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A Systems Biology Approach For Predicting Essential Genes and Deciphering Their Dynamics Under Stress In Streptococcus sanguinis

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A Systems Biology Approach For Predicting Essential Genes and Deciphering Their Dynamics Under Stress In *Streptococcus sanguinis*

A thesis submitted in partial fulfillment of the requirements for the degree of
Doctor of Philosophy at Virginia Commonwealth University.

By

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A	Alanine
A_{260}	Absorbance at 260 nanometer
ABC	ATP-Binding Cassette
B. pertussis	Bordetella pertussis
B. subtilis	*Bacillus subtilis*
BC	Betweenness centrality
BCA	bicinchoninic acid
BHI	brain heart infusion
BLASTP	Basic Local Alignment Search Tool
C	Cysteine
C3	Complement factor 3
C5A	Complement factor 5A
CC	Closeness centrality
CDM	chemically defined medium
CLSI	Clinical & Laboratory Standards Institute
COG	clusters of orthologous groups
D	Aspartic acid
DC	Degree centrality
DEG	Database of Essential Genes
DNA	deoxyribonucleic acid

DTT	Dithiothreitol
E	Glutamic acid
E. coli MG1655,	*Escherichia coli* MG1655,
Ef	Elongation factor
F	Phenylalanine
G	Glycine
GI	GenInfo Identifier
H	Histidine
HUVEC	human umbilical vein endothelial cells
I	Isoleucine
K	Lysine
KDa	Kilo Daltons
KEGG	Kyoto Encyclopedia of Genomes and Genes
KOR	knockout-rate hypothesis
L	Leucine
LC-MS	Liquid chromatography–mass spectrometry
M	Methionine
M. genitalium G37	*Mycoplasma genitalium* G37
M. pulmonis	*Mycoplasma pulmonis*
M. smegmatis	*Mycobacterium smegmatis*
M. tuberculosis H37Rv	*Mycobacterium tuberculosis* H37Rv
MALDI-TOF/TOF	Matrix-assisted laser desorption ionization/ Time of Flight

MIC	minimum inhibitory concentration
mM.	Milli-molar
mRNA	messenger RNA
N	Asparagine
NCBI	National Center for Biotechnology Information
ng	nanogram
NH_4HCO_3	Ammonium Bicarbonate
OD	Optical density
P	Proline
P. aeruginosa PA14	*Pseudomonas aeruginosa* PA14
P. aeruginosa PAO1	*Pseudomonas aeruginosa* PAO1
P. gingivalis 33277	*Porphyromonas gingivalis* 33277
P. gingivalis TDC60	*Porphyromonas gingivalis* TDC60
P. gingivalis W83	*Porphyromonas gingivalis* W83
PTS	Phosphotransferase system
Q	Glutamine
R	Arginine
RNA	ribonucleic acid
RNA-seq	RNA- sequencing
rpm	Rotations per minute
S	Serine
S. agalactiae	*Streptococcus agalactiae*
S. aureus	*Staphylococcus aureus*

S. gordonii	*Streptococcus gordonii*
S. mutans	*Streptococcus mutans*
S. oralis	*Streptococcus oralis*
S. parasanguinis	*Streptococcus parasanguinis*
S. pneumoniae	*Streptococcus pneumoniae*
S. pyogenes	*Streptococcus pyogenes*
S. sanguinis	*Streptococcus sanguinis*
SDS	Sodium dodecyl sulfate
sec	second
SF	surfactant
STM	signature-tagged mutagenesis
T	Threonine
T_{10}	Time at 10 minutes
T_{20}	Time at 20 minutes
T_{30}	Time at 30 minutes
TCC	Tricarboxylic cycle
Tn-seq	Transposon sequencing
V	Valine
v:v	Volume to volume ratio
W	Tryptophan
Y	Tyrosine
µL	Microliter
σ-factor	Sigma factor

Abstract

A Systems Biology Approach For Predicting Essential Genes and Deciphering Their Dynamics Under Stress in *Streptococcus sanguinis*

By Fadi El-Rami, M.Sc., B.Sc.

A dissertation submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy at Virginia Commonwealth University.

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Infectious diseases are the top leading cause of death worldwide. Identifying essential genes, genes indispensable for survival, has been proven indispensable in defining new therapeutic targets against pathogens, major elements of the minimal set genome to be harnessed in synthetic biology, and determinants of evolutionary relationships of phylogenetically distant species. Thus, essentiality studies promise valuable revenues that can decipher much of biological complexities.

Taking advantage of the available microbial sequences and the essentiality studies conducted in various microbial models, we proposed a framework for the prediction of essential genes based on our experimentally verified knowledge of the pathways involved in three essential

functions: genetic information processing, cell wall biosynthesis, and energy metabolism. We investigated physiological pathways in Kyoto Encyclopedia of Genes and Genomes (KEGG) database and developed a bioinformatics approach to predict essential genes in 13 different microbial species. Our *in silico* findings matched to a high degree the experimental data derived from essentiality studies conducted on the same microbial models, providing insights about the microbial lifestyles, including energy resources, cell wall structure, and ecological preferences, but not virulence tools and mechanisms.

Furthermore, we believe that essential genes have survived the evolutionary purifying selection due to their evolved capacity to re-wire genetic and protein networks in response to any emerging stress. In this sense, an environmental specificity (stress) provides a dominant determinant of an essential gene set. The new challenge was understanding the contribution of the essential genome in *S. sanguinis* to the coping mechanisms to different clinically relevant stress factors, namely temperature elevation (43°C) and sub-inhibitory concentration of ampicillin, an abundantly prescribed antibiotic for prophylaxis and treatment against *S. sanguinis*. The current project investigated the transcriptomic and proteomic profiles of essential genes and proteins, using RNA-seq and mass spectrometry respectively, under the impact of the two stressors separately, to elucidate the essential genome and proteome dynamics on a temporal basis and define "pathogenesis signatures" as potential therapeutic targets. We believe that the current findings will help characterize a bacterial model for studying the dynamics of essential genes and assist in designing evidence-based guidelines for drug prescription in clinical practice.

Introduction

I. *Streptococcus sanguinis* SK36

General Description of *Streptococcus sanguinis* SK36. *Streptococcus sanguinis* SK36 (*S. sanguinis*) is a Gram-positive, facultative anaerobic, cocci-shaped bacterium that inhabits the oral cavity in high abundance, despite competition against 700 species [1,2]. It is described as a Janus-faced microorganism: on one hand, it is an oral commensal that competes with pathogenic bacteria for colonization of oral cavity through the production of bactericidal hydrogen peroxide that has been shown to eliminate an etiologic agent of dental caries, namely *Streptococcus mutans* [3,4]. On the other hand, *S. sanguinis* has been related to the formation of biofilms in oral cavity, also called dental plaques [5-8], and has been defined as an opportunistic pathogen that is among the leading etiologic agents of infective endocarditis in patients with heart valve defects [9-12] and bacteremia in neutropenic patients [13,14].

Discovery of *S. sanguinis*. *S. sanguinis* was previously named *S. sanguis* and *Streptococcus* s.b.e. of Loewe when it was originally identified in the mid 1940's from the blood of subacute bacterial endocarditis human patients [15,16]. It was initially classified by a battery of serological and metabolic features:

1) It changes the color of blood in a blood agar plate into green, a phenomenon termed the "Greening effect".

2) It hydrolyzes the amino acid arginine within 48 hours.

3) It ferments inulin, but not raffinose, in a week.

4) it cannot produce slime on 5% sucrose-gelatin agar in one day.

5) it exhibits a type-specific precipitation reaction in serum from immune hosts within 20 minutes [17].

6) It produces a dextran if cultured with sucrose, the founding theory of its biofilm formation potential [18].

Genomic Description of *S. sanguinis*. In comparison to many oral streptococci, the genome of *S. sanguinis* (2.388 Mb) is larger than other streptococci, ranging from 177 to 590 kb. In addition, its GC% (43.4%) is relatively higher than other streptococci [19]. Its genome encodes 2,704 predicted proteins (more than many streptococcal species), 61 tRNAs, and four rRNA operons (less than many streptococcal species). Although *S. sanguinis* has a superior potential for DNA transformation from external environment, only a few operons have been shown to be acquired via horizonatal gene transfer, such as a region responsible for vitamin B_{12} biosynthesis and utilization of ethanolamine and propanediol. Armed with a plethora of cell adhesion molecules, *S. sanguinis* employs its armamentum for binding and attachment to diverse soft and solid, mobile and stationary surfaces in the oral cavity, which entitles it to be a “primary colonizer” in a heavily populated oral niche. *S. sanguinis* genomes encompasses genes that encode enzymes needed for fatty acid biosynthesis, glycolysis, and *de novo* amino acid biosynthesis of most amino acids, except leucine, isoleucine, valine, lysine, and tryptophan. To compensate for that, *S. sanguinis* relies heavily on import of vital nutrients and for this purpose, its genome encompasses around 150 genes that encode for around 50 putative transporters, which are predicted to import many sugars (glucose, fructose, mannose, lactose, maltose, trehalose), metals (zinc, manganese, iron, cobalt, copper, nickel, molybdenum), amino acids (methionine, proline, glycine, cysteine, arginine, histidine, leucine, isoleucine, valine), peptides, lipids, and many other compounds (bacitracin, spermidine, putrescine).

Pathogenesis. *S. sanguinis* is an early colonizer of the solid surfaces of the mouth, initiating the first stage for biofilm formation, which later develops through recruitment of poly-species and ultimately the establishment of biofilm structure [5-7]. Biofilm structures in oral cavities have been linked to dental plaques and caries' formation [5]. Moreover, *S. sanguinis* is an opportunistic pathogen and among the leading etiologic agents of infective endocarditis [9-12].

Using comparative genomics approach, *S. sanguinis* orthologs, homologous genes of *S. sanguinis* genes in different species, were identified in other bacterial models which are phylogenetically relevant to *S. sanguinis* and where functional clues of *S. sanguinis* orthologs were elucidated based on experimental findings. Three sets of virulence determinants were defined as gene sets involved in endocarditis, immune evasion, tissue adherence and biofilm formation. Many *S. sanguinis* orthologs were identified as contributors to infective endocarditis: the orthologs of SSA_0260 in *S. parasanguinis*[20] and *S. mutans* [21]; SSA_0613 in *S. mutans* [22] and *S. oralis* [23]; and SSA_0829 in *S. gordonii* [24]. Orthologs of *S. sanguinis* were shown to be involved in diverse host immune evasion techniques: ortholog of SSA_0886 in *S. pneumoniae* was shown to possess a extracellular matrix degradation activity [25]; ortholog of SSA_1023 in *S. lugdunensis* binds Von Willebrand factor [26]; ortholog of SSA_1761 in *S. pneumoniae* was a putative hemolysin [27]; ortholog of SSA_1882 in *S. pyogenes* was shown to be a C5A surface peptidase [28]; ortholog of SSA_2108 in *S. pneumoniae* was shown to bind plasminogen [29]; and ortholog of SSA_1991 in *S. pneumoniae* was shown to be a surface C3 protease [30]. Finally, various orthologs of *S. sanguinis* were shown to be involved in biofilm formation and host tissue adherence: orthologs of SSA_0227, SSA_0805, SSA_1019, and SSA_1666 in *Staphylococcus* *aureus* [31] were shown to be involved in collagen binding; orthologs of SSA_0907 in *S. gordonii* [32] and *S. pneumoniae* [33] were shown to bind fibronectin; ortholog of SSA_1990 in *S. agalactiae* was shown to bind laminin [34]; orthologs of SSA_1631 and SSA_1632 in *S. pneumoniae* were shown to encode pilus subunits [35]; and orthologs of SSA_1984 in *S. epidermidis* [36] and SSA_1219 in *S. gordonii* [37] and in *S. mutans* [38] were shown to be adhesins.

Numerous studies investigated the contribution of *S. sanguinis* genes to endocarditis through various pathogenesis mechanisms. An elegant study using signature-tagged mutagenesis (STM) screened *in vivo* 800 *S. sanguinis* mutants and identified 5 hypovirulent mutants using a rabbit model for endocarditis. Genes attributed to decreased virulence in the endocarditis model were: *purB* gene encoding adenylosuccinate lyase that is involved in de novo purine synthesis [39]; an ortholog of *BacA* from *S. pneumoniae* that encodes undecaprenol kinase and amplifies resistance against bacitracin [40]; an ortholog of *thrB* gene in *S. pneumoniae* that encodes homoserine kinase and is responsible for the biosynthesis of the amino acid threonine [41]; and an ortholog of *nrdD* in S. pneumoniae that encodes anaerobic ribonucleotide reductase that sustains survival under anaerobic conditions [42]. The final virulence determinant was a hypothetical gene. Using the same approach (STM), pro-lipoprotein diacylglyceryl transferase (SSA_1546), signal peptidase II (SSA_1069), ssaB gene (SSA_0260) were shown to be a potent virulence determinants in infective endocarditis as their respective mutants showed decreased competiveness against the wild type strain in a rabbit endocarditis model [43].

Furthermore, gene products of SSA_0374, SSA_1663 [44], and SSA_0829 [45] involved in platelets aggregation can be ascribed as virulence determinants in endocarditis [46]. The cell surface molecule, ecto-5'-nucleotidase (Nt5e), was shown to slow down platelet aggregation and enhance survival conditions of *S. sanguinis* in valve vegitations [47]. Recently, NADH oxidase-encoding gene nox was experimentally verified as an endocarditis virulence determinant where nox mutant produced less hydrogen peroxide and demonstrated reduced virulence in a rabbit endocarditis model [48].

Further studies investigated the potential of *S. sanguinis* to induce cytotoxicity through infecting human umbilical vein endothelial cells (HUVEC) and attributed this capability to the presence of glucosyltransferase, the sialic acid-binding protein *Hsa*, and the hydrophobicity/coaggregation proteins *CshA* and *CshB* [49]. Another study identified the secretion of a metalloprotease (SSA_1106) that cleaves IgA antibody and termed IgA-specific metallo-endopeptidase [50]. The adhesion function of SsaB adhesion (SSA_0260) to saliva-coated hydroxyapatite was experimentally verified [51].

II. Essential Genes

Advances in Essentiality Studies. Genomic studies have flooded the NCBI database (https://www.ncbi.nlm.nih.gov/genome/) with prokaryotic (95,070), eukaryotic (4,146), viral (7,187), plasmid (9,148), and organelle (9,662) sequences, taking advantage of the technological advancements that reduced the time and cost of sequencing. However, attention nowadays is diverted to genetic functional analysis, with the aim of linking gene sequences to functional roles and significance in physiological networks that satisfy needs of survival. Early genome-scale studies, using chromosomal (positional), functional (system level), or phylogenetic (evolutionary) context analysis, coined the term “essential genes” to identify genes that are indispensable for survival, and whose knock out has a lethal consequence [52,53]. Essential genes have been proven indispensable in defining new therapeutic targets against pathogens [54], major elements of the minimal set genome that modulate pathways to be harnessed in synthetic biology [55], and determinants of evolutionary relationships of phylogenetically distant species [56]. In conclusion, essentiality studies promise valuable revenues that can decipher much of biological complexities.

Essential genes have been systematically detected using multiple approaches, ranging from single gene deletions [57,58], transposon mutagenesis [52,59,60], or antisense RNA [61,62] Essentiality studies provided rich information regarding essential functions and elucidated new links between genotypes and phenotypes in a specific ecological context. However, using different techniques led to different findings and amplified the effect of technical bias in defining essential genes. A major example illustrates the differences in 2 sets of *E. coli* K-12 essential genomes owing to the different experimental designs. All in all, essentiality experiments deepened our understanding of evolution, bacterial behavior, and provided invaluable tools for synthetic biology[63].

Essential genes, owing to their essential function(s), have been characterized by a set of distinct genomic features: localization on leading strand, usage of optimal codons, and high mRNA expression [64-66]. They have been linked to conservation and slower "evolutionary clock" in comparison to non-essential genes, as emphasized in the knockout-rate hypothesis (KOR) [67,68]. Although the KOR theory has been controversial in linking gene essentiality to evolutionary conservation in eukaryotic models, such as mice [68] and yeast [69], it has established the essentiality-conservation link in prokaryotic models [70,71], such as *E. coli* [72] and *Pseudomonas aeruginosa* [73]. A recent study showed that among 23 bacterial species tested for the link between essentiality and conservation, the link was established for orthologous essential genes involved in genetic information processing pathways (DNA replication, transcription, translation, and ribosomal biogenesis) and some energy production pathways (carbohydrate, lipid, and coenzyme metabolism) [74].

Further analysis of essential genes subdivided them into two groups:

1) Ones that are “absolutely essential for cell viability under any conditions”. These are minor fraction of identified essential genes and are involved mainly in genetic machinery: information storage and processing.

2) Ones that are essential in “context of special conditions”, also called accessory essential genes, and included majorly genes involved in metabolic pathways. They are essential during specific cultural conditions [53,75,76]. Upon culturing *P. aeruginosa* in 6 different media and conducting essentiality study using Tn-seq method, 199 condition-specific essential genes contributing to 11-23% of essential genome were identified [77].

At a higher resolution of essentiality, functional units of proteins, domains, were categorized into essential domains based on their localization on essential proteins. Although essential proteins contain at least one essential domain, some essential proteins contained more than one essential domain[78]. Moreover, only 16% of all domains were found in all kingdoms of life and the correlation between phylogenetic conservation and essentiality was not strong.

