Electron transfer flavoprotein, beta subunit
rmAC3151 ubiE1		Ubiquinone/menaquinone biosynthesis methyltransferase
rmAC3152 atpG	3.6.3.14	Vacuolar (H ⁺)-ATPase G subunit
rmAC3154 atpI	3.6.3.14	V-type ATP synthase subunit I
rmAC3155 atpC1	3.6.3.14	H ⁺ ATP synthase subunit C
rmAC3156 atpE	3.6.3.14	V-type ATP synthase subunit E
rmAC3157 ntpC	3.6.3.14	V-type ATP synthase subunit C
rmAC3158 atpF	3.6.3.14	V-type ATP synthase subunit F
rmAC3159 ntpA	3.6.1.34	V-type sodium ATP synthase subunit A
rmAC3160 ntpB	3.6.1.34	V-type sodium ATP synthase subunit B
rmAC3161 bop		Bacteriorhodopsin
rmAC3162 atpD	3.6.3.14	V-type ATP synthase subunit D
rmAC3164 erf1		Peptide chain release factor eRF1
rmAC3166 minD3		Septum site-determining protein MinC
rmAC3167		Putative DNA binding
rmAC3168 pcbD-2		Probable hydrolase
rmAC3169 argS	6.1.1.19	Arginyl-tRNA synthetase
rmAC3170		M50 metalloproteinase
rmAC3171 usp19		Universal stress protein
rmAC3173 lysS	6.1.1.6	Lysyl-tRNA synthetase
rmAC3174 pyrH	2.7.4.-	Probable uridylate kinase
rmAC3177 thiL		Thiamine monophosphate kinase
rmAC3179 rps19E		30S ribosomal protein S19E
rmAC3183 hisS	6.1.1.21	Histidyl-tRNA synthetase
rmAC3188 truA	4.2.1.70	tRNA pseudouridine synthase A

rmAC3189 pepF	3.4.24.-	Oligoendopeptidase F
rmAC3190 pan1		Proteasome-activating nucleotidase 1 (Proteasome regulatory subunit)
rmAC3191 deoR1		Transcriptional regulator of sugar metabolism
rmAC3194 ugpC		Sn-glycerol-3-phosphate transport system ATP-binding
rmAC3195 malFG-7		Sugar ABC transporter, permease protein
rmAC3196 malFG-8		ABC transporter, permease protein
rmAC3197 malE2		Trehalose/maltose binding protein
rmAC3198 pkn-2		putative cell surface protein OR Serine/threonine protein kinase-related prote
rmAC3199 argDC	4.1.1.19	Pyruvyl-dependent arginine decarboxylase
rmAC3203 infB		Translation initiation factor IF-;
rmAC3204 hcp1		Halocyanin precursor-like
rmAC3205		PRC-barrel domain, possible photosystem reaction centre subunit I
rmAC3207		Ribbon-helix-helix protein, copG family
rmAC3210 pgi	5.3.1.9	Glucose-6-phosphate isomerase
rmAC3214 secF		Protein-export membrane protein SecF
rmAC3215 secD		Protein-export membrane protein SecC
rmAC3216 mhB	3.1.26.4	RNAase HII
rmAC3218 mic		Mechanosensitive ion channel
rmAC3219 BacA		Bacitracin resistance protein
rmAC3225 usp22		Universal stress protein
rmAC3226 ssf		Sodium/solute symporter
rmAC3228 acs5	6.2.1.1	putative Acetyl-coenzyme A synthetase
rmAC3229 boa		Bacterio-opsin activator-like protein
rmAC3230 acs3	6.2.1.1	Acyl-coenzyme A synthetase
rmAC3232 graD4c		Glucose-1-phosphate thymidyltransferase
rmAC3235 glmS2	2.6.1.16	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing]
rmAC3236		Sugar transferase involved in lipopolysaccharide synthesis
rmAC3238 rfh3	2.7.7.24	Glucose-1-phosphate thymidyltransferase
rmAC3239 ugd2	1.1.1.22	UDP-glucose 6-dehydrogenase
rmAC3240		putative membrane-bound metal-dependent hydrolase
rmAC3243 galE7		UDP-glucose 4-epimerase
rmAC3245 galE5	5.3.1.2	UDP-glucose 4-epimerase
rmAC3246 sqdB		UDP-sulfoquinovose synthase
rmAC3249 guaB4		Inosine-5'-monophosphate dehydrogenase related protein I'
rmAC3250 codA		Cytosine deaminase (Cytidine/deoxycytidylate deaminase family protein)
rmAC3251 yjiD3		NADH dehydrogenase
rmAC3258 tgt		Archaeosine tRNA-ribosyltransferase
rmAC3259 galE1	5.1.3.2	UDP-glucose 4-epimerase
rmAC3261 tgt		Archaeosine tRNA-ribosyltransferase
rmAC3264		Putative molybdenum-binding protein (transcriptional regulator)
rmAC3265 pstB3		Phosphate ABC transporter, ATP-binding protein
rmAC3266 modB		Molybdenum ABC transporter, permease protein
rmAC3267		Molybdate Transport Protein
rmAC3268 purQ	6.3.5.3	Phosphoribosylformylglycinamide synthase
rmAC3271		small putative GAF containing sensor
rmAC3272 purU	3.5.1.10;2.1.2.1	Formyltetrahydrofolate deformylase
rmAC3274 pap2b	3.1.3.9	Glucose-6-phosphatase
rmAC3275 purC	6.3.2.6	Phosphoribosylaminoimidazole-succinocarboxamide synthase
rmAC3276 nce3		Na+/Ca2+-exchanging protein
rmAC3280 sop1		Sensory rhodopsin I (SR-I)
rmAC3281 htr		MCP domain signal transducer (soluble)
rmAC3284 ftsZ5		Cell division protein
rmAC3285 nolA		NADH dehydrogenase/oxido-reductase-like protein
rmAC3286 tmk	2.7.4.9	Thymidylate kinase
rmAC3289 trkA3		TRK potassium uptake system protein
rmAC3290 trh5		Transcription regulator
rmAC3295 ykfD		Oligopeptide ABC transporter ATP-binding
rmAC3296 oppD2		Oligopeptide ABC transporter, ATPase component
rmAC3297 oppC		Oligopeptide ABC transporter, permease protein
rmAC3298 dppB		Dipeptide ABC transporter permease
rmAC3299 dppA		Dipeptide ABC transporter dipeptide-binding
rmAC3303 ppiB1	5.2.1.8	Peptidyl-prolyl cis-trans isomerase sir1251
rmAC3304 yfhM		Epoxide hydrolase-related protein
rmAC3306 trpD1	2.4.2.18	Anthranilate phosphoribosyltransferase
rmAC3307 nirD		Heme biosynthesis protein
rmAC3308 hlx5		HoxA-like transcriptional regulator
rmAC3310		transcription regulator
rmAC3312 cyp1	1.14.14.1;1.6.2	Cytochrome P450
rmAC3316 arsC		Putative arsenate reductase
rmAC3320 mhA		ribonuclease H-like protein
rmAC3322		transcription regulator
rmAC3323 ipp	3.6.1.1	Inorganic pyrophosphatase
rmAC3325	3.1.6.-	sulfatase, Arylsulfatase A like
rmAC3326 ftsZ4		Cell division protein
rmAC3329 hcp3		Halocyanin precursor-like
rmAC3334 dnaJ2		Chaperone protein Dna.
rmAC3337		Putative transcriptional regulator
rmAC3339 dnaK		Chaperone protein dnaK
rmAC3340 grpE		Heat shock protein, GrpE protein (HSP-70 cofactor)
rmAC3342 truB	4.2.1.70	tRNA pseudouridine synthase B
rmAC3343 cmk	2.7.4.14	Cytidylate kinase
rmAC3344 htlB		Htr-like protein
rmAC3345 bcp2		Bacterioferritin comigratory protein
rmAC3346 adk	2.7.4.3	Adenylate kinase
rmAC3347 kinA3		Signal-transducing histidine kinase homolog
rmAC3348 thrB	2.7.1.39	Homoserine kinase
rmAC3349 kinA5		Signal-transducing histidine kinase homolog
rmAC3353 noxA2		NADH oxidase
rmAC3360 carB	6.3.5.5	Carbamoylphosphate synthetase, large subunit
rmAC3361 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC3363 carA	6.3.5.5	Carbamoyl-phosphate synthase small chain
rmAC3365 thr3		Transcription regulator
rmAC3370		signal transducing histidine kinase
rmAC3371 yprA2		ATP-dependant helicase
rmAC3372 fecE		Iron (III) ABC transporter ATP-binding protein
rmAC3374 hemU		Iron(III) citrate transport system permease protein FecI
rmAC3375 hemV		Iron (III) ABC transporter ATP-binding
rmAC3378	6.3.3.2	5-formyltetrahydrofolate cyclo-ligase
rmAC3379 htlD		Similar to ESCHERICHIA COLI protein kinase GP:GI-606149 (HTR-like protein)
rmAC3381 lpdA1	1.8.1.4	Dihydrolipoamide dehydrogenase
rmAC3384		DNA binding protein, putative transcriptional regulator
rmAC3385 ntrC		signal receiver domain-protein (PF00072)
rmAC3387 tnp		Transposase
rmAC3391 ppnK	2.7.1.23	Probable inorganic polyphosphate/ATP-NAD kinase
rmAC3392 kaiC2		Circadian regulator
rmAC3394 usp4		Universal stress protein
rmAC3395 usp24		Universal stress protein family