III. Stress Response Network

The ability of *S. sanguinis* to thrive abundantly in the oral cavity despite severe competition with more than 700 microbial species reflects a high level of adaptation skills to various environmental stress conditions. Usually, bacteria cope with stress through harnessing a specific adaptive response that is directed specifically to a given stress, such as synthesizing catalase and superoxide dismutase in response to oxidative stress [79] or exhibit a ‘general stress response’ [80] with a wide range protection against various stressors, such as slow growth rate accompanied with smaller cell size and thicker cell wall. A third type of newly identified stress response has been coined “cross-stress behavior”[81], an adaptive mechanism that assists stressed cells under impact of one stressor to develop stress resistance against another stressor. In either case, the adaptive responses of *S. sanguinis* owe a lot of their flexibility and robustness to the presence of stress response proteins, which include chaperones with assigned functions of folding and preventing aggregation of proteins in highly dense cell cytosol [82,83]. In *S. sanguinis*, the only chaperone systems that exhibit essentiality among all proteins whose functional category is protein folding (GO#0006457), namely GroELS and DnaKS, are major players in maintaining proteostasis in the cell. GroEL chaperone (also called chaperonin), in collaboration with its cofactor GroES, hinders newly synthesized and pre-existing proteins, especially large polypeptides, from falling into “kinetic traps” during their folding intermediates and forming aggregates [84]. The binding of cylinder-shaped GroEL with dome-shaped GroES traps the unfolded or misfolded protein in an enclosed chamber and provides a safe folding environment to its native state away from densely packed cell cytosol [85,86]. Chaperone DnaK, with assistance of co-chaperone DnaJ and nucleotide exchange factor GrpE, is responsible for protein folding of nascent or misfolded proteins as well as protein disaggregation. Interestingly, DnaK shares with Trigger factor the task of folding emerging nascent polypeptide from ribosomes [87,88].

Antibiotic as a stressor. Colonizing the oral cavity in abundance, *S. sanguinis* are frequently exposed continuously to antibiotics which perpetuate as sub-inhibitory concentrations for long time periods, either directly through antibiotics’ prescriptions and ingestion by patients or indirectly through anthropogenic antibiotic usage and transfer of antibiotics through animal food products to humans [89,90]. Some studies estimated that out of total antibiotic prescriptions for clinical purposes, 7% and 10% of total prescriptions are provided by dentists in the United Kingdom [91] and Spain [92] respectively. Ampicillin and amoxicillin are members of β-lactam family of antibiotics family that differ only in one hydroxyl group and have same spectrum of activity against Gram-positive bacteria, although the latter has better intestinal absorption and consequently higher serum levels than ampicillin [93]. They are considered the drugs of choice for many dental practices [94-96] and, controversially, prophylactic drugs for susceptible patients to infective endocarditis [97-106]. Misuse and abuse of antibiotics by many dentists worldwide exacerbate the situation by further exposing the oral microbiota, including *S. sanguinis*, to these drugs [107-110]. It was shown that almost half of the prescribed antibiotics to humans are excreted in an active form, raising questions about the diluted residual doses and their impact on bacterial communities [111].

Since 1946, early observations questioned the paradoxical behavior of *S. sanguinis* in response to drugs prescribed prophylactically against infective endocarditis *in vitro*, where they were shown to be susceptible, versus *in vivo*, where they demonstrated resistance against the same drugs [112,113]. Many theoretical interpretations have been provided. A major suggestion attributed this antibacterial resistance pattern *in vivo* to the physical barriers that block the access of antibiotics to the bacteria, such as aggregated platelets and fibrin on damaged heart valves and biofilm structures [114-117]. However, this concept is challenged by findings that antibiotics can in fact successfully diffuse through biofilms, weakening the barrier argument of "protected niches" [118-120]. Another hypothesis to explain the *in vivo* antibiotic resistance pattern was first initiated with the work of Walsh McDermott [121] in 1958 who introduced the concept of "adaptive plasticity" as bacteria modulating their metabolism and growth rate to cope with the environmental stress, such as antibiotics, and "playing dead" by slowing down or halting replication, thus becoming indifferent to antibiotics [122,123]. However, after clearance of antibiotics, persistent bacteria relapse albeit with an antibiotic susceptible profile [124]. This scenario is more acceptable in context of *S. sanguinis* lifestyle, where cases of antibiotics resistance have been rarely reported [125,126]. Surprisingly, no homolog for the persistence initiation toxin protein *hipA* (from *Escherichia coli* [127]) can be identified in *S. sanguinis* proteome, bringing back questioning to square one: how does *S. sanguinis* respond to sub-inhibitory concentrations of antibiotics? How does *S. sanguinis* modulate its essential genes and pathways to thrive in a stressful environment which happens to be the norm rather than exception?

Heat as a global stressor. Bacterial response against heat shock is a well conserved mechanism that has been shaped by evolutionary selective pressure in every bacterial model [83,128-130]. Bacteria are constantly exposed to temperature shifts that impact their response mechanisms at different transcriptomic, metabolomic, and proteomic angles as orchestrated by alternative sigma factors, in many cases. Heat shock response has been intensively investigated in the bacterial prototype model, *E. coli*, where it was shown that alternative sigma factor *RpoS*, which encodes sigma factor σ^S, coordinates heat shock response through selectively targeting a set of operons and pathways that encompass more than 140 genes [80,131,132]. In many Gram-positive bacteria such as *B. subtilis* and *S. aureus, SigB* operon encoding *sigB* (σ^B) impacts the expression of around 200 genes contributing to heat shock response and involved in cell wall biosynthesis, membrane transporters, molecular chaperone systems, and intermediary metabolism[133-136]. A study by Fleury et al. [137] has shown that heat induces transcriptomic up-regulation of classical chaperones, DnaK and GroESL, as well as many components of the pentose phosphate pathway, gluconeogenesis, oxidative stress, and DNA damage repair. Despite the fact that energy production was reduced in heat-stressed bacterial systems, the energy-demanding DNA repair mechanisms were up-regulated, reflecting a bias in energy consumption geared towards the indispensable pathways. Interestingly, many streptococcal species lack an alternative sigma factor and recently a study investigating the transcriptomic stress response of *S. mutans* showed two-component systems, sugar transporters, heat shock proteins, components of glucans biosynthesis and glycolysis to be differentially expressed under heat shock [138]. However, using our essential gene-based approach combined with systems biology tools will highlight the “priority list” of pathways that consume the scarce energy reserves as a reward for their utmost importance and contribution to survival in a specific stressful environment.

IV. Systems Biology Approach

With the daily feeding of genomic databases with new microbial sequences and harnessing of –omics approach, the investigation of essential genes and functions to decode microbial behavior in health and disease is systematically feasible. Despite the whole genome sequencing and further identification of essential genes set in *S. sanguinis,* our understanding of the survival strategies, metabolism, and physiology under stress remains incomplete.

Systems biology approach has emerged as a natural result of technological advances, availability of huge databases loaded continuously with biological data, and the need to tackle biological problems using the “bird’s eye” perspective at a specific time point with minimal effect of technical bias [139-143]. It is based on high-throughput but less time-consuming techniques that screen whole components of a biological system: mRNA, protein, metabolites, etc. Systems biology techniques have been widely adopted by the industry for high-throughput testing with the aim of identifying novel drug targets [89,144-146]

However, the systems biology techniques have basic limitations: the detection ranges of different technologies are variable, the absence of complete gene/protein annotations even for many model organisms, and data interpretation challenges [147-149]. For example, lipids and volatile compounds demand discrete testing on various instrument platforms in LC-MS metabolomics systems and analysis is always challenging [148]. Despite those aforementioned obstacle, with the continuous flow of data from all –omics systems into reference databases, refinement of better statistical algorithms for big data analysis, and further discovery of hypothetical gene/protein functions, the future looks promising with integrated pipelines for biological systems analysis that exhibit precision along with time and cost efficiency [89,142,150,151].

In conclusion, despite the tremendous advances in sequencing technologies and the consequent dissection of complete genomes, our understanding of complex molecular interactions driving physiological mechanisms within a bacterial cell is fragmentary [59]. Bacteria adjust their intracellular web of molecular interactions to adaptively respond to a continuously emerging environmental stresses. The current project used whole-genome RNA-seq and mass spectrometric analysis to investigate the dynamics of essential transcriptome and proteome to elucidate involvement of essential genes in adaptive responses against antibiotics and heat stress.

For Aim 1, we plan to design a prediction framework for essential genes based on our knowledge of essential pathways using our bacterial model, *S. sanguinis*, to predict conserved essential proteins in bacterial systems based on KEGG annotations and a Basic Local Alignment Search Tool (BLASTP) approach. We plan to harness the network parameters of essential genes in *S. sanguinis* essential network to provide deep insights to elucidate bacterial behavior and identify patterns of genetic interactions that may serve as drug targets.

For Aim 2, using RNA-seq technology, we will quantitate the relative mRNA expression of all 2270, including 218 essential genes, *S. sanguinis* genes when the bacterial model is under two growth stresses.

For Aim 3, we will quantitate the relative bacterial proteome in the same two stress conditions used previously, with special emphasis on the essential proteins, as a means to understand protein essentiality with respect to adaptive responses against different stressors using mass spectrometry.

Chapter One

A Prediction Framework for the Analysis of Essential Genes in Bacteria

Fadi E. El-Rami, Hardik Parikh, and Ping Xu

Fadi E. El-Rami performed the prediction manually, analysis and presentation of data in two departmental seminars. Hardik Parikh wrote the BLASTP codes and conducted the bioinformatics work. Ping Xu supervised the whole work as an advisor.

Background

Infectious diseases are the top leading cause of death worldwide. Identifying essential genes, genes indispensable for survival, provides new opportunities for tackling old riddles of microbial pathogenesis, understand evolutionary trends of gene transfer, bolster synthetic biology, and present new therapeutic targets [152-154]. Regardless of the experimental design harnessed for the identification of essential genes, the time, effort, and financial toll is considerably high. Taking advantage of the available microbial sequences and the high throughput essentiality studies already conducted in various microbial models and deposited in Database of Essential Genes (DEG) database version 14.7 (http://www.essentialgene.org/), we investigated pathways of essential genes using bioinformatics approach to predict essential genes in different microbial species.

In silico programs for the prediction of prokaryotic essential genes have become abundant recently owing to the availability of thousands of sequenced and annotated microbial genomes in public repositories on one hand and the experimental data derived from essentiality studies conducted in various microbial models (data from 46 essentiality studies involving 40 bacterial models are deposited in DEG version 14.7) on the other hand. The earliest prediction models for the prediction of essential genes relied on the comparative genomics approach, where the experimental data from a handful of microbial models then were used as "training set" and orthologs, gene homologs in different species, of experimentally defined essential genes were defined in various organisms [155,156]. This approach had limited success for many reasons: it didn't factor in the ecological impact on bacterial genome, the role of horizontal gene transfer was under-appreciated [157] as mobile genetic elements like plasmids that have been shown to harbor genes involved in vital functions [158], gene duplication in a genome leading to neo-functionalization [154,159,160]. The high expectations for defining the minimal set genome using this approach dropped dramatically as the common set of orthologous essential genes between 4 bacterial models was shown to be 34 only [161], which definitely don't fulfill the diverse essential functions of a cell. To circumvent these limitations, we defined a new approach for the prediction framework of essential genes based on using a comparative genomics approach in relevance to the experimentally defined set of essential genes defined in *S. sanguinis* [162] as they are focused on three essential functions: genetic information processing, cell wall biosynthesis, and energy production (Fig. 1). Adopting the concept of a network biology approach solidified our findings by measuring the network parameters [163,164] of our essential genes in the predicted model and later investigating the network parameters impact on the conservation of these essential genes to fine-tune the prediction framework [24-28]. This approach can be further enhanced and applied to a larger set of microbial sequences using machine learning methods [163,165].

Compiling experimental data from essentiality studies conducted on *B. subtilis*, *S. aureus* NCTC 8325, *S. pneumoniae* TIGR4 and *S. sanguinis* SK36, we compared distribution patterns of essential genes along functional pathways and constructed a prediction framework of essential functions in Gram-positive bacterial strains. We further extended our studies to encompass *Escherichia coli* MG1655, *Mycobacterium tuberculosis* H37Rv, *Mycoplasma genitalium* G37, *Mycoplasma pulmonis, Porphyromonas gingivalis* W83, *Porphyromonas gingivalis* 33277, *Porphyromonas gingivalis* TDC60, *Pseudomonas aeruginosa* PAO1, and *Pseudomonas aeruginosa* PA14.

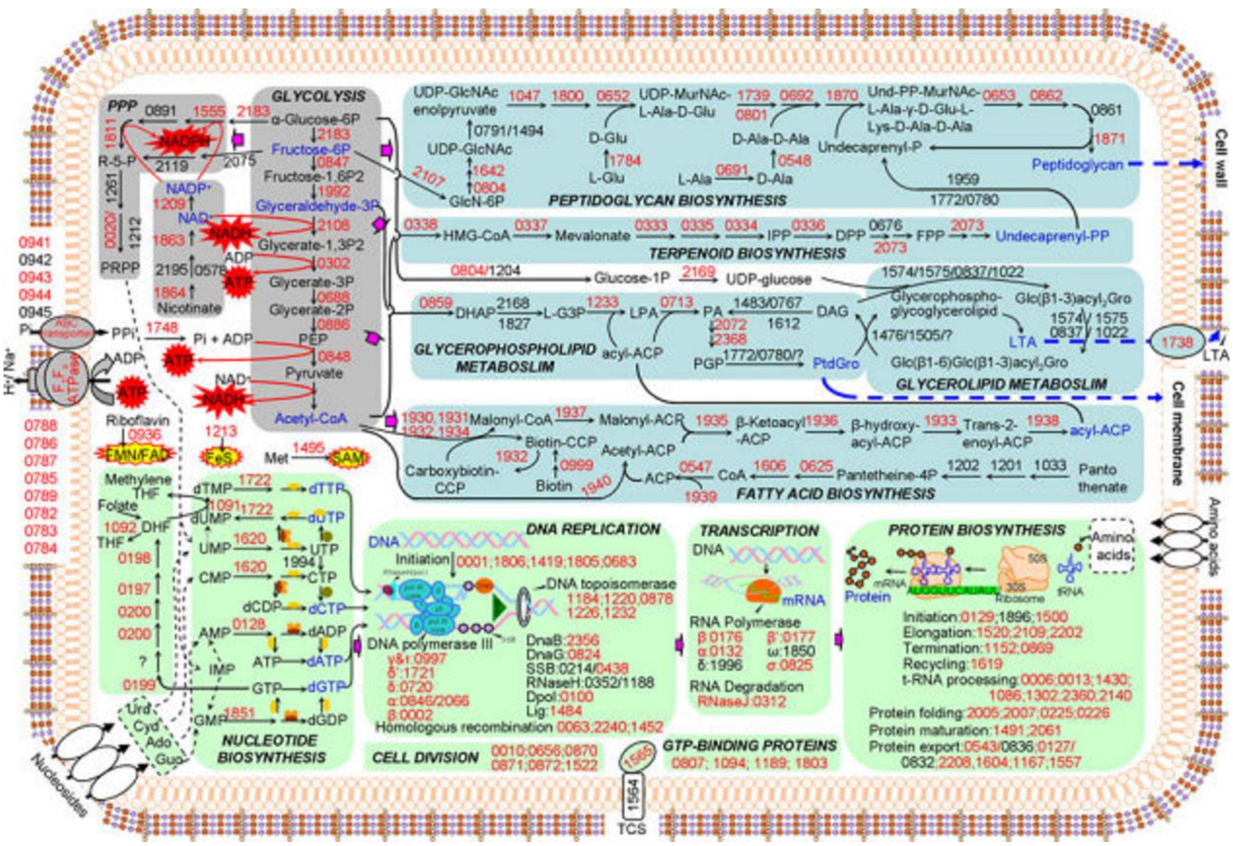

GLYCOLYSIS
α-Glucose-6P
2183
Fructose-6P
0847
Fructose-1,6P2
1992
Glyceraldehyde-3P
2108
Glycerate-1,3P2
0302
Glycerate-3P
0688
Glycerate-2P
0886
PEP
0848
Pyruvate
Acetyl-CoA
PPP
0891
1555
2183
1811
NADPH
R-5-P
2119
2075
1261
0020/
1212
PRPP
NADP+
1209
NAD+
1863
NADH
ADP
ATP
2195
0578
1864
Nicotinate
0941
0942
0943
0944
0945
Pi
ABC transporter
PPi
1748
Pi + ADP
ADP
H+/ Na+
F1F0-ATPase
ATP
NAD+
NADH
0788
0786
0787
0785
0789
0782
0783
0784
Riboflavin
0936
FMN/FAD
1213
FeS
Met
1495
SAM
UDP-GlcNAc enolpyruvate
1047
1800
0652
UDP-MurNAc-L-Ala-D-Glu
1739
0801
0692
1870
Und-PP-MurNAc-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala
0653
0862
0861
1871
0791/1494
UDP-GlcNAc
1642
0804
GlcN-6P
2107
D-Glu
1784
L-Glu
D-Ala-D-Ala
0548
L-Ala
0691
D-Ala
Undecaprenyl-P
Peptidoglycan
1959
1772/0780
PEPTIDOGLYCAN BIOSYNTHESIS
Cell wall
0338
HMG-CoA
0337
Mevalonate
0333
0335
0334
IPP
0336
DPP
0676
2073
FPP
2073
Undecaprenyl-PP
TERPENOID BIOSYNTHESIS
0804/1204
Glucose-1P
2169
UDP-glucose
1574/1575/0837/1022
Glycerophospho-glycoglycerolipid
Glc(β1-3)acyl₂Gro
1574
1575
0837
1022
LTA
1738
LTA
Glc(β1-6)Glc(β1-3)acyl₂Gro
1476/1505/?
GLYCEROLIPID METABOSLIM
0859
DHAP
2168
1827
L-G3P
1233
LPA
0713
PA
1483/0767
1612
DAG
2072
2368
PGP
1772/0780/?
PtdGro
acyl-ACP
GLYCEROPHOSPHOLIPID METABOSLIM
Cell membrane
1930,1931
1932,1934
Malonyl-CoA
1937
Malonyl-ACP
1935
β-Ketoacyl-ACP
1936
β-hydroxy-acyl-ACP
1933
Trans-2-enoyl-ACP
1938
acyl-ACP
Biotin-CCP
1932
Carboxybiotin-CCP
0999
Biotin
1940
Acetyl-ACP
ACP
0547
1939
CoA
1606
0625
Pantetheine-4P
1202
1201
1033
Panto thenate
FATTY ACID BIOSYNTHESIS
Methylene THF
Folate
1092
DHF
THF
0198
0197
0200
0200
?
0199
dTMP
1722
dTTP
1091
dUMP
1722
dUTP
UMP
1620
UTP
1994
CMP
1620
CTP
dCDP
dCTP
AMP
0128
dADP
ATP
dATP
IMP
GTP
dGTP
GMP
1851
dGDP
NUCLEOTIDE BIOSYNTHESIS
Urd
Cyd
Ado
Guo
Nucleosides
DNA REPLICATION
DNA
Initiation
0001;1806;1419;1805;0683
DNA topoisomerase
1184;1220,0878
1226,1232
DNA polymerase III
γ&τ:0997
δ':1721
δ:0720
α:0846/2066
β:0002
DnaB:2356
DnaG:0824
SSB:0214/0438
RNaseH:0352/1188
Dpol:0100
Lig:1484
Homologous recombination 0063;2240;1452
CELL DIVISION
0010;0656;0870
0871;0872;1522
1565
1554
TCS
TRANSCRIPTION
DNA
mRNA
RNA Polymerase
β:0176
β':0177
α:0132
ω:1850
δ:1996
σ:0825
RNA Degradation
RNaseJ:0312
GTP-BINDING PROTEINS
0807; 1094; 1189; 1803
PROTEIN BIOSYNTHESIS
Protein
mRNA
50S
30S
Ribosome
tRNA
Amino acids
Amino acids
Initiation:0129;1896;1500
Elongation:1520;2109;2202
Termination:1152;0869
Recycling:1619
t-RNA processing:0006;0013;1430;
1086;1302;2360;2140
Protein folding:2005;2007;0225;0226
Protein maturation:1491;2061
Protein export:0543/0836;0127/
0832;2208;1604;1167;1557