rmAC3399		DNA binding protein, putative transcriptional regulator
rmAC3403 pgm	5.4.2.1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
rmAC3404 kpA	2.7.-.-	Probable RNA 2'-phosphotransferase
rmAC3405		Acetyltransferase (GNAT) family
rmAC3408 nadC1	2.4.2.19	nicotinate-nucleotide pyrophosphorylase
rmAC3409 nadB	1.4.3.16	L-aspartate oxidase
rmAC3410 nadA		Quinolinate synthetase
rmAC3411	3.5.-.-;3.5.1.25	metal dependent Amidohydrolase superfamily protein
rmAC3412 mvaA	1.1.1.34	3-hydroxy-3-methylglutaryl-coenzyme A reductase
rmAC3415		
rmAC3419 icd	1.1.1.42	Isocitrate dehydrogenase
rmAC3420 ans		Asparaginase family protein
rmAC3421 map	3.4.11.18	Methionine aminopeptidase
rmAC3423 hit1		Histidine triad protein
rmAC3424		Rieske [2Fe-2S] domain protein
rmAC3425 cef		Cation efflux system protein (Zinc/cadmium)
rmAC3427 doxD2		terminal quinol oxidase subunit
rmAC3429 deoC1	4.1.2.4	Deoxyribose-phosphate aldolase
rmAC3434 udp1	2.4.2.3	Uridine phosphorylase
rmAC3436 pch2		Potassium channel homolog
rmAC3441 hat5		GNAT family Acetyltransferase
rmAC3442 asbA	3.5.1.1	L-asparaginase
rmAC3447 arsR		transcription regulator
rmAC3451		Putative DNA binding
rmAC3455 ykfB3		Chloromuconate cycloisomerase
rmAC3456 bcp1		Bacterioferritin comigrating protein
rmAC3458		Anhydrase, family 3 protein
rmAC3460 usp26		Universal stress protein
rmAC3462 thrS	6.1.1.3	Threonyl-tRNA synthetase
rmAC3466 arsB		Arsenite transport protein
rmAC3467 pspA1		transcription regulator
rmAC3471 pyrG	6.3.4.2	CTP synthase
rmAC3472 guaA1	6.3.5.2	GMP synthase (glutamine-hydrolyzing)
rmAC3474		Metallo-beta-lactamase superfamily protein
rmAC3476 yafB-5		Oxidoreductase, aldo/keto reductase family
rmAC3480 moaB2		Molybdenum cofactor biosynthesis protein
rmAC3482 ark-6		Putative signal-transducing histidine kinase
rmAC3483 fabG2		3-oxoacyl-[acyl-carrier protein] reductase
rmAC3484 idi	5.3.3.2	Probable isopentenyl-diphosphate delta-isomerase
rmAC3489 pqeE		Coenzyme PQQ synthesis protein
rmAC3490 boa2		Bacterio-opsin activator-like protein
rmAC3494		putative Bacterial regulatory protein, arsR family
rmAC3495 aspB2	2.6.1.1	Aspartate aminotransferase
rmAC3497 yqeF	2.3.1.9	Acetyl-coA acetyltransferase
rmAC3501		transcription regulator
rmAC3504		Flavin containing amine oxidoreductase
rmAC3505 thrC1	4.2.99.2	Threonine synthase
rmAC3506 adh2	1.1.1.1;1.6.5.5	Alcohol dehydrogenase
rmAC3507 usp3		Universal stress protein
rmAC3508 usp7		Universal stress protein
rmAC3509 dnaJ1		chaperone
rmAC3511 nop10P		Nucleolar RNA-binding protein, Nop10p family
rmAC3512 eif2A		Probable translation initiation factor 2 alpha subunit (eIF-2-alpha)
rmAC3513 rps27E		30S ribosomal protein S27e
rmAC3514 rpl44E		50S ribosomal protein L44E
rmAC3518 dgs		Dolichol-P-glucose transferase
rmAC3519		GtrA-like family protein
rmAC3523 apt1	2.4.2.7	Adenine phosphoribosyltransferase
rmAC3529		NADH-Ubiquinone/plastoquinone (complex I)
rmAC3530 nuoL1		NADH dehydrogenase I, L subunit
rmAC3531 ndhG2		NADH dehydrogenase/oxidoreductase
rmAC3533 mnhG1		putative Na/H antiporter
rmAC3535 mnhG2		Multisubunit Na+/H+ antiporter, MnhG subunit
rmAC3537 mnhE		Na/H antiporter subunit
rmAC3539 dfp		Pantothenate metabolism flavoprotein
rmAC3544 htpX4	3.4.24.-	Protease heat shock protein HtpX
rmAC3545 trxB4		Thioredoxin reductase
rmAC3546 pan2		Proteasome-activating nucleotidase 2 (Proteasome regulatory subunit)
rmAC3549		putative HD family metal dependent phosphohydrolase
rmAC3551 trzA4		Chlorohydrolase family protein
rmAC3553 usp18		universal stress protein
rmB0004 cdc6b		Cell division control protein 6 homolog 1 (CDC6 homolog 1)
rmB0006		Acetamidase/formamidase family protein
rmB0008 tnp		Probable transposase for insertion sequence element ISH1
rmB0018 flaA1		Flagellin A precursor
rmB0027		Acetyltransferase (GNAT family)
rmB0028 tnp		Probable transposase for insertion sequence element ISH1
rmB0029 yhcR4		phosphoesterase
rmB0033		Tautomerase
rmB0036 nadC2		Sodium dependent transporter
rmB0038 usp11		Universal stress protein
rmB0041 xseA2	3.1.11.6	Probable exodeoxyribonuclease VII large subunit
rmB0042 exoVIIIB	3.1.11.6	Exonuclease VII small subunit
rmB0046 tnp		phage integrase
rmB0049 apbE		thiamin biosynthesis protein
rmB0052		regulatory protein, arsR family
rmB0062 parA3		Chromosome partitioning protein, ParA family ATPase
rmB0063 cdc6a		Cell division control protein 6 homolog 1 (CDC6 homolog 1)
rmB0070 speE	2.5.1.16	Spermidine synthase
rmB0074		transcription regulator
rmB0075		glycosyl transferase
rmB0083 ski-1	2.4.1.-	Putative 2-component system sensor kinase
rmB0087 ski-2		Sensor protein
rmB0089		transcription regulator
rmB0092 aldY7	1.2.1.3	Aldehyde dehydrogenase
rmB0094 tnp		Putative transposase (VNG6486H) (VNG6040H)
rmB0095 aldY6	1.2.1.3	Aldehyde dehydrogenase
rmB0097 hcp7		Halocyanin precursor-like
rmB0102 suhB2	3.1.3.25	Inositol-1-monophosphatase
rmB0103 rbsB-3		Putative ABC transporter, substrate binding protein
rmB0104 malFG-9		Sugar ABC transport system, permease protein
rmB0105 malFG-10		Sugar ABC transporter, permease protein
rmB0106 ugpC2		Sugar ABC transporter, ATP-binding subunit
rmB0107		very putative carbohydrate responsive phospholipase
rmB0112		putative DNA binding domain
rmB0113 gatA2	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit A
rmB0122 tnp		Probable transposase for insertion sequence element ISH1

rmB0133		putative redox sensing protein
rmB0143		Probable transposase
rmB0146		Putative ISH8 transposase (VNG6331H
rmB0148		Transcription initiation factor IIB (TFIIB
rmB0156		putative light and redox sensing histidine kinase
rmB0157		padR like DNA binding protein
rmB0167		Calcium-binding protein homolog
rmB0171		putative acyltransferase
rmB0175	1.1.1.205	Inosine Monophosphate Dehydrogenase
rmB0180		putative 22-domain light- and oxygen-sensing histidine kinase
rmB0183		Transposase
rmB0187		putative cupir
rmB0192		Universal stress protein 1
rmB0197	1.8.1.4	Dihydrolipoamide dehydrogenase
rmB0198		Dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E
rmB0199	1.2.4.1	Pyruvate Dehydrogenase
rmB0200	1.2.4.1	Pyruvate dehydrogenase E1 component, alpha subunit
rmB0202		Branched-chain amino acid ABC transporter, ATP-binding protein
rmB0203		Branched-chain amino acid ABC transporter, ATP-binding protein
rmB0204		High-affinity branched-chain amino acid transport protein
rmB0205		Branched-chain amino acid ABC transporter, permease protein
rmB0206	2.6.1.1	Aspartate aminotransferase
rmB0207		putative extracellular ligand binding protein
rmB0209	4.1.3.18	Acetolactate synthase large subunit
rmB0210		UDP-glucose 4-epimerase
rmB0212		Aminopeptidase
rmB0214		bacterial luciferase family monooxygenase
rmB0215		thioesterase
rmB0217	6.2.1.1	Acyl-coenzyme A synthetase
rmB0218		F420-dependent NADP reductase
rmB0219		Succinate-semialdehyde dehydrogenase
rmB0221		putative metal dependent phosphohydrolase
rmB0222		Transcription regulator KdgF
rmB0224		Branched-chain amino acid ABC transporter, ATP-binding protein
rmB0225		Branched-chain amino acid ABC transporter, ATP-binding protein
rmB0227		Branched-chain amino acid ABC transporter, permease protein
rmB0229	3.5.1.11	Penicillin acylase (Penicillin amidase)
rmB0230	3.5.1.11	Penicillin G amidase
rmB0231	6.2.1.30	Phenylacetyl-CoA ligase
rmB0235		Transcriptional regulator, IclR family
rmB0237	4.2.1.17	Enoyl-CoA hydratase
rmB0238	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase
rmB0240	2.3.1.9	Acetyl-CoA acetyltransferase
rmB0241	2.3.1.41	Acyl carrier protein synthase
rmB0242	2.3.1.9;2.3.1.11	3-ketoacyl-CoA thiolase
rmB0243		Phenylacetyl-coenzyme A ligase
rmB0244		Phenylacetic acid degradation protein Paa
rmB0245		Monoamine oxidase regulatory protein
rmB0246	1.2.1.3	Aldehyde dehydrogenase
rmB0249		Phenylacetic acid degradation protein PaaC
rmB0250		PacF protein
rmB0252		Phenylacetic acid degradation protein PaaC
rmB0253		transcription regulator
rmB0254	4.2.1.17	Enoyl-CoA hydratase
rmB0255		amidohydrolase
rmB0257	4.1.3.6;4.1.2.2	Citrate lyase, beta chain
rmB0259	2.1.1.79	Cyclopropane-fatty-acyl-phospholipid synthase
rmB0260		Molybdenum cofactor biosynthesis protein
rmB0261		Propionyl-CoA carboxylase, beta subunit
rmB0263	6.4.1.16	Carbamoyl phosphate synthase L chain
rmB0264	1.3.99.3	Acyl-CoA dehydrogenase
rmB0265	6.2.1.1	Acyl-coenzyme A synthetase
rmB0267		3-octaprenyl-4-hydroxybenzoate carboxy-lyase
rmB0270		Zinc-transporting ATPase
rmB0275		putative-iron binding protein
rmB0277		thioredoxin
rmB0283	6.3.5.2	GMP synthase
rmB0290		Sodium-dependent phosphate transporter
rmB0291		Universal stress protein
rmB0295		gaf only light sensing histidine kinase
rmB0296		Signal-transducing histidine kinase homolog
rmB0297		Two-component response regulator
rmB0299		nineteen domain light and oxygen sensing histidine kinase
rmB0301		HoxA-like transcriptional regulator
rmB0302		Response regulator
rmB0303		Putative ISH8 transposase
rmB0309	2.3.1.9	3-ketoacyl-CoA thiolase
rmB0310		Fmn oxidoreductase protein
rmB0311		Glycerol-3-phosphate-binding protein
rmB0312		ABC transporter, permease protein
rmB0314		Sn-glycerol-3-phosphate transport system permease
rmB0315		Sugar ABC transporter, ATP-binding protein
rmB0316	3.1.4.46	Glycerophosphoryl diester phosphodiesterase
rmB0317		unknown L-arabinose operon protein AraI
rmB0318		Magnesium transporter accessory protein
rmB0319		ABC transporter, phosphate-binding protein
rmB0320		Phosphonate ABC transporter, ATP-binding protein
rmB0321		Phosphonate ABC transporter permease protein
rmB0322		Phosphonate ABC transporter, permease protein
rmB0324		Fad-dependent monooxygenase
rmB0325		Cell division protein
rmB0326		2', 3'-cyclic nucleotide 2'-phosphodiesterase
rmB0335		parA/minD like Bacterial Cell Division Regulator