Figure 1. Experimentally defined essential genes in *S. sanguinis* SK36 [162].

The three functional categories associated with essential genes and pathways are colored as follows: blue for maintenance of cell envelope, grey for energy production, and green for genetic information processing. Numbers are for gene loci, excluding the preceding (SSA_): red numbers indicate essential genes; black numbers indicate nonessential genes; solid arrow indicates an enzymatic reaction; dashed arrow indicates a multistep pathway. Ado, adenosine; Cyd, cytidine; DAG, 1,2-diacylglycerol; DHAP, dihydroxyacetone phosphate; DHF, dihydrofolate; L-G3P, sn-glycerol 3-phosphate; Guo, guanosine; LPA, lysophosphatidic acid; LTA, lipoteichoic acid; PA, phosphatidic acid; PGP, phosphatidylglycerophosphate; PPP, pentose phosphate pathway; TCS, two-component system; THF, tetrahydrofolate; Urd, uridine. Essential genes associated with ribosome and aminoacyl-tRNA biosynthesis are not indicated here, nor are SSA_0575, SSA_0800 and SSA_1903, which could not be categorized into these pathways. Essential genes associated with ribosome and aminoacyl-tRNA biosynthesis are not indicated in this figure.

Materials and Methods

Manual prediction framework. We used the essential pathways derived from our essentiality study with *S. sanguinis* as a reference for essential functional categories, namely cell wall biosynthesis, genetic information processing, and energy production [162]. Using genome annotations as provided in pathways in the KEGG database, we compared the distribution of predicted essential genes across same pathways in different bacterial species. Essential genes are aligned in continuous pathways that are interconnected to each other. When a certain pathway is absent in *S. sanguinis*, data mining and evidence-based conclusions are the alternative method to pursue the prediction process.

Protein sequence alignment code. The protein sequences from 2774 bacterial species were downloaded and a database was formatted in VCU godel account that contained orderly arrangement of all amino acid sequences and their respective identifiers. We designed Python scripts to run comparisons of essential gene products across species to detect homologs (Significant matches: E-value < 1e-5). We then analyzed the distribution patterns of essential proteins via KEGG and identified essential pathways with the highest percentage of essential proteins. All databases and scripts are located in godel folder: ping-essential. The same scripts were used for the identification of orthologs (homologs in different species) and paralogs (homologs within same species).

Measurement of essential proteins' conservation patterns. We developed a bioinformatics approach to measure the conservation ratio of every experimentally-detected essential protein in *S. sanguinis* SK36. We extracted the amino acid sequences of all proteins from 2774 bacterial species deposited in NCBI. After designing a program based on reciprocal hit approach to detect orthologs of every *S. sanguinis* SK36 essential proteins (as a query) against all bacterial proteins (as subject) using BLASTP, we accepted an ortholog as a significant match any sequence alignment with the following cutoff values: minimal sequence identity of 50% and E value ≤1e^{-5}. We clustered essential proteins based on their COG annotation and then compared the conservation of essential proteins based on their COG annotation using Prism 5 software for illustration.

Construction of essential genes' network. Essential pathways were visualized using Cytoscape 3.4 software. The information regarding the essential genes and their respective interaction partners was inferred from KEGG. Manual construction of essential pathways was conducted as described by the manufacturer. The final graph was double checked manually for erroneous interactions.

Network parameters. Different network parameters were investigated to elucidate essentiality: degree centrality, betweenness centrality, and closeness centrality as follows:

Degree centrality (DC): Total number of edges incident upon a node.

$$DC(u) = \sum_{u} edge(u, v)$$

Betweenness centrality (BC): fraction of all shortest paths passing through the node.

$$BC(u) = \sum_{i \in V} \sum_{j \in V} \frac{p(i, u, j)}{p(i, j)}, i \neq u \neq j$$

Closeness centrality (CC): inverse of the average node distance from all other nodes.

$$CC(u) = \frac{N - 1}{\sum_{v \in V} dis(u, v)}$$

Results

Designing a framework for prediction of essential genes. We designed our framework for the prediction of essential genes based on our knowledge of essential genes, functions, and pathways that we concluded form the essentiality study of *S. sanguinis*. We used the KEGG pathways for comparison of pathways and predicting essential genes based on the saturation of pathways by predicted essential genes that contribute to an essential core functional category: genetic information processing, cell wall biosynthesis, and energy production. We further sub-divided each functional category into pathways that contribute to each functional class: peptidoglycan biosynthesis, terpenoid backbone biosynthesis, glycerophospholipid and glycerolipid metabolism, amino sugar metabolism, and fatty acid biosynthesis are pathways that contribute to cell wall biosynthesis; The pentose phosphate pathway, transcription, translation, DNA replication and repair, nucleotide (purine and pyrimidine) biosynthesis contribute to genetic information processing; Glycolysis and pyruvate metabolism contribute to energy production.

We faced many hurdles in defining a predicted essential pathway. First, given the pleiotropic nature of many essential genes and their involvement in multiple pathways (Fig. 2), we tracked the essential genes in all pathways and predicted a pathway to be essential based on harboring a proportionally large number of essential genes involved in a sequential cascade of reactions (Fig. 3). Second, many essential functions are conducted more than one essential protein, also called paralogs or, in the case of paralogous enzymes, isozymes (Fig. 3), as well as many other genes occupying an alternative pathway. We dealt with such scenarios by predicting all paralogs, isozymes, alternative pathways to be essential. Third, we encountered a lot of missing genes that show a pathway as disconnected. The enormous numbers of hypothetical genes, almost one-third in most genomes, contribute to these pathway gaps and only experimental findings can resolve this issue.

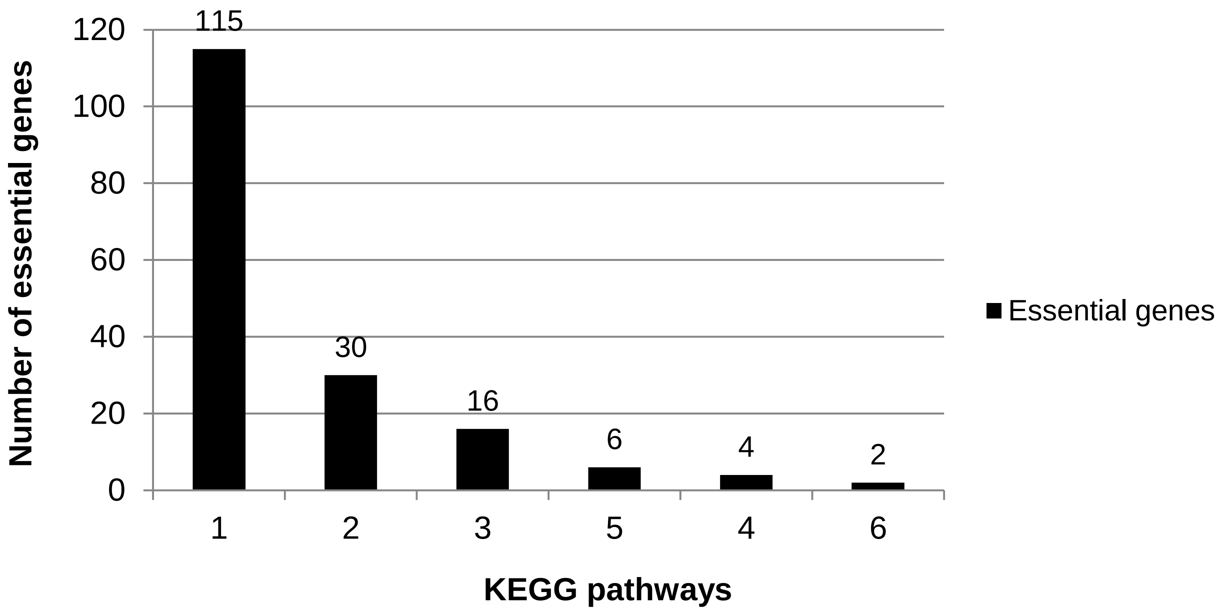
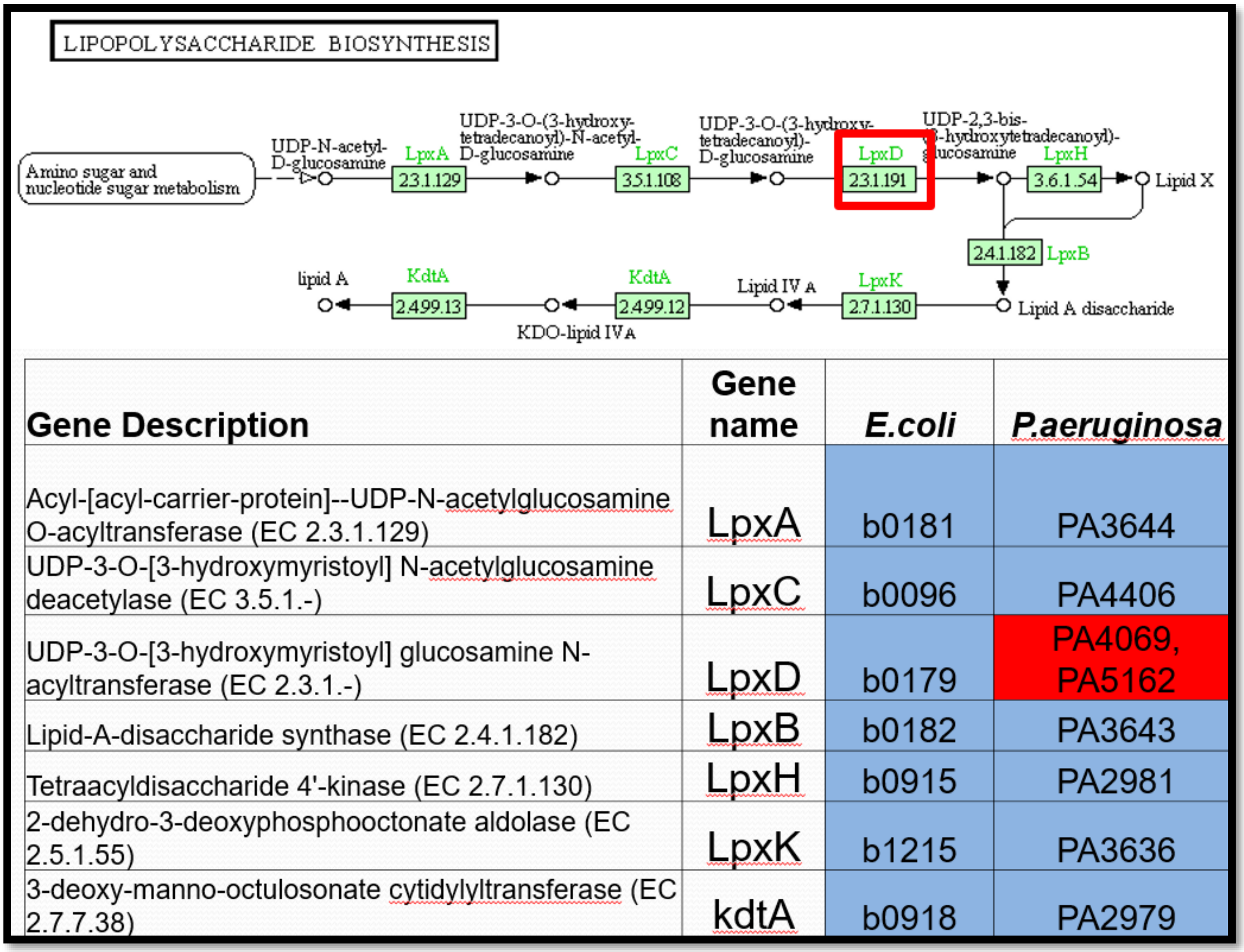

115
30
16
6
4
2
120
100
80
60
40
20
0
1
2
3
5
4
6
Number of essential genes
KEGG pathways
■ Essential genes

Figure 2. **Involvement of essential genes in *S. sanguinis* SK36 physiological pathways as described by KEGG database**. The count of KEGG pathways (x-axis) in which essential genes are involved (y-axis and number at top of every chart bar) is shown in this bar chart.

To further identify the pleiotropic functions of *S. sanguinis* essential genes, we measured the number of pathways in which every essential gene is involved, as described by KEGG database (Fig. 2). Although the majority of essential genes (115 genes) were shown to be involved in one pathway, we need not to underestimate the moonlighting effect of many essential genes in *S. sanguinis* that are yet to be experimentally defined. Of special emphasis are many components of the genetic processing machinery (ribosomal components of 50S and 30S subunits, elongation factor Ef-Tu, threonyl-tRNA synthetase, Alanyl-tRNA synthetase, leucyl-tRNA synthetase) which are underappreciated pleiotropic players in *S. sanguinis*, although they have been established as pleiotropic players in many model species (http://www.moonlightingproteins.org/). Another major factor to ponder is the absence of "genetic pathways" in KEGG database, with more focus on metabolic pathways.



Gene Description	**Gene name**	***E.coli***	***P.aeruginosa***
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)	LpxA	b0181	PA3644
UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-)	LpxC	b0096	PA4406
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-)	LpxD	b0179	PA4069, PA5162
Lipid-A-disaccharide synthase (EC 2.4.1.182)	LpxB	b0182	PA3643
Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)	LpxH	b0915	PA2981
2-dehydro-3-deoxyphosphooctonate aldolase (EC 2.5.1.55)	LpxK	b1215	PA3636
3-deoxy-manno-octulosonate cytidylyltransferase (EC 2.7.7.38)	kdtA	b0918	PA2979

Figure 3. A schematic example for the prediction framework of essential genes.
The example provided demonstrates the prediction of essential genes using the lipopolysaccharide pathway in *E. coli* and *P. aeruginosa* bacterial models. The genes in the green boxes are predicted to be essential. In the case of *P. aeruginosa*, the presence of two homologs (Paralogs PA4069 and PA5162) indicates two genes with same function. We predict both genes to be essential.

Linking essential genes across databases. Genes are labelled differently across different databases: The genes are labelled in DEG database through DEG codes (unique identifiers), in NCBI database through GI number and gene ID (unique identifiers), and in KEGG database through KO numbers and gene symbols. We unified the genes' nomenclature across all databases by blasting the amino acid sequences of all proteins and using GI number or gene locus as a unique identifier of every protein.

Validation of essential genes' prediction framework. We compared our lists of predicted essential genes to the experimentally verified lists of essential genes as deposited in DEG database (Table 1). We calculated the accuracy of our prediction framework as follows:

$$\text{Accuracy percentage} = \frac{\text{common genes between experimental and predicted genes} \times 100}{\text{Experimentally verified essential genes}}$$

Table 1. Comparison of experimentally verified essential genes to our predicted list.