Table C

Genes implicated in denitrification

ORF	GENE	Function
rrnAC2619	<i>amt</i>	Ammonium transporter
rrnAC2779	<i>asnC1</i>	Transcription regulator, AsnC family
rrnAC2622	<i>asnC4</i>	Transcription regulator, AsnC family
rrnAC3005	<i>cobH</i>	Precorrin-3B C17-methyltransferase
rrnAC1215	<i>dmsA</i>	Dimethylsulfoxide reductase
pNG7151	<i>fdhA</i>	Formate dehydrogenase alpha subunit
pNG7318	<i>fdnG</i>	Formate dehydrogenase alpha subunit
rrnAC2621	<i>glnB</i>	Nitrogen regulatory protein P-II
rrnAC1252	<i>lrp</i>	Leucine responsive regulatory protein
rrnAC1186	<i>moaE</i>	Molybdenum cofactor biosynthesis protein
rrnAC1317	<i>mobA</i>	Molybdopterin-guanine dinucleotide biosynthesis protein A
rrnAC1705	<i>moaE1</i>	Molybdenum cofactor biosynthesis protein
rrnAC2486	<i>nadE1</i>	NH(3)-dependent NAD(+) synthetase
rrnAC2627	<i>narB</i>	Nitrate reductase
rrnAC1199	<i>narG</i>	Nitrate reductase, alpha chain
rrnAC1200	<i>narH</i>	Nitrate reductase, beta chain
rrnAC1204	<i>narJ</i>	Chaperone protein
rrnAC2625	<i>nirA1</i>	Ferredoxin-nitrite reductase
rrnAC2992	<i>nirA2</i>	Ferredoxin-nitrite reductase
rrnAC2853	<i>nirK</i>	nitrite reductase, copper containing
rrnAC0810	<i>nitA</i>	Nitrilase
rrnAC0392	<i>nosD2</i>	copper binding protein
rrnAC0396	<i>nosY1</i>	ABC-type transport system involved in multi-copper enzyme maturation, permease component
rrnAC3052	<i>nosY2</i>	ABC-type transport system involved in multi-copper enzyme maturation, permease component
rrnAC0390	<i>nosZ</i>	Nitrous-oxide reductase
pNG7136	<i>noxA1</i>	NADH oxidase
rrnAC3353	<i>noxA2</i>	NADH oxidase
rrnAC0389	<i>pcy</i>	copper-binding plastocyanin like protein
rrnAC0616	<i>pecE</i>	Pectinesterase
rrnAC1196	<i>petB2</i>	Cytochrome B6
pNG6034	<i>pNG6034</i>	transcription regulator
pNG6047	<i>pNG6047</i>	putative metal-binding transcription regulator
rrnAC1206	<i>prp</i>	protein phosphatase
rrnAC2829	<i>rpoE'</i>	DNA-directed RNA polymerase subunit E'
rrnAC0391	<i>rrnAC0394</i>	ABC transporter, ATP-binding protein
rrnAC0394	<i>rrnAC1655</i>	ABC transporter, ATP-binding protein
rrnAC0811	<i>rrnAC2084</i>	ABC transporter, ATP-binding protein
rrnAC1194	<i>rrnAC1195</i>	Putative Rieske iron-sulfur protein
rrnAC1195	<i>rrnAC0391</i>	unknown
rrnAC1197	<i>rrnAC0811</i>	unknown
rrnAC1202	<i>rrnAC1194</i>	unknown
rrnAC1203	<i>rrnAC1197</i>	unknown
rrnAC1205	<i>rrnAC1202</i>	unknown
rrnAC1655	<i>rrnAC1203</i>	unknown
rrnAC2084	<i>rrnAC1205</i>	putative ABC-type phosphate transport system, permease component
rrnAC2699	<i>rrnAC2699</i>	putative inosine monophosphate dehydrogenase
rrnAC3053	<i>rrnAC3053</i>	ABC transporter, ATP-binding protein
rrnAC2073	<i>trp2</i>	ABC transporter, ATP-binding protein
rrnAC0479	<i>trp5</i>	ABC transporter, ATP-binding protein
rrnAC0450	<i>yjiD1</i>	NADH dehydrogenase
rrnAC1301	<i>yjiD2</i>	NADH dehydrogenase

Table D

Genes implicated in arginine catabolism

ORF	GENE	Function
rrnAC2672	arcB	Ornithine carbamoyltransferase
rrnAC0453	arg1	Arginase
rrnAC0383	arg2	Arginase
rrnAC0078	argB1	Acetylglutamate kinase
rrnAC2676	argB2	Acetylglutamate kinase
rrnAC2678	argC	N-acetyl-gamma-glutamyl-phosphate reductase
rrnAC2675	argD	Acetylornithine aminotransferase
rrnAC2683	argG	Argininosuccinate synthase
rrnAC2681	argH	Argininosuccinate lyase
rrnAC0933	argK	ArgK protein
rrnAC3363	carA	Carbamoyl-phosphate synthase small chain
rrnAC3360	carB	Carbamoylphosphate synthetase, large subunit
rrnAC1929	eif5A	Translation initiation factor 5A (eIF-5A) (Hypusine-containing protein)
rrnAC0384	gdhA1	NADP-specific glutamate dehydrogenase
rrnAC0775	gdhA2	NAD(P)-specific Glutamate dehydrogenase
rrnAC2674	gltCP	Glutamate Carboxypeptidase
pNG7157	gudB	NAD(P)-specific glutamate dehydrogenase
rrnAC0637	mcmA1	Methylmalonyl-CoA mutase, subunit alpha
rrnAC1275	mcmA2	Methylmalonyl-CoA mutase, subunit alpha
rrnAC0934	mcmA3	Putative methylmalonyl-CoA mutase
rrnAC0077	mvk	Mevalonate kinase
rrnAC2426	nusA2	Transcription termination factor NusA
rrnAC2679	rimK	Ribosomal protein S6 modification protein
rrnAC2829	rpoE'	DNA-directed RNA polymerase subunit E'
rrnAC2460	rrnAC2460	Unknown
rrnB0068	rrnB0068	Unknown
rrnB0069	rrnB0069	Unknown
rrnAC1927	speB1	Agmatinase
rrnB0070	speE	Spermidine synthase
rrnAC0710	trpD2	Anthranilate synthase, component II
pNG7325	trpG2	Anthranilate synthase component II
pNG7125	ureA	Urease gamma subunit
pNG7123	ureB	Urease beta subunit
pNG7124	ureC	Urease alpha subunit
pNG7127	ureD	Urease accessory protein UreD
pNG7128	ureE	Urease accessory protein UreE
pNG7129	ureF	Urease accessory protein F, UreF
pNG7126	ureG	Urease accessory protein UreG
rrnAC2873	potC2	Spermidine/putrescine ABC transporter permease
rrnAC0908	potA4	Spermidine/putrescine ABC transporter, ATP-binding protein
rrnAC2870	potA2	Spermidine/putrescine ABC transporter, ATP-binding protein
rrnAC2868	potD2	Spermidine/putrescine ABC transporter, spermidine/putrescine binding protein
pNG7349	potB1	Spermidine/putrescine ABC transporter, permease protein
pNG7347	potA1	Putrescine ABC transporter, ATP-binding protein
rrnAC0145	potA3	Spermidine/putrescine ABC transporter, ATP-binding protein
rrnAC2872	potB2	Spermidine/putrescine ABC transporter, permease protein
pNG7350	potC1	Spermidine/putrescine ABC transporter, permease protein (PotC)
pNG7067	speB2	Agmatinase
rrnAC0223	camH3	Creatinine amidohydrolase
pNG7096	camH1	Creatinine amidohydrolase
pNG7341	camH2	Creatinine amidohydrolase
rrnAC0198	odc	Ornithine Decarboxylase
rrnAC2941	ocd2	Ornithine cyclodeaminase
rrnAC0227	ocd3	Ornithine cyclodeaminase
rrnAC0038	ocd1	Ornithine cyclodeaminase

Table E

Proteins with PAS, PAC, GAF, and Histidine Kinase domains

PF00015: Methyl accepting chemotaxis (MCP)

Gene Name	start	stop	e-value
rmAC0013	469	757	2.00E-59
rmAC2760	475	763	5.90E-56
rmAC0976	338	628	3.00E-56
rmAC2425	484	772	9.70E-64
rmAC0701	508	796	1.30E-63
pNG7084	337	630	1.20E-47
rmAC1752	376	636	4.40E-39
rmAC0183	235	492	1.20E-46
rmAC0552	163	437	3.90E-42
rmAC2728	466	756	1.00E-54
rmAC2495	259	547	5.30E-59
rmAC3281	137	395	9.10E-63
rmAC0404	161	432	7.30E-23
rmAC0942	155	443	3.80E-58
rmAC0371	420	619	0.0078
rmAC2091	70	327	5.90E-48
rmAC2633	14	288	7.80E-24
rmAC2618	48	303	7.40E-23