Organisms	Organism type	Genome size	Total Genes	Experimental essential genes	Predicted Essential genes	Accurate % (common genes)
Streptococcus sanguinis SK36	Gram positive	2.4 Mb	2270	218	215	98.6%(215 genes)
Bacillus subtilis 168	Gram positive	4.22 Mb	4175	273	364	94.5%(258 genes)
Mycobacterium tuberculosis H37Rv	Gram-positive, acid-fast	4.41 Mb	3906	614	638	48.2%(514 genes)
Mycoplasma genitalium G37	no cell wall	0.58 Mb	475	378	227	58.5%(221 genes)
Mycoplasma pulmonis UAB CTIP	no cell wall	0.96 Mb	749	311	344	75.2%(234 genes)
Porphyromonas gingivalis TDC60	Gram negative	2.35 Mb	2118	NA	395	NA
Porphyromonas gingivalis ATCC 33276	Gram negative	2.35 Mb	1,869	463	396	67.4%(312 genes)
Porphyromonas gingivalis W83	Gram negative	2.34 Mb	1858	759	393	39.7%(301 genes)
Pseudomonas aeruginosa UCBPP-PA14	Gram negative	6.54 Mb	5,873	434	422	63% (273 genes)
Pseudomonas aeruginosa PAO1	Gram negative	6.26 Mb	5572	337	421	67% (226 genes)
Staphylococcus aureus NCTC 8325	Gram positive	2.82 Mb	2767	401	301	63.3% (254 genes)
Streptococcus pneumoniae TIGR4	Gram positive	2.16 Mb	2105	243	341	74.5% (181 genes)

Functional distribution of predicted essential genes. We investigated the functional categorization of predicted essential genes and their identified orthologs in Gram-positive bacterial models. We noticed a pattern of essential functional categorization being dominated by the "genetic information processing" category in all Gram-positive bacteria (Fig. 4). This concurs with another finding were investigated the conservation of the *S. sanguinis* experimentally verified essential proteins among 2774 bacterial proteomes and found that pathways involved in "genetic information processing", namely translation and transcription, exhibit a high degree of conservation (Fig. 5).

Based on COG functional categories, we found that *S. sanguinis* essential genes are unevenly distributed in functional categories (Fig. 5), biased towards translation (33.2% of essential genes), replication and repair (10.7%), lipid metabolism (9%), and cell wall/membrane/envelop biogenesis (7.6%). Given the fact that essential *S. sanguinis* genes are only 218 genes (9.6% of genome) [162], it is unsurprising that essential genes do not outnumber non-essential genes in any functional category. With 752 non-essential genes defined as hypothetical genes, the functional categories most enriched with non-essential genes are "General functional prediction only" (11.7% of non-essential genes) and "Function unknown" (10.6%). COG categories related to energy production were shown to be highly enriched with non-essential genes: Amino Acid metabolism and transport (11%) and carbohydrate metabolism and transport (9%). This may be explained by the fact that the essentiality study for *S. sanguinis* was conducted in a nutrient-rich brain heart infusion (BHI) medium, where the need for many genes involved in biosynthesis of carbohydrate and amino acids was abrogated. Finally, in comparison to essential genes, non-essential genes are less biased to essential genes-favored categories: translation (4.6 % of non-essential genes), replication and repair (5 %), lipid metabolism (1.1 %), and cell wall/membrane/envelop biogenesis (5.8 %), reflecting an interplay between essential and non-essential genes within same functional category and pathways that can be explained by presence of alternative pathways, gene paralogs, and culture conditions.

Table 2. Orthologs of the predicted essential proteins in 4 Gram-positive bacterial species.

Gene description	*S. sanguinis*	*Bacillus subtilis*	*S. aureus*	*S. pneumoniae*	Function
phosphoglycerate kinase	SSA_0302	BSU33930	SAOUHSC_00796	SP_0499	E
4'-phosphopantetheinyl transferase	SSA_0547	BSU04620	SAOUHSC_02306	SP_1699	E
6-phosphofructokinase	SSA_0847	BSU29190	SAOUHSC_01807	SP_0896	E
triosephosphate isomerase	SSA_0859	BSU33920	SAOUHSC_00797	SP_1574	E
phosphopyruvate hydratase	SSA_0886	BSU33900	SAOUHSC_00799	SP_1128	E
biotin--protein ligase	SSA_0999	BSU22440	SAOUHSC_01473	SP_1900	E
S-adenosylmethionine synthetase	SSA_1495	BSU30550	SAOUHSC_01909	SP_0762	E
dephospho-CoA kinase	SSA_1606	BSU29060	SAOUHSC_01795	SP_0971	E
manganese-dependent inorganic pyrophosphatase	SSA_1748	BSU40550	SAOUHSC_02140	SP_1534	E
nicotinate phosphoribosyltransferase	SSA_1864	BSU31750	SAOUHSC_02133	SP_1421	E
pyridoxal-phosphate dependent aminotransferase	SSA_1213	BSU27510	SAOUHSC_01727	SP_1094	E
ribonuclease P protein component	SSA_2140	BSU41050	SAOUHSC_03054	SP_2042	G
dihydrofolate reductase	SSA_1092	BSU21810	SAOUHSC_01434	SP_1571	G
adenylate kinase	SSA_0128	BSU01370	SAOUHSC_02490	SP_0231	G
ribosome biogenesis GTP-binding protein YsxC	SSA_1094	BSU28190	SAOUHSC_01777	SP_1568	G
GTPase ObgE	SSA_0807	BSU27920	SAOUHSC_01753	SP_1079	G
GTP-binding protein EngA	SSA_1803	BSU22840	SAOUHSC_01492	SP_1709	G
peptidyl-tRNA hydrolase	SSA_0006	BSU00530	SAOUHSC_00475	SP_0005	G
30S ribosomal protein S19	SSA_0111	BSU01200	SAOUHSC_02508	SP_0213	G
30S ribosomal protein S17	SSA_0116	BSU01250	SAOUHSC_02503	SP_0218	G
translation initiation factor IF-1	SSA_0129	BSU01390	SAOUHSC_02489	SP_0232	G
30S ribosomal protein S11	SSA_0131	BSU01420	SAOUHSC_02486	SP_0235	G
DNA-directed RNA polymerase subunit beta'	SSA_0177	BSU01080	SAOUHSC_00525	SP_1960	G
molecular chaperone GroEL	SSA_0226	BSU06030	SAOUHSC_02254	SP_1906	G
30S ribosomal protein S18	SSA_0440	BSU40890	SAOUHSC_00350	SP_1539	G
aspartyl/glutamyl-tRNA	SSA_0569	BSU06670	SAOUHSC_02118	SP_0438	G
aspartyl/glutamyl-tRNA amidotransferase subunit B	SSA_0571	BSU06690	SAOUHSC_02116	SP_0436	G
isoleucyl-tRNA synthetase	SSA_0661	BSU15430	SAOUHSC_01159	SP_1659	G
DNA primase	SSA_0824	BSU25210	SAOUHSC_01663	SP_1072	G
DNA gyrase subunit B	SSA_0878	BSU00060	SAOUHSC_00005	SP_0806	G
phenylalanyl-tRNA synthetase subunit beta	SSA_0914	BSU28630	SAOUHSC_01093	SP_0581	G
DNA polymerase III subunits gamma and tau	SSA_0997	BSU00190	SAOUHSC_00442	SP_0865	G

Gene description	*S. sanguinis*	*Bacillus subtilis*	*S. aureus*	*S. pneumoniae*	Function
tRNA CCA-pyrophosphorylase	SSA_1086	BSU22450	SAOUHSC_01474	SP_1554	G
peptide chain release factor 1	SSA_1152	BSU37010	SAOUHSC_02359	SP_1020	G
ribosomal biogenesis GTPase	SSA_1189	BSU16050	SAOUHSC_01214	SP_1155	G
DNA topoisomerase IV subunit B	SSA_1232	BSU18090	SAOUHSC_01351	SP_0852	G
tRNA (guanine-N(1)-)-	SSA_1302	BSU16030	SAOUHSC_01210	SP_0779	G
ribonuclease Z	SSA_1430	BSU23840	SAOUHSC_01598	SP_0674	G
NAD-dependent DNA ligase LigA	SSA_1484	BSU06620	SAOUHSC_02122	SP_1117	G
translation initiation factor IF-3	SSA_1500	BSU28870	SAOUHSC_01786	SP_0959	G
lysyl-tRNA synthetase	SSA_1529	BSU00820	SAOUHSC_00493	SP_0713	G
SRPR, signal recognition particle-	SSA_1557	BSU15950	SAOUHSC_01205	SP_1244	G
ribosome recycling factor	SSA_1619	BSU16520	SAOUHSC_01236	SP_0945	G
DNA polymerase III subunit delta'	SSA_1721	BSU00310	SAOUHSC_00442	SP_0936	G
methionyl-tRNA formyltransferase	SSA_1848	BSU15730	SAOUHSC_01183	SP_1735	G
seryl-tRNA synthetase	SSA_1925	BSU00130	SAOUHSC_00009	SP_0411	G
elongation factor G	SSA_2109	BSU01120	SAOUHSC_00529	SP_0273	G
glutamyl-tRNA synthetase	SSA_2144	BSU00920	SAOUHSC_00509	SP_2069	G
tryptophanyl-tRNA synthetase II	SSA_2375	BSU11420	SAOUHSC_00933	SP_2229	G
phosphoglucosamine mutase	SSA_0804	BSU01770	SAOUHSC_02405	SP_1559	C
bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	SSA_1642	BSU00500	SAOUHSC_00471	SP_1267	C
1-acyl-sn-glycerol-3-phosphate acyltransferase	SSA_0713	BSU09540	SAOUHSC_01837	SP_1624	C
glycerol-3-phosphate acyltransferase PlsY	SSA_1233	BSU18070	SAOUHSC_01350	SP_0851	C
acetyl-CoA carboxylase subunit	SSA_1930	BSU29200	SAOUHSC_01808	SP_0427	C
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	SSA_2368	BSU16920	SAOUHSC_01260	SP_2222	C
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	SSA_0652	BSU15200	SAOUHSC_01147	SP_0688	C
D-alanyl-alanine synthetase A	SSA_0691	BSU04560	SAOUHSC_02318	SP_1671	C
D-Ala-D-Ala adding enzyme	SSA_0692	BSU04570	SAOUHSC_02317	SP_1670	C
UDP-N-acetylenolpyruvoylglucosamine reductase	SSA_1047	BSU15230	SAOUHSC_00752	SP_1390	C
UDP-N-acetylmuramoylalanyl-D-	SSA_1739	BSU15180	SAOUHSC_00954	SP_1530	C
UDP-N-acetylmuramate--L-alanine ligase	SSA_1800	BSU29790	SAOUHSC_01856	SP_1521	C
phospho-N-acetylmuramoyl-pentapeptide-transferase	SSA_1870	BSU15190	SAOUHSC_01146	SP_0337	C
cell division protein FtsZ	SSA_0656	BSU15290	SAOUHSC_01150	SP_1666	C

Abbreviations: G, genetic information processing; E, energy production; C, cell wall biosynthesis.

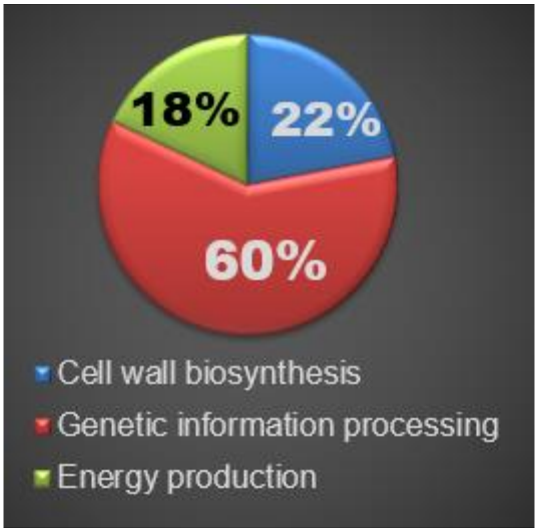


Figure 4. Functional categorization of the orthologs of the predicted essential genes in 4 Gram-positive bacterial species. Abbreviations: G, genetic information processing; M, metabolism and energy production; C, cell wall biosynthesis.

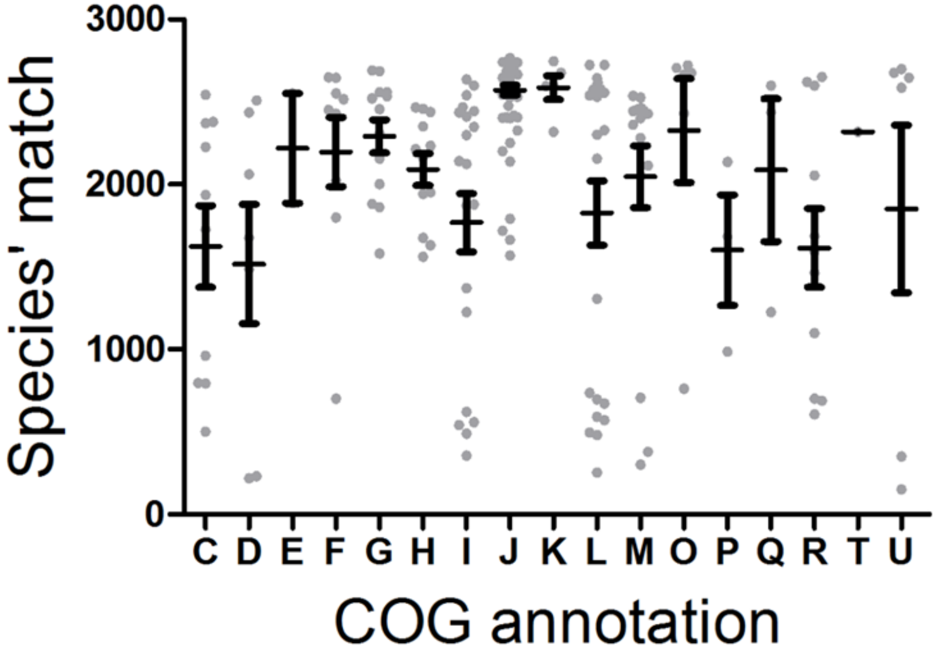
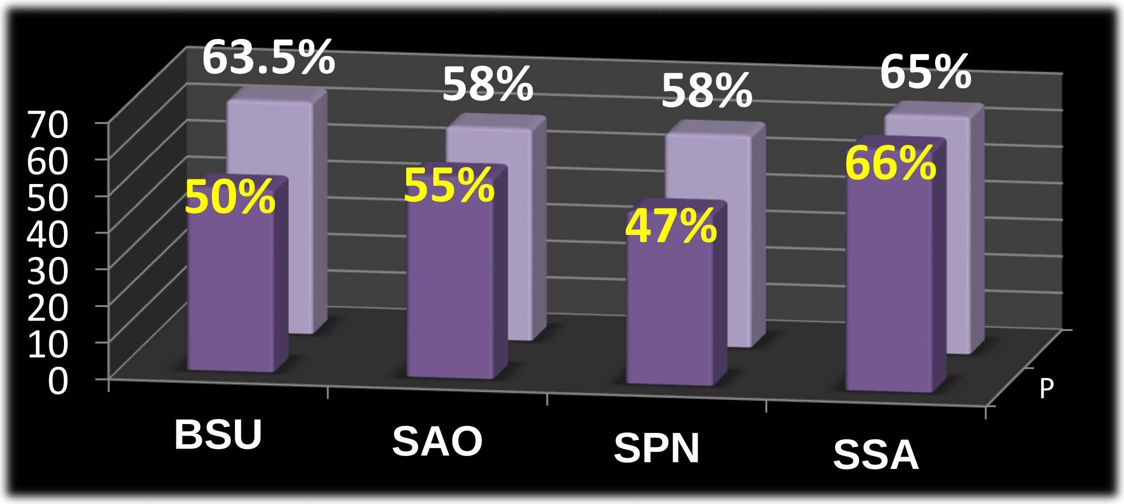

3000
2000
1000
0
Species' match
C
D
E
F
G
H
I
J
K
L
M
O
P
Q
R
T
U
COG annotation

Figure 5. Conservation of *S. sanguinis* essential proteins' orthologs across 2774 bacterial proteomes based on COG annotation. *S. sanguinis* were blasted against proteomes of 2774 bacteria and a best match was identified with E-value < 10^{-5} and identity >50%. Essential proteins were grouped according to their COG annotations into the following functional categories: C, energy production and conversion; D, Cell cycle control and mitosis; E, Amino Acid metabolism and transport; F,Nucleotide metabolism and transport; G, Carbohydrate metabolism and transport; H, Coenzyme metabolism; I, Lipid metabolism; J, Translation; K, Transcription; L, Replication and repair; M, Cell wall/membrane/envelop biogenesis; O, Post-translational modification, protein turnover, chaperone functions; P, Inorganic ion transport and metabolism; Q, Secondary Structure; R, General Functional Prediction only; T, Signal Transduction; U, Intracellular trafficking and secretion; N, Cell motility, secretion, and vesicular transport; S, Function unknown; V, Defense mechanisms.

Detection of essential genes' paralogs. We investigated the presence of paralogs among essential genes detected in the 4 Gram-positive bacterial strains (Fig. 6). For every set of predicted essential genes belonging to a bacterial strain, we identified all possible paralogs and then calculated the percentage distribution of those paralogs into 3 functional groups: cell wall biosynthesis, genetic information processing, and energy production. We found that the percentages of predicted essential genes with paralogs outweighed those without paralogs only in cell wall biosynthesis category, reflecting the effect of gene duplication as an adaptive evolutionary tool in response to ecological selective pressures.

Finally, we compared the paralogs of the essential genes' orthologs among the 4 bacterial strains. We found that orthologs involved in cell wall biosynthesis have a high ratio of paralogs with respect to orthologs, while the other two functional groups have a low paralog/ortholog ratio.


40
20
0
28%
15%
28%
17%
40%
23%
26%
18%
BSU
SAO
SPN
SSA
P


70
60
50
40
30
20
10
0
63.5%
58%
58%
65%
50%
55%
47%
66%
BSU
SAO
SPN
SSA
P

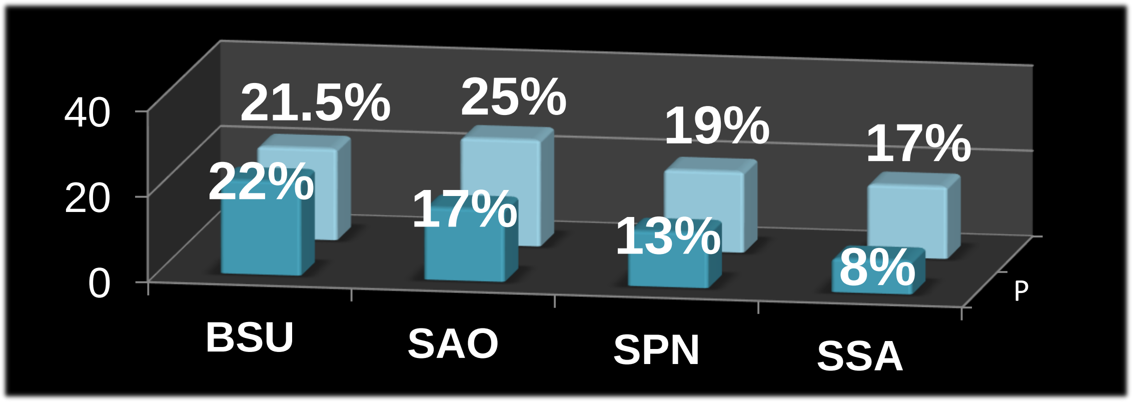
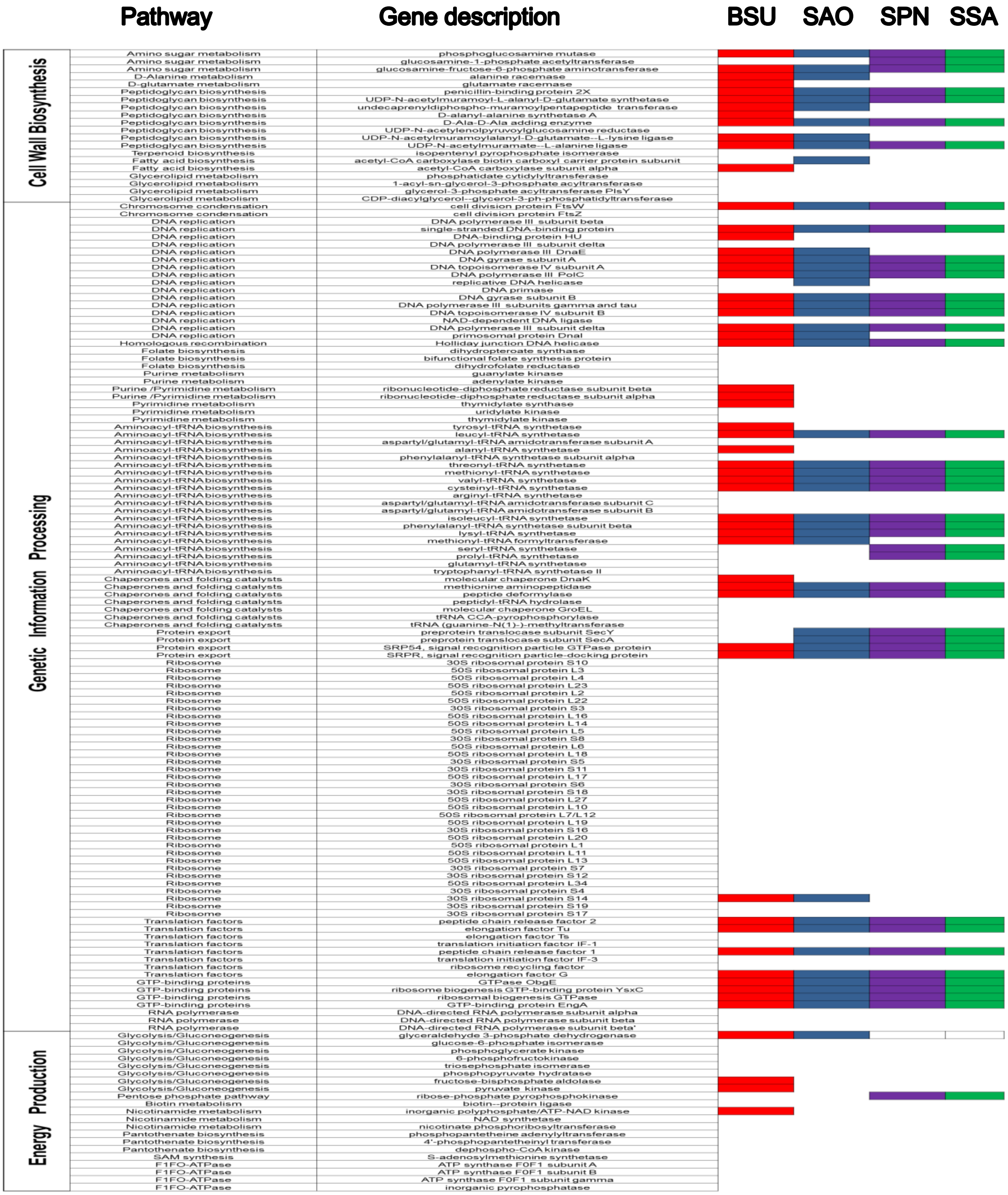

40
20
0
21.5%
25%
19%
17%
22%
17%
13%
8%
BSU
SAO
SPN
SSA
P

Figure 6. Distribution pattern of paralogs among essential functions. Comparison of percentages of predicted essential genes involved in genetic information processing (Upper), cell wall biosynthesis (middle), and energy production (lower) that have paralogs (P) vs essential genes in same functional category that lack paralogs (NP) in four Gram-positive bacterial strains. Abbreviations: BSU: *Bacillus subtilis* 168; SSA: *Streptococcus sanguinis* SK36; SPN: *Streptococcus pneumoniae* TIGR4; SAO: *Staphylococcus aureus* NCTC 8325.

Table 3. **A comparative analysis of paralogs of all orthologs derived from predicted essential genes**. The paralogs for all shared orthologs derived from the predicted essential genes in 4 Gram-positive bacterial strains were measured across different functional pathways.



	Pathway	Gene description	BSU	SAO	SPN	SSA
Cell Wall Biosynthesis	Amino sugar metabolism	phosphoglucosamine mutase	🟥	🟦	🟪	🟩
	Amino sugar metabolism	glucosamine-1-phosphate acetyltransferase			🟪	🟩
	Amino sugar metabolism	glucosamine-fructose-6-phosphate aminotransferase	🟥	🟦	🟪	🟩
	D-Alanine metabolism	alanine racemase	🟥	🟦		
	D-glutamate metabolism	glutamate racemase	🟥			
	Peptidoglycan biosynthesis	penicillin-binding protein 2X	🟥	🟦	🟪	🟩
	Peptidoglycan biosynthesis	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	🟥	🟦	🟪	🟩
	Peptidoglycan biosynthesis	undecaprenyldiphospho-muramoylpentapeptide transferase	🟥	🟦		
	Peptidoglycan biosynthesis	D-alanyl-alanine synthetase A	🟥			
	Peptidoglycan biosynthesis	D-Ala-D-Ala adding enzyme	🟥	🟦	🟪	🟩
	Peptidoglycan biosynthesis	UDP-N-acetylenolpyruvoylglucosamine reductase				
	Peptidoglycan biosynthesis	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase	🟥	🟦		
	Peptidoglycan biosynthesis	UDP-N-acetylmuramate--L-alanine ligase	🟥	🟦	🟪	🟩
	Terpenoid biosynthesis	isopentenyl pyrophosphate isomerase				
	Fatty acid biosynthesis	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit		🟦		
	Fatty acid biosynthesis	acetyl-CoA carboxylase subunit alpha	🟥			
	Glycerolipid metabolism	phosphatidate cytidylyltransferase				
	Glycerolipid metabolism	1-acyl-sn-glycerol-3-phosphate acyltransferase				
	Glycerolipid metabolism	glycerol-3-phosphate acyltransferase PlsY				
	Glycerolipid metabolism	CDP-diacylglycerol--glycerol-3-ph-phosphatidyltransferase				
Genetic Information Processing	Chromosome condensation	cell division protein FtsW	🟥	🟦	🟪	🟩
	Chromosome condensation	cell division protein FtsZ				
	DNA replication	DNA polymerase III subunit beta				
	DNA replication	single-stranded DNA-binding protein	🟥	🟦	🟪	🟩
	DNA replication	DNA-binding protein HU	🟥			
	DNA replication	DNA polymerase III subunit delta				
	DNA replication	DNA polymerase III DnaE	🟥	🟦		
	DNA replication	DNA gyrase subunit A	🟥	🟦	🟪	🟩
	DNA replication	DNA topoisomerase IV subunit A	🟥	🟦	🟪	🟩
	DNA replication	DNA polymerase III PolC	🟥	🟦	🟪	🟩
	DNA replication	replicative DNA helicase		🟦		
	DNA replication	DNA primase				
	DNA replication	DNA gyrase subunit B	🟥	🟦	🟪	🟩
	DNA replication	DNA polymerase III subunits gamma and tau	🟥	🟦	🟪	🟩
	DNA replication	DNA topoisomerase IV subunit B	🟥	🟦	🟪	🟩
	DNA replication	NAD-dependent DNA ligase				
	DNA replication	DNA polymerase III subunit delta	🟥	🟦	🟪	🟩
	DNA replication	primosomal protein DnaI	🟥	🟦		
	Homologous recombination	Holliday junction DNA helicase	🟥	🟦	🟪	🟩
	Folate biosynthesis	dihydropteroate synthase				
	Folate biosynthesis	bifunctional folate synthesis protein				
	Folate biosynthesis	dihydrofolate reductase				
	Purine metabolism	guanylate kinase				
	Purine metabolism	adenylate kinase				
	Purine /Pyrimidine metabolism	ribonucleotide-diphosphate reductase subunit beta	🟥			
	Purine /Pyrimidine metabolism	ribonucleotide-diphosphate reductase subunit alpha	🟥			
	Pyrimidine metabolism	thymidylate synthase	🟥			
	Pyrimidine metabolism	uridylate kinase				
	Pyrimidine metabolism	thymidylate kinase				
	Aminoacyl-tRNA biosynthesis	tyrosyl-tRNA synthetase	🟥			
	Aminoacyl-tRNA biosynthesis	leucyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	aspartyl/glutamyl-tRNA amidotransferase subunit A				
	Aminoacyl-tRNA biosynthesis	alanyl-tRNA synthetase	🟥			
	Aminoacyl-tRNA biosynthesis	phenylalanyl-tRNA synthetase subunit alpha				
	Aminoacyl-tRNA biosynthesis	threonyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	methionyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	valyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	cysteinyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	arginyl-tRNA synthetase				
	Aminoacyl-tRNA biosynthesis	aspartyl/glutamyl-tRNA amidotransferase subunit C				
	Aminoacyl-tRNA biosynthesis	aspartyl/glutamyl-tRNA amidotransferase subunit B				
	Aminoacyl-tRNA biosynthesis	isoleucyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	phenylalanyl-tRNA synthetase subunit beta	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	lysyl-tRNA synthetase	🟥	🟦	🟪	🟩
	Aminoacyl-tRNA biosynthesis	methionyl-tRNA formyltransferase	🟥	🟦		
	Aminoacyl-tRNA biosynthesis	seryl-tRNA synthetase			🟪	🟩
	Aminoacyl-tRNA biosynthesis	prolyl-tRNA synthetase			🟪	🟩
	Aminoacyl-tRNA biosynthesis	glutamyl-tRNA synthetase				
	Aminoacyl-tRNA biosynthesis	tryptophanyl-tRNA synthetase II				
	Chaperones and folding catalysts	molecular chaperone DnaK	🟥			
	Chaperones and folding catalysts	methionine aminopeptidase	🟥	🟦	🟪	🟩
	Chaperones and folding catalysts	peptide deformylase	🟥	🟦	🟪	🟩
	Chaperones and folding catalysts	peptidyl-tRNA hydrolase				
	Chaperones and folding catalysts	molecular chaperone GroEL				
	Chaperones and folding catalysts	tRNA CCA-pyrophosphorylase				
	Chaperones and folding catalysts	tRNA (guanine-N(1)-)-methyltransferase				
	Protein export	preprotein translocase subunit SecY		🟦	🟪	🟩
	Protein export	preprotein translocase subunit SecA		🟦	🟪	🟩
	Protein export	SRP54, signal recognition particle GTPase protein	🟥	🟦	🟪	🟩
	Protein export	SRPR, signal recognition particle-docking protein	🟥	🟦	🟪	🟩
	Ribosome	30S ribosomal protein S10				
	Ribosome	50S ribosomal protein L3				
	Ribosome	50S ribosomal protein L4				
	Ribosome	50S ribosomal protein L23				
	Ribosome	50S ribosomal protein L2				
	Ribosome	50S ribosomal protein L22				
	Ribosome	30S ribosomal protein S3				
	Ribosome	50S ribosomal protein L16				
	Ribosome	50S ribosomal protein L14				
	Ribosome	50S ribosomal protein L5				
	Ribosome	30S ribosomal protein S8				
	Ribosome	50S ribosomal protein L6				
	Ribosome	50S ribosomal protein L18				
	Ribosome	30S ribosomal protein S5				
	Ribosome	30S ribosomal protein S11				
	Ribosome	50S ribosomal protein L17				
	Ribosome	30S ribosomal protein S6				
	Ribosome	30S ribosomal protein S18				
	Ribosome	50S ribosomal protein L27				
	Ribosome	50S ribosomal protein L10				
	Ribosome	50S ribosomal protein L7/L12				
	Ribosome	50S ribosomal protein L19				
	Ribosome	30S ribosomal protein S16				
	Ribosome	50S ribosomal protein L20				
	Ribosome	50S ribosomal protein L1				
	Ribosome	50S ribosomal protein L11				
	Ribosome	50S ribosomal protein L13				
	Ribosome	30S ribosomal protein S7				
	Ribosome	30S ribosomal protein S12				
	Ribosome	50S ribosomal protein L34				
	Ribosome	30S ribosomal protein S4				
	Ribosome	30S ribosomal protein S14	🟥	🟦		
	Ribosome	30S ribosomal protein S19				
	Ribosome	30S ribosomal protein S17				
	Translation factors	peptide chain release factor 2	🟥	🟦	🟪	🟩
	Translation factors	elongation factor Tu	🟥	🟦	🟪	🟩
	Translation factors	elongation factor Ts				
	Translation factors	translation initiation factor IF-1				
	Translation factors	peptide chain release factor 1	🟥	🟦	🟪	🟩
	Translation factors	translation initiation factor IF-3				
	Translation factors	ribosome recycling factor				
	Translation factors	elongation factor G	🟥	🟦	🟪	🟩
	GTP-binding proteins	GTPase ObgE	🟥	🟦	🟪	🟩
	GTP-binding proteins	ribosome biogenesis GTP-binding protein YsxC	🟥	🟦	🟪	🟩
	GTP-binding proteins	ribosomal biogenesis GTPase	🟥	🟦	🟪	🟩
	GTP-binding proteins	GTP-binding protein EngA	🟥	🟦	🟪	🟩
	RNA polymerase	DNA-directed RNA polymerase subunit alpha				
	RNA polymerase	DNA-directed RNA polymerase subunit beta				
	RNA polymerase	DNA-directed RNA polymerase subunit beta'				
Energy Production	Glycolysis/Gluconeogenesis	glyceraldehyde 3-phosphate dehydrogenase	🟥	🟦		
	Glycolysis/Gluconeogenesis	glucose-6-phosphate isomerase				
	Glycolysis/Gluconeogenesis	phosphoglycerate kinase				
	Glycolysis/Gluconeogenesis	6-phosphofructokinase				
	Glycolysis/Gluconeogenesis	triosephosphate isomerase				
	Glycolysis/Gluconeogenesis	phosphopyruvate hydratase				
	Glycolysis/Gluconeogenesis	fructose-bisphosphate aldolase	🟥			
	Glycolysis/Gluconeogenesis	pyruvate kinase	🟥			
	Pentose phosphate pathway	ribose-phosphate pyrophosphokinase			🟪	🟩
	Biotin metabolism	biotin--protein ligase				
	Nicotinamide metabolism	inorganic polyphosphate/ATP-NAD kinase	🟥			
	Nicotinamide metabolism	NAD synthetase				
	Nicotinamide metabolism	nicotinate phosphoribosyltransferase				
	Pantothenate biosynthesis	phosphopantetheine adenylyltransferase				
	Pantothenate biosynthesis	4'-phosphopantetheinyl transferase				
	Pantothenate biosynthesis	dephospho-CoA kinase				
	SAM synthesis	S-adenosylmethionine synthetase				
	F1FO-ATPase	ATP synthase F0F1 subunit A				
	F1FO-ATPase	ATP synthase F0F1 subunit B				
	F1FO-ATPase	ATP synthase F0F1 subunit gamma				
	F1FO-ATPase	inorganic pyrophosphatase				

Biological significance of predicted essential genes in Gram-negative bacterial models. We predicted our set of essential genes in many Gram-negative bacterial models, looking for clues that essential genes can provide regarding the behavior of bacteria: substrate bias, habitat, virulence (Supplementary table 1).