PF00512: Histidine kinase (N-terminal) domain

Gene Name	start	stop	e-value
pNG7156	1100	1161	1.50E-16
rmAC1626	731	792	2.10E-13
rmAC3379	451	514	6.00E-16
rmAC0848	546	607	2.30E-14
rmAC3440	341	409	0.00036
rmAC2692	487	546	7.50E-11
rmAC2533	427	488	3.70E-17
rmAC3361	804	865	9.50E-17
rmAC0086	583	647	4.90E-12
rmAC0574	404	465	1.50E-13
rmAC0075	524	585	5.40E-19
rmAC0991	430	494	1.60E-13
rmAC2372	427	488	5.80E-16
rmAC2416	831	892	2.60E-13
rmAC2219	111	170	1.30E-11
rmAC1806	393	454	3.00E-13
rmAC0247	177	238	5.20E-12
rmAC2044	532	593	9.60E-15
pNG7155	438	499	2.20E-18
rmAC3050	628	689	2.40E-07
rmAC0410	417	484	7.30E-07
rmAC0487	256	319	2.10E-14
rmAC2477	146	207	6.40E-12
rmB0299	1746	1814	7.80E-10
rmAC1391	201	266	7.00E-13
rmB0156	750	814	0.00049
rmAC1096	251	310	1.10E-08
rmAC2461	159	220	6.00E-12
rmAC0477	167	228	4.20E-14
rmAC0988	435	505	6.20E-17
rmAC1114	349	410	1.40E-15
rmB0296	144	208	0.0003
rmB0180	2097	2165	0.0076
rmAC0475	135	191	0.00014
rmAC3370	178	242	0.00859999
rmAC0789	358	420	2.30E-05
rmAC2945	254	313	0.0014
rmAC1495	1082	1147	9.10E-05
rmAC3482	348	409	0.00085
rmAC0301	251	310	0.0018
rmB0133	477	541	0.0019
rmAC0413	307	367	0.0027
rmAC0794	308	369	4.40E-13
rmB0295	444	509	0.0011
rmAC0964	176	237	0.0033
rmAC1486	194	255	0.0022
rmAC0412	144	204	0.0057
rmAC1501	378	448	0.0005
rmAC3349	863	927	0.039
rmAC1693	107	169	0.0076
rmAC3347	128	193	0.0093
rmAC2997	147	211	0.0052

PF02518: Histidine kinase (C-terminal) domain

Gene Name	start	stop	e-value
pNG7156	1199	1299	4.90E-21
rmAC0456	33	179	4.90E-36
rmAC0457	42	191	3.30E-17
rmAC2205	392	534	1.40E-32
rmAC2550	48	161	0.00011
rmAC1626	829	934	1.70E-28
rmAC3379	552	670	1.70E-28
rmAC0848	644	745	2.70E-29

PF00072: Response regulator receiver domain

Gene Name	start	stop	e-value
pNG7156	12	133	5.30E-12
pNG7159	11	131	8.20E-07
rmAC1626	100	224	8.30E-21
rmAC2204	5	135	6.60E-25
rmAC3379	37	157	3.20E-10
rmAC0848	8	129	7.80E-22
rmAC2533	5	129	2.20E-11
rmAC3361	5	126	4.80E-22
rmAC0574	19	138	0.0014
rmAC0075	13	133	1.60E-14
rmAC2372	8	132	1.10E-23
rmAC2416	21	145	2.90E-26
rmAC1806	8	136	2.10E-18
rmAC2044	8	129	8.90E-29
pNG7155	4	124	3.60E-25
rmAC3050	113	234	3.50E-22
pNG7223	22	146	3.50E-23
rmAC0487	7	132	6.70E-26
rmAC0356	9	133	1.10E-23
rmAC1142	4	128	9.40E-27
rmB0296	7	133	3.20E-15
rmAC2109	7	132	7.90E-22
rmAC0411	10	140	4.20E-17
rmAC2211	9	130	1.60E-26
rmAC0339	9	130	9.90E-24
rmAC0475	6	126	0.00088
rmAC0674	63	187	1.90E-22
rmAC2194	2	119	2.20E-35
rmAC1118	7	121	8.00E-27
rmAC0536	24	138	3.60E-19
rmAC1495	8	120	7.40E-05
rmAC1663	74	188	0.059
rmAC3308	7	121	2.50E-22
rmAC0301	4	117	0.00096
rmAC0794	5	131	0.00065
rmAC0794	5	131	0.0024
pNG4019	9	126	2.10E-22
rmAC0412	7	133	3.40E-14
rmAC0361	5	119	2.60E-13
rmB0301	119	231	1.10E-22
rmAC3271	5	124	3.10E-05
rmB0297	6	135	8.20E-14
rmAC1494	3	122	9.30E-19
rmAC2168	4	116	1.80E-11

PF00672: HAMP domain

Gene Name	start	stop	e-value
rmAC0013	291	360	3.60E-16
rmAC2760	297	366	1.10E-16
rmAC2425	280	350	3.80E-10
rmAC0701	304	374	4.80E-12
rmAC2728	288	357	5.40E-15
rmAC2495	60	130	3.80E-08
rmAC0371	331	399	4.20E-10
rmB0156	251	319	0.0001
rmAC0988	341	410	5.90E-18
rmAC0558	53	122	1.00E-05

PF00785: PAC domain

Gene Name	start	stop	e-value
pNG7156	346	385	0.0058
pNG7156	635	677	0.0014
pNG7156	891	933	1.80E-07
rmAC1626	310	352	2.30E-05
rmAC1626	435	477	0.0017
rmAC1626	559	601	2.40E-09
rmAC1626	683	725	4.00E-05
rmAC0848	330	372	8.00E-19
rmAC2692	282	323	1.60E-10
rmAC2533	372	414	4.70E-08
rmAC3361	211	252	0.0032
rmAC3361	493	536	1.50E-07
rmAC3361	620	662	8.00E-05
rmAC3361	753	791	0.014
rmAC0086	293	335	0.023
rmAC0086	404	445	0.079
rmAC0086	528	570	5.70E-11
rmAC0574	225	266	1.20E-12
rmAC0574	349	391	9.40E-07
rmAC0075	222	263	0.0037
rmAC0075	346	388	2.20E-17
rmAC0075	471	511	0.0069
rmAC0991	376	417	0.0047
rmAC2416	229	271	0.004

PF02518: Histidine kinase (C-terminal) domain cont.

Gene Name	start	stop	e-value
rmAC3440	446	545	0.009
rmAC2692	584	684	1.30E-21
rmAC2533	525	645	5.80E-30
rmAC3361	902	1004	5.20E-27
rmAC0086	685	800	7.90E-29
rmAC0574	502	628	1.50E-18
rmAC0075	622	722	4.10E-25
rmAC0991	531	635	3.60E-28
rmAC2372	525	641	1.30E-26
rmAC2416	929	1045	1.60E-24
rmAC2219	209	324	1.20E-27
rmAC1806	491	624	4.60E-24
rmAC0247	275	396	8.90E-20
rmAC2044	636	781	6.90E-23
pNG7155	542	646	2.10E-24
rmAC3050	732	835	9.50E-28
rmAC0410	526	636	8.30E-39
rmAC0487	357	459	7.00E-17
rmAC2477	246	347	5.80E-24
rmB0299	1856	1966	1.80E-36
rmAC1391	303	405	1.30E-24
rmB0156	856	963	1.60E-23
rmAC1096	349	449	3.50E-19
rmAC2461	257	373	4.20E-27
rmAC0477	265	396	3.00E-27
rmAC0988	542	642	8.70E-27
rmAC1114	446	575	1.20E-21
rmB0296	252	366	6.10E-25
rmB0180	2203	2306	1.50E-14
rmAC0475	231	329	5.90E-18
rmAC3370	284	391	1.20E-30
rmAC0789	461	569	2.30E-14
rmAC2945	360	462	3.90E-14
rmAC1495	1187	1293	7.30E-24
rmAC3482	451	561	6.00E-14
rmAC0301	347	447	6.50E-17
rmB0133	581	684	9.30E-21
rmAC0413	413	519	2.60E-27
rmAC2789	451	553	5.10E-22
rmAC0130	360	465	2.20E-20
rmB0295	550	656	3.60E-21
rmAC2616	322	427	3.70E-22
rmAC0964	278	385	2.50E-19
rmAC1486	296	404	3.30E-15
rmAC0412	249	355	1.30E-24
rmAC1501	488	595	1.80E-11
rmAC2694	226	331	6.70E-20
rmAC3349	969	1075	2.10E-23
rmAC1693	216	320	2.40E-08
rmAC3347	234	342	8.00E-16
rmAC1346	299	406	4.30E-14
rmAC2997	252	358	7.80E-18
rmAC2337	262	409	3.40E-14