Looking into *Mycoplasma pulmonis* UAB CTIP and *Mycoplasma genitalium* G37, our predicted sets of essential genes provided clues about these parasitic bacteria using host-dependent metabolites for survival: glucose as primary source for glycolysis and pentose-phosphate pathway, no essential genes in TCA cycle, and small number of ATP synthase subunits (16 essential genes). Added to the finding that no essential genes were predicted in amino acid and cofactor biosynthesis, it was evident the dependency on host-derived metabolites for these products. Perhaps that explained the abundance of predicted essential genes among ABC transporters (28 genes).

E. coli K-12 substr. MG1655 demonstrated a lifestyle of a free living and an intestinal bacterium. It was predicted to possess 24 essential genes for LPS biosynthesis, 37 genes for cell wall biogenesis, 20 genes involved in carbohydrate metabolism and another 39 genes involved in amino acid metabolism, in addition to 43 essential genes contributing to co-enzymes metabolism. All this contributes to a profile of a bacterium characterized by a metabolic independency that can adapt to versatile environments, especially if couples to 33 essential genes involved in transcription, 23 genes for translation, and 51 involved in ribosomal biogenesis, boosting its potential for growth and protein synthesis in diverse conditions.

P. gingivalis ATCC 33277, *P. gingivalis* TDC60, and *P. gingivalis* W83, two periodontal pathogens were investigated for their essential genome. Both lacked predicted essential genes involved in complete glycolysis and pentose phosphate pathways, but predicted essential genes were enriched in amino acid biosynthesis pathways, reflecting the fact that *P. gingivalis* is asaccharolytic. In addition, we didn't detect any predicted essential genes that contribute to additional pathogenicity between the two strains.

P. aeruginosa UCBPP-PA14 and *P. aeruginosa* PAO1 are two free living bacterial species that are prevalent nosocomial pathogens. Pseudomonas demonstrate nutritional versatility as predicted essential genes were enriched in pathways related to amino acid biosynthesis, succinate and citrate metabolism. Their energy production is dependent on ATP synthetase, porphyrin & ubiquinones, as our pattern of predicted essential genes shows.

Networks parameters of predicted essential genes. Based on KEGG database, we extracted pathways loaded with predicted essential genes and constructed a network that harbors the most of these predicted genes as nodes to investigate the network parameters (Fig. 7). We calculated the network parameters (DC, BC, CC) of predicted essential genes based on this constructed graph (Table 4) and we further investigated the conservation of the predicted essential genes with the highest network parameters among 2774 bacterial species (Table 5).

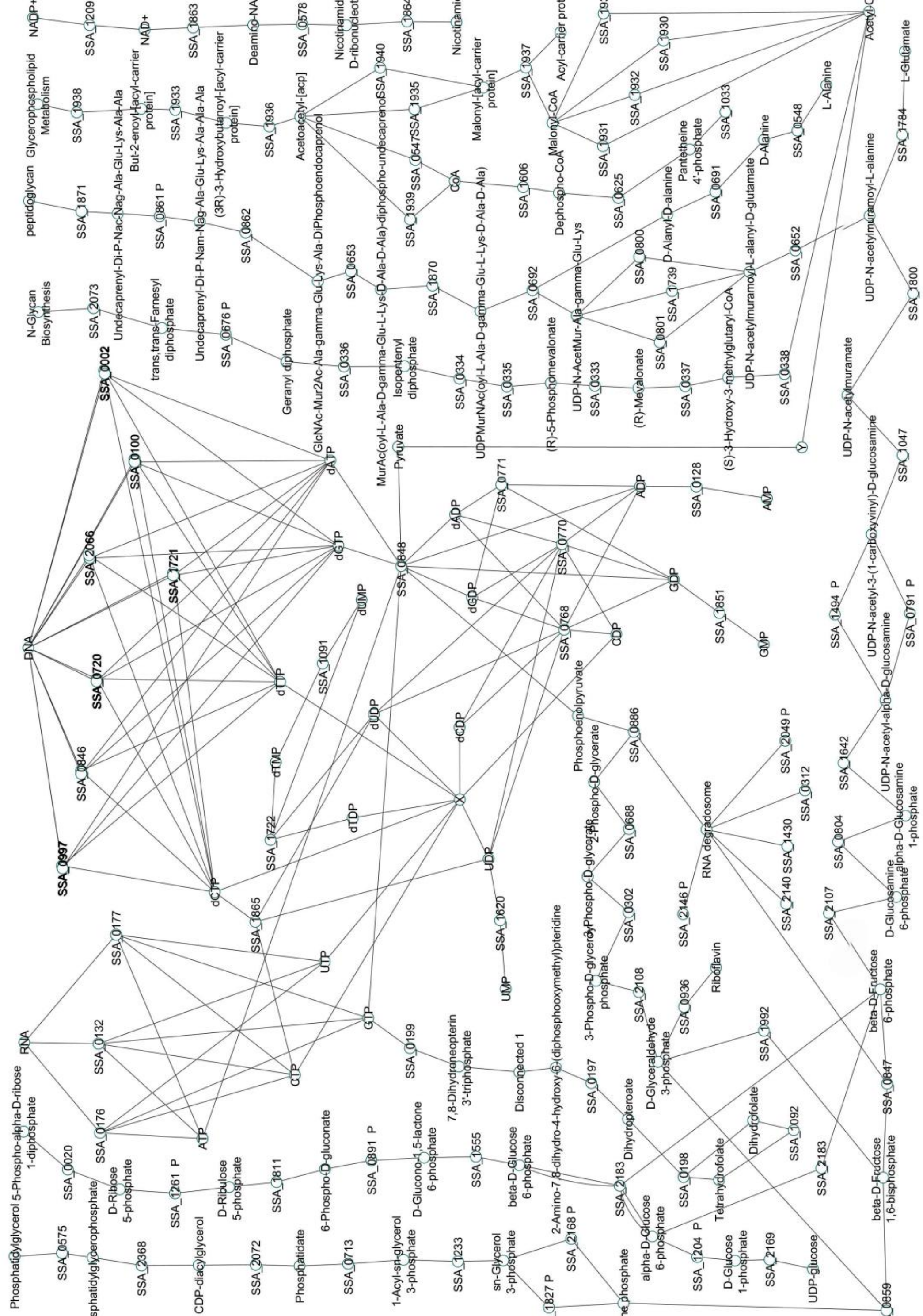
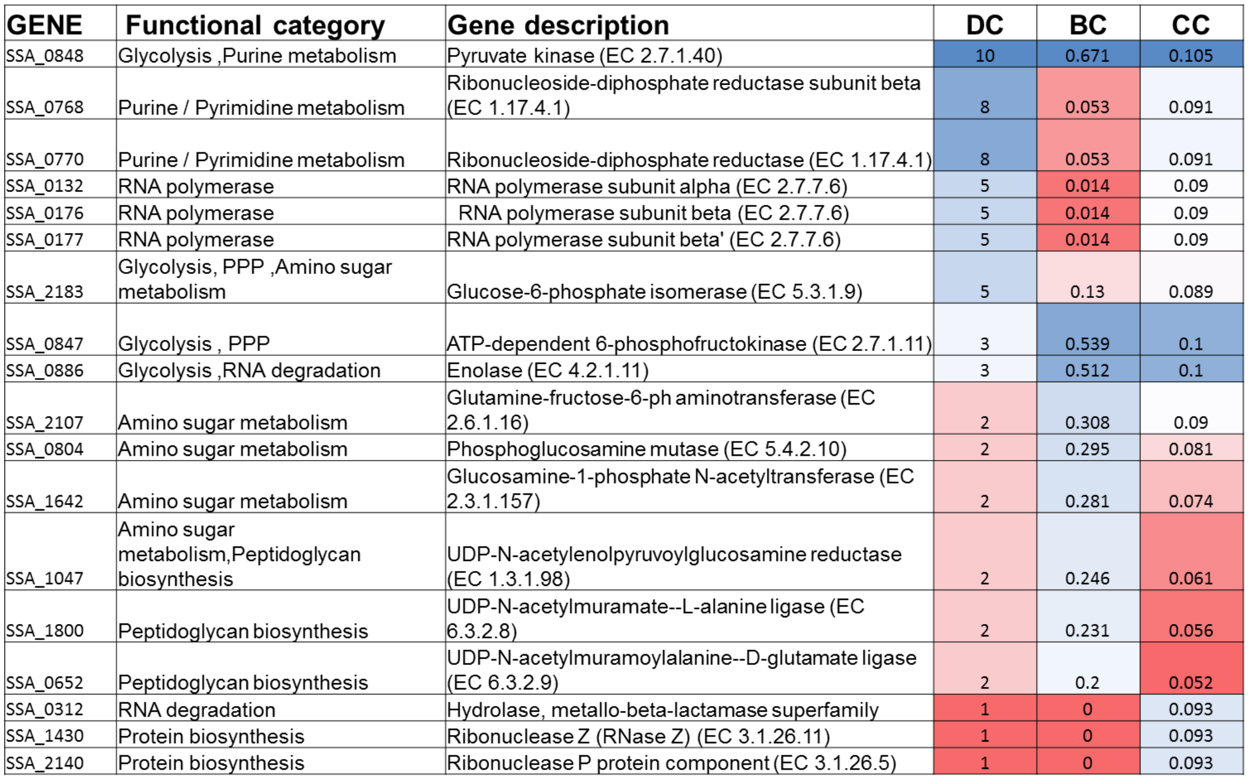

NADP+
SSA_1209
NAD+
SSA_1863
Deamino-NAD+
SSA_0578 P
Nicotinamide D-ribonucleotide
SSA_1864
Nicotinamide
Glycerophospholipid Metabolism
SSA_1938
But-2-enoyl-[acyl-carrier protein]
SSA_1933
(3R)-3-Hydroxybutanoyl-[acyl-carrier protein]
SSA_1936
Acetoacetyl-[acp]
SSA_1940
SSA_1935
Malonyl-[acyl-carrier protein]
SSA_1937
Acyl-carrier protein
SSA_1934
SSA_1930
Acetyl-CoA
L-Glutamate
peptidoglycan
SSA_1871
Undecaprenyl-Di-P-Nac-Nag-Ala-Glu-Lys-Ala-Ala
SSA_0861 P
Undecaprenyl-Di-P-Nam-Nag-Ala-Glu-Lys-Ala-Ala
SSA_0862
GlcNAc-Mur2Ac-Ala-gamma-Glu-Lys-Ala-DiPhosphoendocaprenol
SSA_0653
MurAc(oyl-L-Ala-D-gamma-Glu-L-Lys-D-Ala-D-Ala)-diphospho-undecaprenol
SSA_1870
SSA_1939
SSA_0547
CoA
SSA_1606
Dephospho-CoA
Malonyl-CoA
SSA_1932
SSA_1931
SSA_0625
Pantetheine 4'-phosphate
SSA_1033
D-Alanine
SSA_0548
L-Alanine
SSA_1784
N-Glycan Biosynthesis
SSA_2073
trans,trans-Farnesyl diphosphate
SSA_0676 P
Geranyl diphosphate
SSA_0336
Isopentenyl diphosphate
SSA_0334
UDPMurNAc(oyl-L-Ala-D-gamma-Glu-L-Lys-D-Ala-D-Ala)
SSA_0335
SSA_0692
(R)-5-Phosphomevalonate
UDP-N-AcetMur-Ala-gamma-Glu-Lys
SSA_0333
(R)-Mevalonate
SSA_0800
SSA_1739
D-Alanyl-D-alanine
SSA_0691
SSA_0801
SSA_0337
(S)-3-Hydroxy-3-methylglutaryl-CoA
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate
SSA_0652
SSA_0338
UDP-N-acetylmuramoyl-L-alanine
SSA_1800
UDP-N-acetylmuramate
SSA_0002
SSA_0100
SSA_2066
SSA_1721
DNA
SSA_0720
SSA_0846
SSA_0997
dATP
dGTP
dTTP
dCTP
Pyruvate
Y
SSA_0771
dADP
ADP
SSA_0128
AMP
SSA_0848
SSA_0770
dGDP
GDP
SSA_1851
GMP
SSA_0768
CDP
dUMP
SSA_1091
dUDP
dTMP
SSA_1722
dTDP
dCDP
X
UDP
SSA_1865
SSA_1620
UMP
UDP-N-acetylglucosamine
SSA_1047
UDP-N-acetyl-3-(1-carboxyvinyl)-D-glucosamine
SSA_1494 P
SSA_0791 P
UDP-N-acetyl-alpha-D-glucosamine
SSA_1642
UDP-N-acetyl-D-glucosamine 1-phosphate
alpha-D-Glucosamine 1-phosphate
SSA_0804
D-Glucosamine 6-phosphate
SSA_2107
Phosphoenolpyruvate
SSA_0886
2-Phospho-D-glycerate
SSA_0688
3-Phospho-D-glycerate
SSA_0302
3-Phospho-D-glyceroyl phosphate
SSA_2108
RNA degradosome
SSA_2049 P
SSA_0312
SSA_1430
SSA_2140
SSA_2146 P
Riboflavin
SSA_0936
D-Glyceraldehyde 3-phosphate
SSA_1992
beta-D-Fructose 6-phosphate
SSA_0647
beta-D-Fructose 1,6-bisphosphate
SSA_0659
RNA
SSA_0177
SSA_0132
SSA_0176
UTP
GTP
CTP
ATP
SSA_0199
7,8-Dihydroneopterin 3'-triphosphate
Disconnected 1
2-Amino-7,8-dihydro-4-hydroxy-6-(diphosphooxymethyl)pteridine
SSA_0197
Dihydropteroate
SSA_0198
Dihydrofolate
SSA_1092
Tetrahydrofolate
SSA_2183
5-Phospho-alpha-D-ribose 1-diphosphate
SSA_0020
D-Ribose 5-phosphate
SSA_1261 P
D-Ribulose 5-phosphate
SSA_1811
6-Phospho-D-gluconate
SSA_0891 P
D-Glucono-1,5-lactone 6-phosphate
SSA_1555
beta-D-Glucose 6-phosphate
SSA_2183
alpha-D-Glucose 6-phosphate
SSA_1204 P
D-Glucose 1-phosphate
SSA_2169
UDP-glucose
Phosphatidylglycerol
SSA_0575
Phosphatidylglycerophosphate
SSA_2368
CDP-diacylglycerol
SSA_2072
Phosphatidate
SSA_0713
1-Acyl-sn-glycerol 3-phosphate
SSA_1233
sn-Glycerol 3-phosphate
SSA_2168 P
SSA_1827 P
Glycerone phosphate

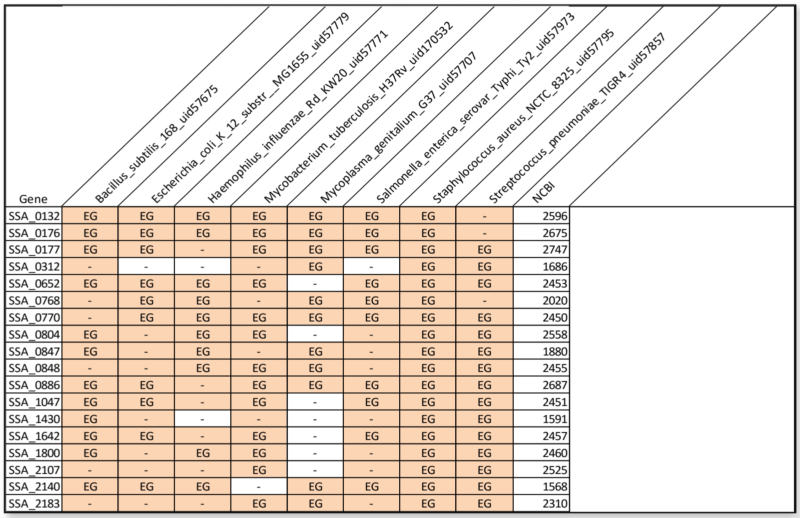
Figure 7. Network scheme encompassing *S. sanguinis* predicted essential genes. Every node represents an essential gene and interactions were shown as edges between nodes, as described in KEGG database.