PF00989: PAS domain

Gene Name	start	stop	e-value
pNG7156	146	208	0.016
pNG7156	689	758	0.015
pNG7156	820	881	2.90E-09
rmAC1626	364	426	0.0069
rmAC1626	485	547	7.30E-11
rmAC1626	609	671	1.50E-13
rmAC1752	163	228	0.0001
rmAC3379	161	229	0.067
rmAC0848	135	200	3.30E-06
rmAC0848	255	321	0.00036
rmAC2692	210	273	2.10E-08
rmAC2533	298	363	0.011
rmAC3361	139	201	4.30E-05
rmAC3361	548	612	0.019
rmAC0404	24	87	2.10E-11
rmAC0086	230	292	1.80E-09
rmAC0086	457	518	9.10E-09
rmAC0574	278	340	0.00093
rmAC0075	271	337	0.0021
rmAC0075	400	462	2.20E-07
rmAC0991	195	254	0.083
rmAC0991	303	365	7.20E-12
rmAC2372	142	204	0.0016
rmAC2416	457	519	1.60E-07
rmAC1806	142	204	0.032
rmAC1687	141	203	2.70E-08
rmAC2044	142	205	0.081
rmAC2044	275	339	1.90E-06
rmAC2044	401	463	3.40E-08
pNG7155	312	374	3.40E-05

PF00785: PAC domain cont.

Gene Name	start	stop	e-value
rmAC2416	528	569	7.20E-06
rmAC2416	654	696	0.00015
rmAC2416	777	818	7.10E-09
rmAC1806	214	256	1.20E-07
rmAC1806	340	380	6.10E-05
rmAC1687	214	255	0.04
rmAC2044	221	263	1.00E-05
rmAC2044	349	389	1.20E-08
pNG7155	383	425	1.90E-08
rmAC3050	324	366	1.80E-05
rmAC0410	81	121	0.0024
rmAC0356	211	248	0.089
rmAC0356	334	375	0.0084
rmAC2477	93	133	0.0015
rmB0299	200	242	8.20E-05
rmB0299	741	778	0.034
rmB0299	984	1024	0.041
rmB0299	1109	1150	5.90E-09
rmB0299	1237	1280	9.00E-10
rmB0299	1366	1407	7.50E-08
rmAC1391	147	188	0.094
rmB0156	411	450	0.00075
rmAC1096	79	119	0.091
rmAC1096	197	238	0.00028
rmAC2461	105	146	3.10E-06
rmAC1142	213	253	0.074
rmB0180	365	405	0.00042
rmB0180	489	529	0.088
rmB0180	729	771	6.80E-17
rmB0180	1024	1066	6.50E-09
rmB0180	1151	1195	0.00073
rmB0180	1277	1320	3.20E-10
rmB0180	1533	1575	6.50E-13
rmB0180	1810	1852	0.0022
rmB0180	1929	1970	0.00029
rmB0180	2050	2091	0.00025
rmAC1495	348	390	0.0062
rmAC1495	636	678	5.40E-08
rmAC1495	908	948	0.00011
rmAC1663	396	438	8.20E-09
rmAC1663	525	568	4.40E-12
rmAC3482	300	342	9.70E-05
rmAC0413	260	301	0.041
rmAC0130	207	249	1.40E-08
rmAC1501	210	252	0.015
rmAC1501	332	372	0.085
rmAC3347	82	122	4.20E-05
pNG7167	142	184	0.0029

PF01590: GAF domain

Gene Name	start	stop	e-value
pNG7156	412	548	3.20E-11
pNG7156	955	1085	0.071
pNG7159	401	532	1.10E-05
pNG7159	577	718	6.00E-07
rmAC3379	299	436	1.50E-09
rmAC0848	394	524	1.70E-05
rmAC2692	345	472	0.0024
rmAC2533	159	287	6.40E-07
rmAC3361	274	404	2.20E-09
rmAC0086	447	591	0.082
rmAC2372	276	405	0.0014
rmAC2416	305	443	0.0016
rmAC0247	32	162	1.30E-07
rmAC1687	446	585	0.0017
pNG7155	155	298	1.60E-11
pNG7223	173	315	2.80E-10
pNG7223	344	481	1.10E-11
pNG7223	675	816	0.035
rmAC0410	261	395	0.0066
rmAC0356	402	540	0.0019
rmB0299	269	405	4.70E-10
rmB0299	1434	1570	5.00E-06
rmB0299	1594	1724	2.00E-06
rmB0156	600	735	0.041
rmAC2070	165	296	1.20E-06
rmB0180	149	283	2.50E-07
rmB0180	798	939	0.0017
rmB0180	1597	1722	0.03
rmAC2211	167	298	5.60E-07
rmAC0019	152	288	3.70E-15
rmAC0019	445	582	0.013
rmAC1495	417	552	0.00055
rmAC1495	700	824	1.50E-08
rmAC1663	600	743	0.00047
rmAC0413	36	171	2.80E-05

PF00989: PAS domain cont.

Gene Name	start	stop	e-value
rmAC3050	374	439	0.038
rmAC0410	8	72	1.30E-06
rmAC0410	133	197	0.027
rmAC0487	135	197	4.00E-05
rmAC0356	139	205	0.00014
rmAC0356	260	324	0.045
rmAC2477	20	85	0.055
rmB0299	10	73	0.077
rmB0299	127	187	6.50E-10
rmB0299	419	481	0.014
rmB0299	545	608	0.0057
rmB0299	669	731	1.90E-05
rmB0299	915	975	7.40E-05
rmB0299	1162	1226	2.20E-05
rmB0156	336	402	2.00E-05
rmAC1096	10	72	3.80E-08
rmAC1096	124	187	0.011
rmAC2461	34	96	3.80E-08
rmAC1114	231	293	0.067
rmAC1142	138	203	0.022
rmAC1142	262	327	2.50E-08
rmAC2070	6	66	0.078
rmB0180	293	354	1.40E-08
rmB0180	413	475	1.90E-09
rmB0180	654	720	0.0002
rmB0180	953	1014	0.05
rmB0180	1332	1395	4.80E-14
rmB0180	1458	1523	0.0056
rmB0180	1736	1800	0.00046
rmB0180	1857	1919	0.00065
rmB0180	1975	2041	0.038
rmAC2211	312	375	0.024
rmAC0339	143	206	4.40E-09
rmAC0674	197	258	0.00011
rmAC0019	295	358	0.037
rmAC1495	148	210	2.70E-07
rmAC1495	276	340	3.90E-05
rmAC1495	562	624	4.10E-10
rmAC1495	834	896	0.014
rmAC1495	960	1026	0.058
rmAC1663	322	384	2.20E-06
rmAC1663	450	514	0.054
rmB0133	347	410	1.50E-07
rmAC2789	240	301	0.0036
rmAC0130	135	197	2.70E-11
rmAC2616	103	166	0.0022
rmAC1486	77	138	4.20E-11
rmAC1501	131	186	0.011
rmAC3349	598	662	0.023
rmAC3347	7	70	0.026

PF01590: GAF domain cont.

Gene Name	start	stop	e-value
rmAC0794	158	286	0.00059
rmB0295	141	273	0.00018
rmAC0964	28	151	0.011
rmAC3271	150	281	1.10E-13

Table F

A. Transcriptional regulators deciphered from Rosetta matches

"Winged helix" repressor DNA binding domain (HTH)

Gene name	CATH I.D., Z-score, Probability
rrnB0084	1.10.10.10,6.3166937,0.402512 1.10.10.10,7.0476996,0.428564 1.10.10.10,7.1844317,0.456303
rrnAC0583	1.10.10.10,6.4040300,0.325012 1.10.10.60,6.5944764,0.339512
rrnB0007	1.10.10.10,7.1844317,0.350016
rrnAC1147	1.10.10.10,7.5344570,0.337471
rrnAC0625	1.10.10.10,7.2360304,0.430226 1.10.10.10,5.6776870,0.325134 1.10.10.10,7.4903582,0.448287
rrnAC0116	1.10.10.10,7.5344570,0.337471
rrnAC3417	1.10.10.10,7.5404154,0.329536 1.10.472.10,8.7259440,0.37916
pNG2009	1.10.10.10,7.7678901,0.389429
pNG3007	1.10.10.10,7.7774391,0.333087
rrnAC0025	1.10.10.10,7.9502897,0.387222 1.10.10.10,7.9038409,0.404731
rrnAC2281	1.10.10.10,7.9751366,0.362329
rrnAC2396	1.10.10.10,8.1009524,0.337038
rrnAC2591	1.10.10.10,8.2136530,0.438271
rrnAC2686	1.10.10.10,8.3831686,0.358225
pNG4044	1.10.10.10,8.7094984,0.397792
pNG1037	1.10.10.10,8.7432908,0.460002
rrnAC0483	1.10.10.10,8.8973467,0.439155

Homeodomain-like

Gene name	CATH I.D., Z-score, Probability
rrnAC2251	1.10.10.60,6.3031714,0.391845
pNG7309	1.10.10.60,6.5540825,0.302340
pNG5134	1.10.10.60,6.6595357,0.319028
rrnAC0363	1.10.10.60,6.7499816,0.338069
rrnB0089	1.10.10.60,7.0747325,0.378860 1.10.10.60,7.2983001,0.394145
rrnAC1712	1.10.10.60,7.1725275,0.352306
rrnAC1994	1.10.10.60,7.7778424,0.326608
pNG6037	1.10.10.60,8.1240629,0.387675

Probable RNA binding domain

Gene name	CATH I.D., Z-score, Probability
rrnAC0095	3.30.70.330,6.9361750,0.309190 3.30.70.330,8.5533252,0.410636

COMPLEX (TRANSCRIPTION REGULATION/DNA) (Nuclear factor-appa-b p52; Transcription factor nfkb)

Gene name	CATH I.D., Z-score, Probability
rrnAC3499	1.10.15.20,5.9527819,0.345372

lambda repressor-like DNA-binding domains

Gene name	CATH I.D., Z-score, Probability
rrnAC0288	1.10.260.10,6.3604714,0.307902
pNG7299	1.10.260.10,6.6220014,0.382065 1.10.472.10,6.8042272,0.316579

Cyclin A domain 1 like, TFIIB-like

Gene name	CATH I.D., Z-score, Probability
rrnAC2059	1.10.472.10,10.003618,0.428198
rrnAC2987	1.10.472.10,10.668899,0.561162
rrnAC3319	1.10.472.10,10.888133,0.450718
rrnAC1658	1.10.472.10,8.1323365,0.334127
rrnB0185	1.10.472.10,8.1439717,0.347310
rrnAC1963	1.10.472.10,8.2489460,0.400757
rrnAC3359	1.10.472.10,8.3102932,0.348436
rrnB0114	1.10.472.10,8.4204319,0.357316
pNG6053	1.10.472.10,8.4762485,0.385119
rrnB0328	1.10.472.10,8.5239949,0.341826
rrnAC3470	1.10.472.10,8.8502856,0.383714
pNG3005	1.10.472.10,8.8508538,0.322573
rrnAC2135	1.10.472.10,8.8552536,0.357576

Classic zinc finger

Gene name	CATH I.D., Z-score, Probability
rrnAC0582	3.30.160.60,6.7390678,0.339400

lambda repressor-like DNA-binding domains

Gene name	CATH I.D., Z-score, Probability
rrnAC0288	1.10.260.10,6.3604714,0.307902
pNG7299	1.10.260.10,6.6220014,0.382065 1.10.472.10,6.8042272,0.316579

Cyclin A domain 1 like, TFIIB-like

Gene name	CATH I.D., Z-score, Probability
rrnAC2059	1.10.472.10,10.003618,0.428198
rrnAC2987	1.10.472.10,10.668899,0.561162
rrnAC3319	1.10.472.10,10.888133,0.450718
rrnAC1658	1.10.472.10,8.1323365,0.334127
rrnB0185	1.10.472.10,8.1439717,0.347310
rrnAC1963	1.10.472.10,8.2489460,0.400757
rrnAC3359	1.10.472.10,8.3102932,0.348436
rrnB0114	1.10.472.10,8.4204319,0.357316
pNG6053	1.10.472.10,8.4762485,0.385119
rrnB0328	1.10.472.10,8.5239949,0.341826
rrnAC3470	1.10.472.10,8.8502856,0.383714
pNG3005	1.10.472.10,8.8508538,0.322573
rrnAC2135	1.10.472.10,8.8552536,0.357576

Classic zinc finger

Gene name	CATH I.D., Z-score, Probability
rrnAC0582	3.30.160.60,6.7390678,0.339400

B. Transcriptional regulators deciphered from Pfam matches

PF00096: C2H2 zinc finger

Gene name	start	stop	bitScore	e-value
rrnAC0806	13	35	18.2	0.017
pNG2032	13	40	12.4	0.43
rrnAC0476	3	25	15.9	0.084
rrnAC1397	32	55	23	0.00063
rrnAC2751	4	27	18.1	0.019

PF00320: GATA zinc finger

Gene name	start	stop	bitScore	e-value
pNG3023	60	96	-9.7	0.4

PF00356: Bacterial regulatory proteins, lacI family (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC0312	100	127	11.9	0.087
rrnAC2622	17	44	8.2	0.26

PF00440: Bacterial regulatory proteins, tetR family (HTH):

Gene name	start	stop	bitScore	e-value
rrnAC2777	10	56	42.8	6.80E-10
pNG5131	1	46	43.6	3.90E-10
pNG7180	15	61	40.5	3.40E-09
pNG7308	16	62	43.8	3.40E-10
pNG5071	16	62	24.2	0.00015
rrnAC1472	17	63	40.9	2.50E-09
rrnAC3384	18	64	66.4	5.30E-17
pNG7183	18	64	42.7	7.50E-10
pNG5067	18	64	39.3	7.50E-09
rrnAC0019	763	813	-5.9	0.29
pNG7307	9	55	54	2.90E-13

PF01047: MarR family (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC0842	10	112	-22.4	0.24
rrnAC3501	11	107	1	0.0032
rrnAC3310	11	109	-17	0.087
rrnAC0230	11	112	-9	0.02
rrnB0222	12	192	-26.1	0.47
pNG6047	13	120	-19	0.13
rrnAC0006	13	150	-7.6	0.016
rrnAC1942	18	110	-25.9	0.45
pNG7046	26	119	-17.5	0.095
pNG7133	28	132	-18.3	0.11
rrnAC2669	31	120	-24.2	0.32
rrnAC2966	3	176	-13.8	0.048
rrnAC0503	4	99	2.1	0.0026
rrnAC3082	58	162	-7.2	0.014
pNG6034	6	101	-9.4	0.022
pNG6091	77	167	-23.8	0.31
rrnAC2285	8	104	-17.9	0.1
rrnAC1645	909	1111	-23.9	0.31
rrnAC3074	97	312	-6.5	0.013

PF01022: Bacterial regulatory protein, arsR family (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC1805	107	196	5.8	0.054
rrnAC0578	10	90	14.8	0.0069
pNG7194	11	90	4.4	0.073
rrnAC2078	11	97	-1.2	0.26
rrnAC0914	16	94	-3.1	0.4
rrnAC3399	17	108	13	0.01
pNG6142	1	77	-1.9	0.3
rrnAC3494	17	89	20.1	0.0021
rrnAC1379	18	107	0.5	0.17
pNG6160	21	116	27.3	3.00E-05
rrnB0089	25	97	3.3	0.094
rrnAC1256	266	362	-3	0.39
rrnAC0001	2	93	0.8	0.17
pNG7045	32	115	13.7	0.0089
rrnAC0961	32	116	28.5	1.30E-05
rrnAC2723	32	132	24.9	0.00017
pNG7312	33	116	1	0.16
rrnB0118	35	135	18.1	0.0033
rrnAC0867	41	127	4.7	0.067
pNG4023	43	125	1.8	0.13
rrnAC3191	4	91	6.8	0.043
pNG6075	51	150	5.9	0.052
rrnB0014	53	136	2.5	0.11
rrnB0052	66	157	40.1	4.40E-09
rrnAC0161	68	147	22	0.0012
pNG7343	7	101	0.2	0.19
pNG7021	7	106	5.5	0.057
pNG7146	71	151	5.5	0.056
pNG6021	72	159	13.1	0.01
rrnAC3447	7	81	37.2	3.20E-08
rrnB0222	9	79	9.4	0.023