Table 4. **Network parameters of predicted essential genes in *S. sanguinis* based on the constructed graph of essential genome.**



GENE	Functional category	Gene description	DC	BC	CC
SSA_0848	Glycolysis ,Purine metabolism	Pyruvate kinase (EC 2.7.1.40)	10	0.671	0.105
SSA_0768	Purine / Pyrimidine metabolism	Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	8	0.053	0.091
SSA_0770	Purine / Pyrimidine metabolism	Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	8	0.053	0.091
SSA_0132	RNA polymerase	RNA polymerase subunit alpha (EC 2.7.7.6)	5	0.014	0.09
SSA_0176	RNA polymerase	RNA polymerase subunit beta (EC 2.7.7.6)	5	0.014	0.09
SSA_0177	RNA polymerase	RNA polymerase subunit beta' (EC 2.7.7.6)	5	0.014	0.09
SSA_2183	Glycolysis, PPP ,Amino sugar metabolism	Glucose-6-phosphate isomerase (EC 5.3.1.9)	5	0.13	0.089
SSA_0847	Glycolysis , PPP	ATP-dependent 6-phosphofructokinase (EC 2.7.1.11)	3	0.539	0.1
SSA_0886	Glycolysis ,RNA degradation	Enolase (EC 4.2.1.11)	3	0.512	0.1
SSA_2107	Amino sugar metabolism	Glutamine-fructose-6-ph aminotransferase (EC 2.6.1.16)	2	0.308	0.09
SSA_0804	Amino sugar metabolism	Phosphoglucosamine mutase (EC 5.4.2.10)	2	0.295	0.081
SSA_1642	Amino sugar metabolism	Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	2	0.281	0.074
SSA_1047	Amino sugar metabolism,Peptidoglycan biosynthesis	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98)	2	0.246	0.061
SSA_1800	Peptidoglycan biosynthesis	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)	2	0.231	0.056
SSA_0652	Peptidoglycan biosynthesis	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	2	0.2	0.052
SSA_0312	RNA degradation	Hydrolase, metallo-beta-lactamase superfamily	1	0	0.093
SSA_1430	Protein biosynthesis	Ribonuclease Z (RNase Z) (EC 3.1.26.11)	1	0	0.093
SSA_2140	Protein biosynthesis	Ribonuclease P protein component (EC 3.1.26.5)	1	0	0.093

Table 5. **Conservation rate of predicted essential genes with high network parameters.**



Gene	Bacillus_subtilis_168_uid57675	Escherichia_coli_K_12_substr__MG1655_uid57779	Haemophilus_influenzae_Rd_KW20_uid57771	Mycobacterium_tuberculosis_H37Rv_uid170532	Mycoplasma_genitalium_G37_uid57707	Salmonella_enterica_serovar_Typhi_Ty2_uid57973	Staphylococcus_aureus_NCTC_8325_uid57795	Streptococcus_pneumoniae_TIGR4_uid57857	NCBI
SSA_0132	EG	EG	EG	EG	EG	EG	EG	-	2596
SSA_0176	EG	EG	EG	EG	EG	EG	EG	-	2675
SSA_0177	EG	EG	-	EG	EG	EG	EG	EG	2747
SSA_0312	-	-	-	-	EG	-	EG	EG	1686
SSA_0652	EG	EG	EG	EG	-	EG	EG	EG	2453
SSA_0768	-	EG	EG	-	EG	EG	EG	-	2020
SSA_0770	-	EG	EG	EG	EG	EG	EG	EG	2450
SSA_0804	EG	-	EG	EG	-	-	EG	EG	2558
SSA_0847	EG	-	EG	-	EG	-	EG	EG	1880
SSA_0848	-	-	EG	EG	EG	-	EG	EG	2455
SSA_0886	EG	EG	-	EG	EG	EG	EG	EG	2687
SSA_1047	EG	EG	-	EG	-	EG	EG	EG	2451
SSA_1430	EG	-	-	-	-	-	EG	EG	1591
SSA_1642	EG	EG	-	EG	-	EG	EG	EG	2457
SSA_1800	EG	-	EG	EG	-	-	EG	EG	2460
SSA_2107	-	-	-	EG	-	-	EG	EG	2525
SSA_2140	EG	EG	EG	-	EG	EG	EG	EG	1568
SSA_2183	-	-	-	EG	EG	-	EG	EG	2310

Colored box= conserved gene homolog detected; colored box with “EG”= conserved essential gene; Empty box= missing gene. NCBI column= number of bacterial species with homologs to the gene listed horizontally on left.

Discussion

In this project, we first collected proteome sets from 13 phylogenetically diverse bacterial species. We extracted the proteome sets from the NCBI database where each protein was defined along with its protein name, code, amino acid length, general description and function. Using the *S. sanguinis* SK36 proteome as a “training set”, we predicted a list of essential genes based on predicted essential functions. We defined essential pathways as those containing abundantly predicted essential proteins consecutively interacting in a cascade, forming a predicted essential pathway. We then assigned network parameters to every protein and ran a BLASTP search using our predicted list of essential proteins from *S. sanguinis* as a query against 13 proteome sets, each from a bacterial species, identifying the best hits as predicted essential proteins in their respective proteome.

Upon comparison of our predicted essential genes against the experimentally defined essential genes, the percentages of concurrence ranged from 98.6% to 39.7%, and this discrepancy can be attributed to many reasons: First, the experimentally defined essential genes encompass a varying proportion of hypothetical genes which lack any functional hint and therefore do not belong to any pathway. In this sense, we cannot “predict” a hypothetical gene to be essential in any pathway. In the case of *S. sanguinis,* the reason we achieved high concurrence between predicted lists and experimentally defined lists is that only three essential genes were hypothetical. Second, NCBI annotations to genes are generally based on parallel annotation of experimentally defined genes in a model species to other bacterial genes. In the case of bacterial genes, *E. coli* is considered in this sense a “reference” for the annotation of other bacterial genes. Given pleiotropic nature of essential genes and distribution of essential and hypothetical domains [78], it is misleading to assume all orthologs contribute to the same functions. Third, essentiality studies were conducted in different experimental designs and settings, overshadowing their impact on the study outcome. For example, two essentiality studies, one using transposon mutagenesis and another using single gene knockout method, identified 609 [52] and 296 [57] essential genes, respectively.

Functionally categorized predicted essential genes fell into three general essential pathways: maintenance of cell envelope, energy production and processing of genetic information, the last pathway harboring the most of essential genes (57% of orthologs among Gram-positive bacteria), providing insights about evolutionary functional conservation. Relevance between outputs of our prediction framework of essential genes and experimental data exceeded 63.3% in all four Gram-positive bacterial models. Taking all these factors together, our prediction framework for essential genes defined in every tested bacterial model a core of essential genes that exhibited the three previously defined essential functions despite all mentioned obstacles.

We investigated in depth the essential functions and how conserved are these function. By identifying the orthologs and paralogs of essential genes, we defined “genetic information processing” and “energy production” as essential functions that are well conserved and undergo less neo-functionalization as highlighted by presence of paralogs. However, in case of “cell wall biosynthesis” essential genes, we have shown that the essential genes we predicted, although less conserved than those involved in “genetic information processing”, undergo a huge duplication process which ultimately leads to neo-functionalization. This may provide insights into the ongoing resistance to drugs targeting the cell wall, such as β-lactam family, where target inactivation is a common resistance mechanism.

We searched for clues that essential genes provide regarding the lifestyles of bacterial models. It was evident using our prediction framework that predicted essential genes provide hints about the habitat and substrate of choice in all tested models. To our surprise, the predicted essential genes did not provide clues regarding the virulence of bacterial models tested. The three strains of *P. gingivalis* demonstrate different pathogenesis patterns but predicted essential genes were not linked to any virulence factor. We believe that with more dependence on *in vivo* models for essentiality studies, we will have deeper insights regarding the linkage of essential genes to virulence.

Furthermore, we defined predicted essential genes involved in energy production (glycolysis) to have higher BC values (also called stress centrality) than others, while essential genes involved in genetic information processing have higher DC and CC values, reflecting connectivity and information centralities, respectively. It can be postulated that essential genes involved in energy production are sensitive to external and internal changes through metabolite-regulation (allosteric modulation) while "genetic information processing" predicted genes have a more global impact through higher connections to all nodes and regulating the synthesis of proteins needed in all pathways [137,166]. This regulatory logic seems conserved across species as demonstrated through the observed correlation of essential genes with high network parameters across 2774 species.

In conclusion, our framework for prediction of essential genes identified "core essential genes" with a high conservation rate that provided insights about the lifestyles of 13 tested bacterial models, except for virulence. With more discoveries of the functional roles of hypothetical essential genes and integrating them into essential networks, we will profoundly enhance predictions of the microbial functional essentiality and shape new prevention and treatment strategies against infectious diseases.

Chapter Two

A Transcriptomic Analysis of Essential Genes Under Stress in *Streptococcus sanguinis*

Fadi E. El-Rami, Todd Kitten, and Ping Xu

Fadi E. El-Rami performed the transcriptomic assays, analysis, and preparation of manuscript. Ping Xu and Todd Kitten supervised the whole work as an advisor and a co-advisor respectively.

Background

Streptococcus sanguinis is a Janus-faced microorganism: an oral commensal with high abundancy in the oral cavity that competes with etiologic agents of dental caries (such as *Streptococcus mutans*) and an opportunistic pathogen and a leading causative agent of infective endocarditis [12]. Deciphering the environmental impact on the genetic network underlying the behavior of this bacterial species in disease settings will enhance our understanding of its genetic complexity and help define therapeutic targets.

Bacterial species display a margin of flexible regulatory mechanisms, as their lifestyles are marked with an incessant exposure to stress. Transcription represents a major genetic regulatory tool that allows bacteria to respond efficiently to radical environmental changes. Thus, transcription constitutes a key factor in stress response mechanisms and dissecting its role in stress response provides invaluable insights into the complexity of bacterial behavior [167,168].

Bacterial genes are mostly organized into clusters of adjacent genes called operons, each under control of a common operator [169]. Transcription is conducted by an RNA polymerase complex composed of a holoenzyme and a σ-factor. Every σ-factor binding to a holoenzyme guides the transcription machinery to a specific promoter which precedes a set of genes [170-172]. Although bacterial species possess various σ-factors, most of them harbor at least one housekeeping σ^{70} [173-175]. Transcription factors serve as transcription regulators that may either enhance (activator) or suppress (repressor) transcription [176,177]. In addition, other regulatory elements interfere in the transcription machinery, such as internal promoters within operons [178], small RNAs (sRNAs) and riboswitches [179]. *S. sanguinis* encodes 117 putative transcription factors, one housekeeping σ^{70} (SSA_0825), an ortholog of the competence-specific sigma factor, ComX (SSA_0016), and surprisingly no other alternative sigma factor [180].

Initially in yeast, research findings have uncovered conserved regulatory strategies for stress response, coined as core stress response (also called common environmental response), in which a common response against diverse environmental insults is characterized by a conserved set of up-regulated genes involved in heat shock, anti-oxidation and carbohydrate metabolism, and another conserved set of down-regulated genes involved in ribosomal biogenesis and translation [181-183]. The significance of core stress response is that it may provide a stressed cell with "cross-protection", where a cell exposed to one stress factor may become "immune" against other stresses [184]. Given this context, cross-protection represents a serious medical complication that jeopardizes the host efficiency of host immune response and antibiotics against bacterial pathogens. For example, research findings have shown that antibiotics resistance against one antibiotic may contribute to cross-resistance against other non-related drugs [185,186] or host bactericidal products [187,188], thus unveiling the imminent emergence of superbugs.

As stress response mechanisms target vital cellular pathways, it is intuitive that at the core of stress response mechanisms are essential genes. Essential genes are genes that are indispensable for survival in a specific environmental context. Essential genes may be up-regulated or down-regulated in different circumstances, but their knockout is detrimental to the cell. Previous findings by Xu et al. [162] has shown that essential genes are involved in three major functional categories, namely: genetic information processing, cell wall biosynthesis, and energy production. Essential genes are highly conserved and involved in at least one essential function, with a strong tendency to be pleiotropic in many pathways due to selective evolutionary pressure that favors neo-functionalization of essential genes [189]. Deciphering the impact of every essential gene through its measuring its transcriptional profile under different stress factors will deepen our understanding of functional essentiality and provide hints about promising drug targets.

Nowadays, the availability of highly sensitive, relatively cheap, and high throughput approaches to measure transcriptomic profiles simultaneously of all genomic elements, namely the protein coding and non-coding DNA sequences, revolutionized our understanding of the intricate regulatory networks to an unprecedented depth, revealing the dynamics and complexity of bacterial transcriptomes under different environmental conditions [190-193].

In this study, we shed light on the transcriptomic profiles of essential genes in stress response mechanisms of *S. sanguinis* against two stress factors: a sub-inhibitory concentration of a commonly prescribed antibiotic in dental practices, ampicillin, and heat as a non-specific host immune response manifested in fever. We compare the transcriptomic findings from the two stressed bacterial samples and define a core stress response as well as a stress-specific response in both scenarios. We believe the current findings will help characterize a bacterial model for further studying the dynamics of essential genes under clinically relevant stress factors and assist in designing an evidence-based dental practice drug prescription guidelines.

Materials and Methods

Bacterial strains, media and growth conditions. *S. sanguinis* SK36 samples were routinely grown in brain heart infusion (BHI) broth (BD, San Jose, CA) under micro-aerobic conditions (7.2% H_2, 7.2% CO_2, 79.6% N_2, and 6% O_2) at 37°C as previously described [194].

Examination of stressed growth *in vitro.* Overnight cultures of *S. sanguinis* SK36 were diluted 1:100 fold in BHI and grown for 4 hours in microaerophilic conditions, and then diluted 20-fold into microplate wells containing fresh BHI and treated with either sub-inhibitory concentration of ampicillin or mild heat shock at mid-log phase (OD_{600} = 0.6). Each sample was tested in triplicate. Growth rates were determined by measuring the OD_{600} using a Synergy H1 Hybrid Reactor microplate reader (BioTek, VT, USA) every 5 minutes under aerobic conditions for 12 hours of untreated and ampicillin-treated triplicate samples. The experiment was performed in triplicate.

Transcriptome analysis by RNA-seq. For RNA-seq, three replicates of *S. sanguinis* SK36 cultures were grown overnight in BHI broth at 37°C in microaerophilic conditions. The next day, cells were diluted 1:100 into 5 ml BHI broth and grown at 37°C for 4.5- 5 hours until OD_{600} of 0.6 was attained, after which 10 ml of RNAprotect Bacteria Reagent (cat.# 76506, Qiagen, CA, USA) was added to each bacterial culture. After 5 min incubation at room temperature, cells were centrifuged and the pellet stored was at -80°C. Cells were lysed using RNeasy mini kit (cat.# 74106, Qiagen, CA, USA) as recommended by the manufacturer and by bead milling conducted using 2 ml Lysing matrix B beads in the Fast Prep 24 for 45 s at level 6. All samples were treated with DNase I RNase-Free DNase Set (cat.# 79254, Qiagen, CA, USA) to deplete DNA. Total RNA concentrations were measured using a NanoDrop 2000 UV-Vis Spectrophotometer (Thermo fisher, DE, USA) with cutoff values for absorbance ratios 260/280 and 260/230 of 2.0 and 2-2.2 respectively. For depletion of ribosomal RNA, all samples were treated with Illumina Ribo-zero Magnetic Kit for Bacteria (cat.# MRZB12424, Roche, USA) and the rRNA-depleted samples were purified using Qiagen RNeasy MinElute Cleanup Kit (cat.# 74204, Qiagen, CA, USA).

RNA concentrations were measured in rRNA-depleted samples using NanoDrop 2000 UV-Vis Spectrophotometer with cutoff values for RNA concentration of 10 ng/µl. Actinomycin D (cat. # A1410-2MG, Sigma-Aldrich, MO, USA) was used for RNA fragmentation and RNA libraries were prepared with NEBNext Ultra Directional RNA Library Prep Kit NEB (cat.# E7420L, New

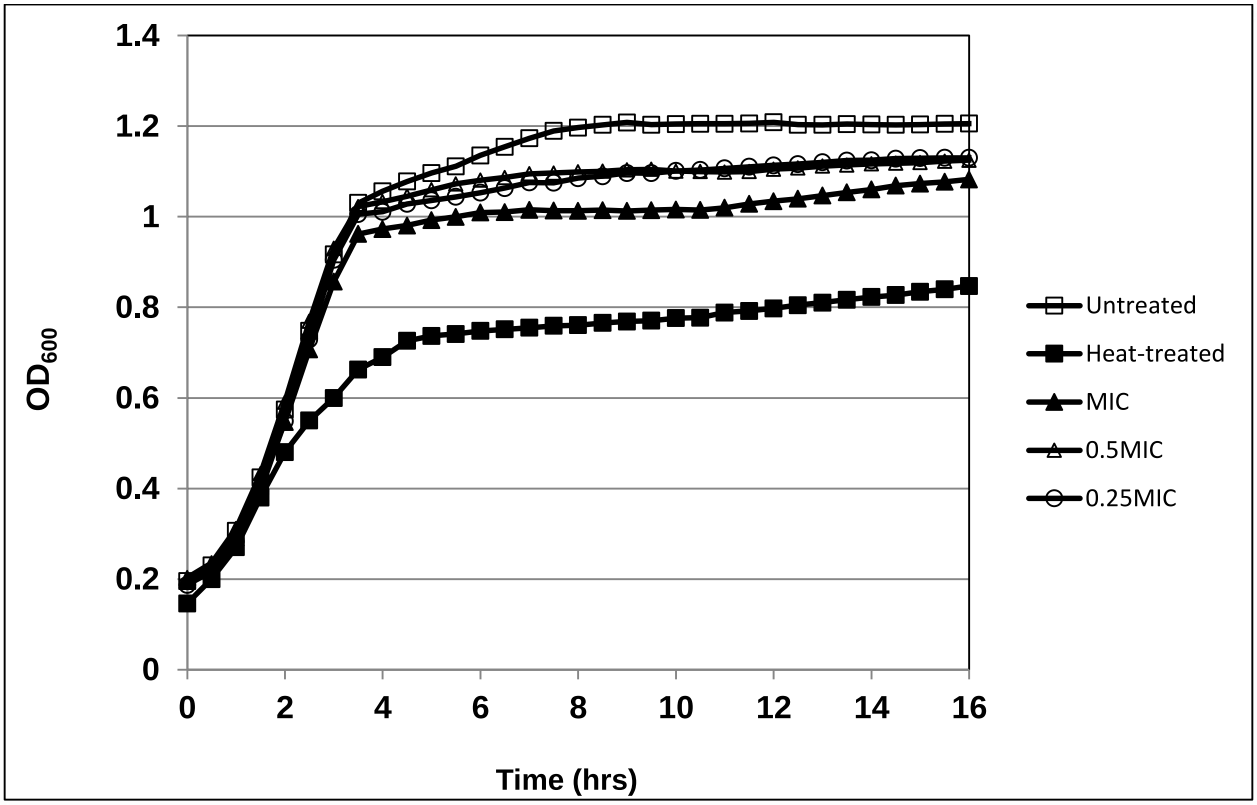
England Biolabs, MA, USA) and NEBNext Multiplex Oligos for Illumina Index Primers Set 1 and set 2 (cat.# E7335L & E7500L respectively, New England Biolabs, MA, USA). The final cDNA products were purified with AMPure XP Beads (cat.# A63880, Beckman Coulter, CA, USA) and band sizes were checked by gel electrophoresis. The quality of the constructed cDNA library was determined using Agilent Bioanalyzer-High Sensitivity DNA Chip and Ribosome Integrity Numbers (RIN) were determined for all samples with a cutoff value of 10. Sequencing was carried out on an Illumina MiSeq platform using reagent Kit v2, with coverage of ~15 M reads each. Reads obtained from sequencing were aligned against the *S. sanguinis* SK36 genome using Rockhopper software and counts of transcripts along with statistical calculations were provided.