PF01325: Iron dependent repressor, N-terminal DNA binding domain (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC3074	101	161	-6	0.18
rrnAC1653	10	68	-7.2	0.24
rrnAC1269	1	56	8.5	0.0064
rrnAC0341	1	58	-9.6	0.41
rrnAC1825	1	60	61.6	1.50E-15
pNG7038	1	60	-3.3	0.097
rrnAC2037	1	60	56.5	5.10E-14
rrnAC0496	1	62	84.9	1.50E-22
pNG6011	4	58	-7.5	0.25
rrnB0222	5	64	-0.4	0.05
rrnAC1645	908	963	-9.1	0.36
rrnAC1338	9	64	-0.9	0.056

PF02573: N-terminal HTH domain of molybdenum-binding protein (HTH):

Gene name	start	stop	bitScore	e-value
rrnAC3264	7	106	58.9	9.40E-15

PF01381: Helix-turn-helix 3 (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC0872	109	166	15.7	0.081
rrnAC2519	132	185	38.5	1.30E-08
rrnAC2428	182	238	14.1	0.12
rrnAC1777	20	68	24.9	0.00017
rrnAC1742	27	81	37.8	2.20E-08
rrnAC1764	40	92	19.4	0.0076
rrnAC2762	685	735	45.3	1.20E-10
rrnAC0535	94	148	47	3.70E-11
rrnAC0440	9	63	53.3	4.80E-13

PF01402: Ribbon-helix-helix protein, copG family

Gene name	start	stop	bitScore	e-value
rrnAC3207	10	51	24.6	0.0002
pNG6157	1	41	15.4	0.036
rrnAC1238	1	42	19	0.0097
rrnAC2002	1	42	21.8	0.0014
pNG5088	1	42	14.2	0.049
rrnAC2856	1	43	7.1	0.33
rrnAC0323	1	43	11	0.12
rrnB0151	14	56	14.9	0.041
pNG7160	2	43	44.7	1.80E-10
rrnAC0583	2	43	12.6	0.076
pNG2039	25	66	25.6	0.0001
pNG5089	4	45	15.7	0.033
rrnAC2748	53	94	22.9	0.00067
rrnAC1567	61	102	18.3	0.016
rrnB0134	67	108	16.6	0.026
rrnAC0316	7	48	11.2	0.11

PF01614: Bacterial transcriptional regulator (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC2801	104	289	-86.1	0.36
rrnB0235	104	290	121.9	1.00E-33
rrnB0222	63	246	65.7	8.90E-19
rrnAC0230	64	246	107.5	2.30E-27
pNG7343	64	249	148.6	9.80E-42
rrnAC1338	64	250	194.9	1.10E-55
rrnAC1964	65	250	150.6	2.40E-42
pNG7021	65	251	139.4	5.60E-39
rrnAC0385	69	258	190.8	1.90E-54
pNG7171	73	262	172.8	5.00E-49
pNG7344	77	274	86.6	4.30E-23
rrnAC1971	79	265	134.9	1.30E-37

PF02796: Helix-turn-helix (HTH)

Gene name	start	stop	bitScore	e-value
pNG4015	28	68	3.1	0.43
rrnAC1941	5	52	4.6	0.27
pNG5137	82	117	4.7	0.27
rrnAC2354	9	55	3.9	0.34

PF02954: Bacterial regulatory protein, Fis family (HTH)

Gene name	start	stop	bitScore	e-value
rrnAC2519	124	160	-0.3	0.44
rrnB0269	184	230	1.4	0.28

PF01638: Transcriptional regulator

Gene name	start	stop	bitScore	e-value
rrnB0301	23	114	86.4	5.10E-23
rrnAC0417	26	115	73.7	3.30E-19
rrnAC1303	26	117	119.7	4.80E-33
pNG6155	39	114	26.6	1.90E-08

PF03551: Transcriptional regulator PadR-like family

Gene name	start	stop	bitScore	e-value
pNG6092	12	91	73.6	3.70E-19
rrnAC3322	15	93	63.6	3.70E-16
pNG5119	1	79	32.3	8.70E-07
pNG1015	17	95	14.9	4.50E-05
pNG2042	17	95	9.8	0.00014
pNG3007	17	95	-14.2	0.033
rrnB0161	1	81	63.8	3.30E-16
rrnAC2383	18	86	-21.7	0.18
pNG4025	19	101	1	0.0011
rrnAC1971	23	84	-14	0.031
rrnAC0435	2	81	76.4	5.10E-20
pNG2006	2	81	68.3	1.40E-17
rrnAC0992	2	81	79.5	5.90E-21
pNG6058	2	81	68.8	9.90E-18
rrnB0157	2	81	45.4	1.10E-10
pNG6074	3	72	-8.8	0.0098
rrnB0074	39	115	-7.2	0.0069
pNG6172	53	133	-22.8	0.23
pNG4043	5	83	-8.4	0.0088
pNG4042	5	85	57.5	2.50E-14
rrnB0112	5	85	46.1	7.10E-11
pNG5140	5	85	31	1.20E-06
rrnAC1521	6	101	-20.9	0.15
rrnAC2270	65	143	24.7	4.90E-06
rrnB0084	6	84	-20.8	0.15
rrnAC1964	8	75	-24.3	0.33
rrnAC0768	8	84	20	1.40E-05
rrnAC0913	9	77	-10.4	0.014

PF04967: HTH DNA binding domain (HTH) (bat like, found in Halobacterium)

Gene name	start	stop	bitScore	e-value
rrnAC2160	151	203	62	1.10E-15
rrnAC1895	154	206	56.9	3.80E-14
rrnAC1217	155	207	80	4.20E-21
rrnAC1786	156	208	63.9	3.10E-16
rrnAC1996	156	208	73.1	5.00E-19
pNG7357	157	209	65.2	1.20E-16
rrnAC3490	158	210	79.3	7.10E-21
rrnAC3451	158	210	64.8	1.60E-16
rrnAC1953	159	211	81.7	1.30E-21
rrnB0253	160	212	68.5	1.30E-17
rrnAC1193	161	213	87.5	2.30E-23
rrnAC2022	162	214	57.4	2.80E-14
rrnAC3486	167	219	78.1	1.60E-20
rrnAC0640	171	223	74	2.80E-19
rrnAC0564	171	223	71.8	1.30E-18
pNG6134	181	233	62.4	8.30E-16
pNG7188	182	234	73.7	3.30E-19

**PF04967: HTH DNA binding domain (HTH) (bat like,
found in Halobacterium) (contd)**

Gene name	start	stop	bitScore	e-value
rrnAC2936	183	235	97.3	2.70E-26
rrnAC2472	183	235	67.2	3.00E-17
rrnB0269	184	236	67.5	2.50E-17
rrnAC0376	184	236	83.7	3.40E-22
rrnAC3167	185	237	88.3	1.40E-23
rrnAC0231	189	241	87.8	2.00E-23
rrnAC2017	190	242	46.8	4.30E-11
rrnAC1541	192	244	59.4	6.70E-15
rrnAC2785	2	44	30.3	1.70E-06
rrnAC0199	42	86	-9.2	0.048
rrnAC2070	468	520	70.2	3.80E-18
rrnAC3229	495	547	92.7	6.30E-25
rrnAC1687	759	811	81.5	1.50E-21
rrnAC0019	759	811	82.4	8.20E-22
pNG7159	890	942	74.7	1.70E-19
rrnAC1663	913	965	87.8	1.90E-23
pNG7223	988	1040	72.8	6.30E-19