Gene expression data. The RNA-seq data was deposited in the Gene Expression Omnibus (GEO) database (http://www.ncbi.nlm.nih.gov/geo/) under the accession number GSE97218 (Ampicillin-treated samples) and GSE97357 (heat-shocked cells).

Data mining from databases. We searched for pathways that contain essential genes as described by the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. For functional enrichment analysis of our genes and proteins dataset, we used the functional annotation tool of DAVID Bioinformatics Resources 6.7 [195].To visualize the maximal number of essential genes on a single map that encompasses all pathways harboring essential genes and integrate the gene expression profiles at different time points, we constructed a network based on data acquired from KEGG using Cytoscape 3.4 software platform [196]. Circos plots were designed to visualize the differential regulation of essential genes [197].

Results

Growth curves of stressed cells. *S. sanguinis* SK36 samples were treated with heat shock and different concentrations of ampicillin at the mid-exponential growth phase (Fig. 8). Based on the CLSI MIC values [198], we tested MIC, 0.5xMIC, and 0.25xMIC values as sub-inhibitory ampicillin concentrations. Both tested concentrations of ampicillin resulted in a slight growth defects in comparison to the untreated samples. It was suggested that ½ MIC was the best dose for testing the impact of sub-inhibitory concentration of ampicillin as it is the highest dose of sub-inhibitory concentration that least affects the growth pattern of *S. sanguinis* among the tested doses. The heat shock was selected based on literature review and the concept of using a mild shock that will not reduce the bacterial growth to a level that hinders sufficient mRNA and protein collection. The growth defect was visible in comparison to untreated cells.



1.4
1.2
1
0.8
0.6
0.4
0.2
0
OD_{600}
0
2
4
6
8
10
12
14
16
Time (hrs)
Untreated
Heat-treated
MIC
0.5MIC
0.25MIC

Figure 8. Growth rates of *S. sanguinis* SK36 samples under stress. Growth rates were measured of *S. sanguinis* treated with different ampicillin concentrations or mild heat shock. Minimal inhibitory concentration (MIC) of ampicillin with respect to *Streptococcus* viridians group is 0.25 µg/ml. All experiments were done in triplicate.

Quantification of differentially expressed genes under different stressors. Differentially expressed genes with statistical significance were counted (Table 6). More genes were differentially expressed in ampicillin treated cells than the heat shocked cells at all three time points. Moreover, the pattern of gene expression was strikingly different with the ampicillin treated cells being more up-regulated while the heat shocked cells we more down-regulated across three times points.

Table 6. Quantification of differentially expressed genes in counts and percentages under different stress factors in *S. sanguinis*. The table includes only findings with statistical significance (p-value <0.05).

	Ampicillin-treated cells		
	T_{10}	T_{20}	T_{30}
Up-regulated	736 (53%)	722 (61%)	652 (50%)
Same	43 (3%)	9 (1%)	8 (1%)
Down-regulated	611 (44%)	445 (38%)	644 (49%)
Total	1390	1176	1304
	Heat-shocked cells		
Up-regulated	439 (48%)	383 (37%)	396 (40%)
Same	13 (1%)	5 (1%)	5 (1%)
Down-regulated	459 (51%)	642 (62%)	587 (59%)
Total	911	1030	988

Moreover, we conducted a functional enrichment analysis of all differentially expressed genes (Table 7). RNA-seq analysis conducted on a temporal basis revealed the impact of gene regulation on global basis at early response phase (T_{10}), at end of bacterial replication phase (T_{20}), and late response phase (T_{30}) post-treatment with sub-inhibitory concentration of ampicillin and heat shock. Starting with ampicillin-treated cells, “Phosphotransferase system” was the functional category most enriched among up-regulated genes at T_{10} (736 genes), T_{20} (722 genes), and T_{30} (652 genes). “Hydrogen ion transport” and “signal transduction through two-component system” were enriched among up-regulated genes at T_{10} and T_{20} only. The enriched functional classes among up-regulated genes point towards modulating gene expression in a direction that potentiates an early stress response mechanism based on sensing the environmental cues, reducing internal proton buildup, and importing energy resources.

“Ribosomal biogenesis” was the functional category most enriched among down-regulated genes at T_{10} (611 genes), T_{20} (445 genes), and T_{30} (644 genes). “Peptidoglycan biosynthesis” was enriched among down-regulated genes at T_{10} and T_{20} only, “DNA replication” at $T_{20,}$ and “fatty acid metabolism” at T_{30}. The enriched functional classes among down-regulated genes demonstrate a global transcriptional inclination towards slowing cell growth as the bacteria acclimate to the antibiotic concentration.

Interestingly, heat-shocked cells demonstrated remarkable differences on the transcriptional levels, with “glycogen synthesis” being the dominant enriched group of up-regulated genes at all time points, indicating a trend towards regulating genes in the directing of energy saving and avoiding glycolysis at stressful conditions. This suggestion is backed up by the down-regulation of genes involved in ribosomal biosynthesis at T_{10}, inducing a stress response to slow down growth and protein biosynthesis, especially histidine and arginine. These amino acids require glutamate as a precursor for their biosynthesis and the down-regulation of glutamate biosynthesis enzyme (SSA_0371) explains the down-regulation of arginine and histidine. This concurs with transcriptional down-regulation of genes involved in peptidoglycan biosynthesis that was observed in ampicillin-treated cells. Thus, it appears that transcriptional down-regulation of genes involved in amino acid biosynthesis, ribosomal biogenesis, and cell wall biosynthesis is a "transcriptional stress signature" of *S. sanguinis* cells that manifests at stressful conditions regardless of the stressor.

Table 7. Functional enrichment and clustering of differentially regulated genes under impact of ampicillin and mild heat shock.

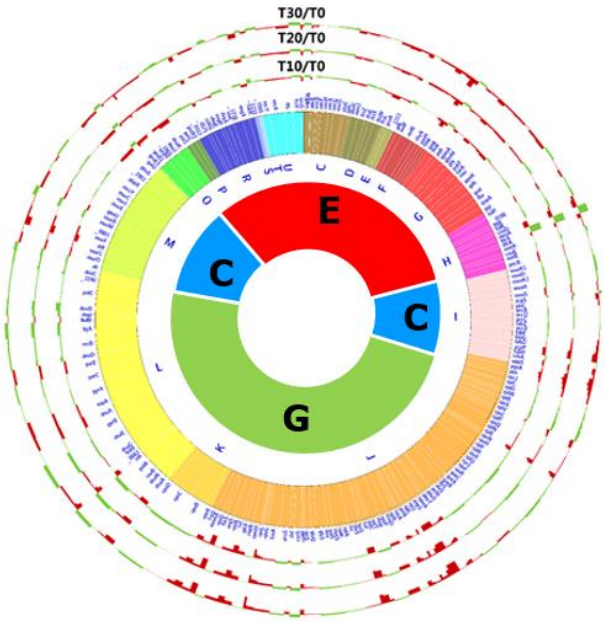
		Ampicillin-treated cells		Heat-shocked cells	
		Functional category	P-value	Functional category	P-value
T_{10}	**Up-regulated**	Phosphotransferase system Hydrogen ion transport Signal transduction	9.85E-05 0.014 0.022	Transmembrane helix Transcription Glycogen biosynthesis	0.00019 0.0054 0.0167
	Down-regulated	Ribosomal biogenesis Peptidoglycan biosynthesis GTP-binding	2.82E-06 1.25E-04 0.0088	Histidine biosynthesis Cell membrane transport Ribosomal biogenesis	0.0002 0.0039 0.042
T_{20}	**Up-regulated**	Phosphotransferase system Signal transduction Hydrogen ion transport	4.84E-04 0.0202 0.0433	Thioredoxin domain Glycogen biosynthesis	0.0028 0.012
	Down-regulated	Ribosomal biogenesis Peptidoglycan biosynthesis DNA replication Aminoacyl-tRNA biosynthesis	7.05E-04 0.0018 0.0104 0.0484	Transmembrane helix Arginine biosynthesis Histidine biosynthesis	4.5E-05 0.0014 0.0022
T_{30}	**Up-regulated**	Phosphotransferase system Metal-binding	8.39E-06 0.044	redox homeostasis Glycogen biosynthesis Phosphotransferase system	5.5E-04 5.6E-04 0.015
	Down-regulated	Ribosomal biogenesis Fatty acid biosynthesis ATP-binding	0.0032 0.0037 0.0107	Transmembrane helix Histidine biosynthesis Arginine biosynthesis	9.1E-04 0.001 0.005

Pathway-dependent interpretation of transcriptomic profiles of essential genes.

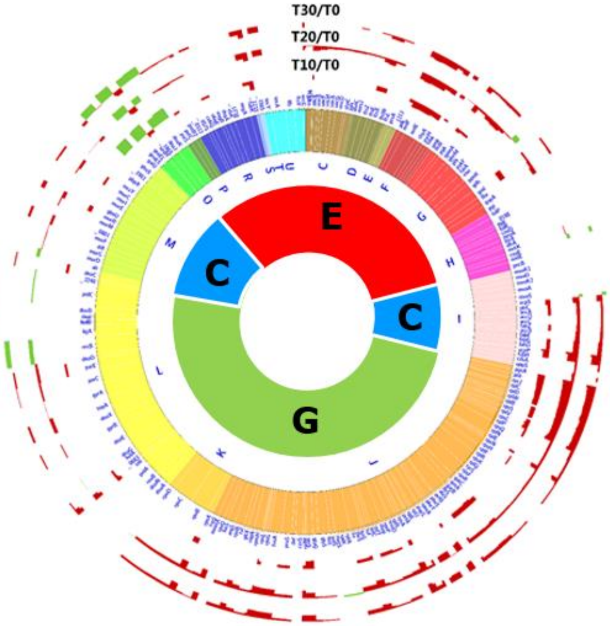
Ribosomal biogenesis. Ribosomes are the main energy consumers in the cell [199]. Unlike heat-shocked cells that showed an total transcriptional shutdown of ribosomal biogenesis genes at all time points, in ampicillin-treated cells, at T_{10}, most essential genes (28 genes) encoding ribosomal proteins showed a significant reduction in the transcript level that extended to T_{30} (Fig. 8, 9, Supplementary Table 2), except for 9 genes: *rpsN* (SSA_2391, 30S ribosomal protein S14), *rplP* (SSA_0114, 50S ribosomal protein L16), *rpsQ* (SSA_0116, 30S ribosomal protein S17), *rplN* (SSA_117, 50S ribosomal protein L14), *rplE* (SSA_0119, 50S ribosomal protein L5), *rpsH* (SSA_0120, 30S ribosomal protein S8), *rplF* (SSA_0122, 50S ribosomal protein L6), *rplR* (SSA_0123, 50S ribosomal protein L18*), rpsE* (SSA_0124, 30S ribosomal protein S5). In addition to their major role in protein synthesis, ribosomes have been implicated in pleiotropic functions, ranging from antibiotic adaptation [200] to fatty acid biosynthesis [201], in which we postulate that these exceptionally up-regulated ribosomal proteins may be involved. Taking into account the transcriptomic down-regulation of most ribosomal proteins, as well as down-regulation of the elements of DNA topoisomerase (SSA_1184, SSA_1220, SSA_1232), and RNA polymerase (SSA_0176, SSA_0825), these findings provide the first "transcrptomic signature" of ampicillin sub-inhibitory treatment that is phenotypically demonstrated in a minor growth defect (Fig. 8).

Amino acid biosynthesis. Our findings show that most genes and proteins involved in translation were down-regulated in stressed cells, with some interesting exceptions (Fig. 9). Although and mRNA transcripts for "ribosomal biogenesis" genes were down-regulated, the opposite result was recorded for some amino-acid tRNA synthetases: valyl-tRNA synthetase (SSA_1819) was transcriptionally up-regulated in heat-treated cells, while histidyl-tRNA synthetase (SSA_2284), prolyl-tRNA synthetase (SSA_2069), cysteinyl-tRNA synthetase (SSA_2044), glycyl-tRNA synthetase (SSA_1879), alanine-tRNA synthetase (SSA_0756), methionine-tRNA synthetase (SSA_1848), isoleucyl-tRNA synthetase (SSA_0661), valyl-tRNA synthetase (SSA_1819),

threonyl-tRNA synthetase (SSA_1571), and phenylalanyl-tRNA synthetase (SSA_0914) were significantly up-regulated.



Ampicillin-treated

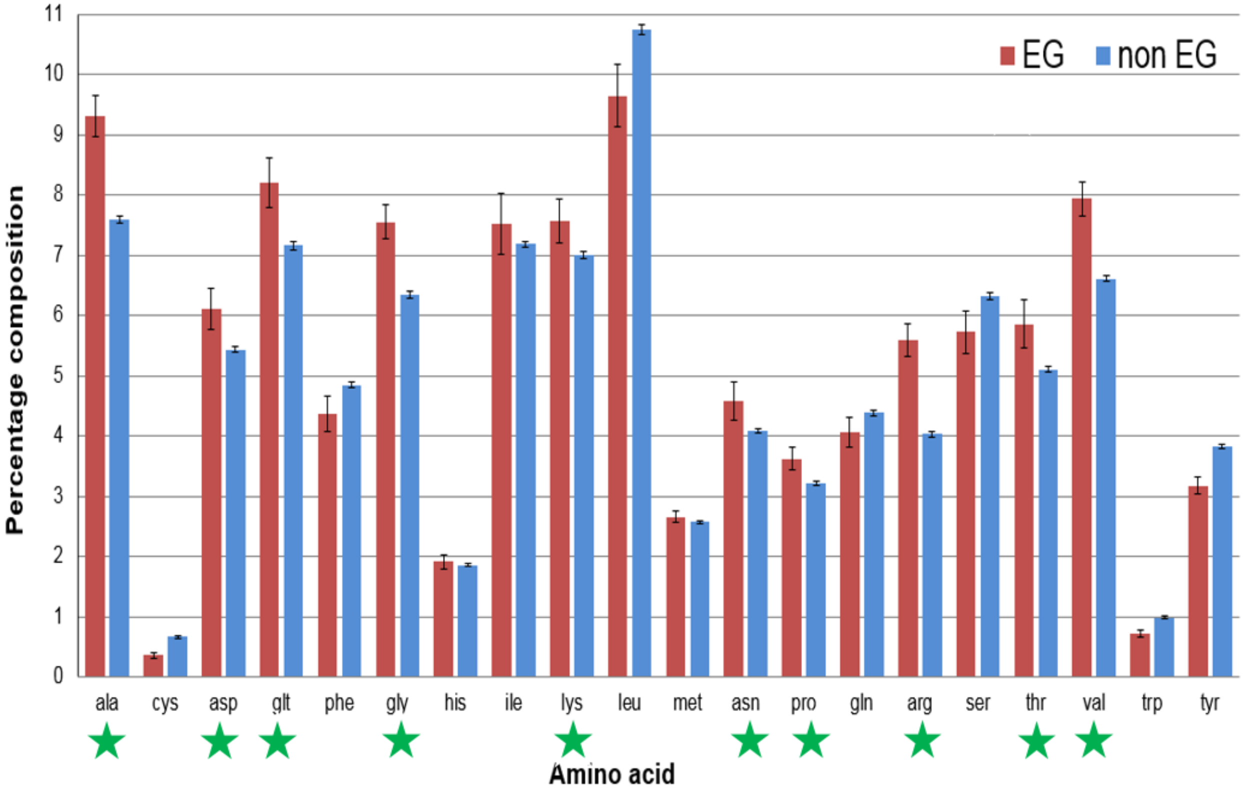


Heat-treated

Figure 9. Differentially regulated essential genes in ampicillin-treated cells (left) and heat-shocked cells (right). Figure was constructed using Circos software. Essential genes were aligned based on their COG annotations. Clustering of COG annotations was done into three essential functions: Genetic information processing (green), cell wall biosynthesis (blue), and energy production (red). Transcriptional up-regulations of genes were shown as green bars. Transcriptional down-regulations of genes were shown as red bars. Transcriptional measures were taken at 10, 20, and 30 minutes after stress exposure, and ratios of transcriptional up- or down-regulation with respect to control (T_0) are symbolized by T_{10} / T_0, T_{20}/T_0, and T_{30}/ T_0 respectively.

In an attempt to understand this translational bias, we measured the amino acid composition of essential and non-essential proteins (Fig. 10). We postulated that because essential proteins demand longer persistence in the cell, they need to contain less “degradation-prone” amino acids as dictated by the N-rule [202]. In other words, we expected essential proteins to encompass less ofthe following amino acids: tyrosine, tryptophan, leucine, phenylalanine, lysine and arginine. We found that essential proteins contain less of these amino acids than non-essential proteins, except for arginine (Fig. 10). Dissecting the amino acid composition of essential proteins provided clues about the biased transcriptomic up-regulation of genes encoding specific amino acid-tRNA synthetases where alanine, glycine, histidine, proline, methionine, and valine have been shown to have higher abundance in the composition of essential proteins than the non-essential proteins.

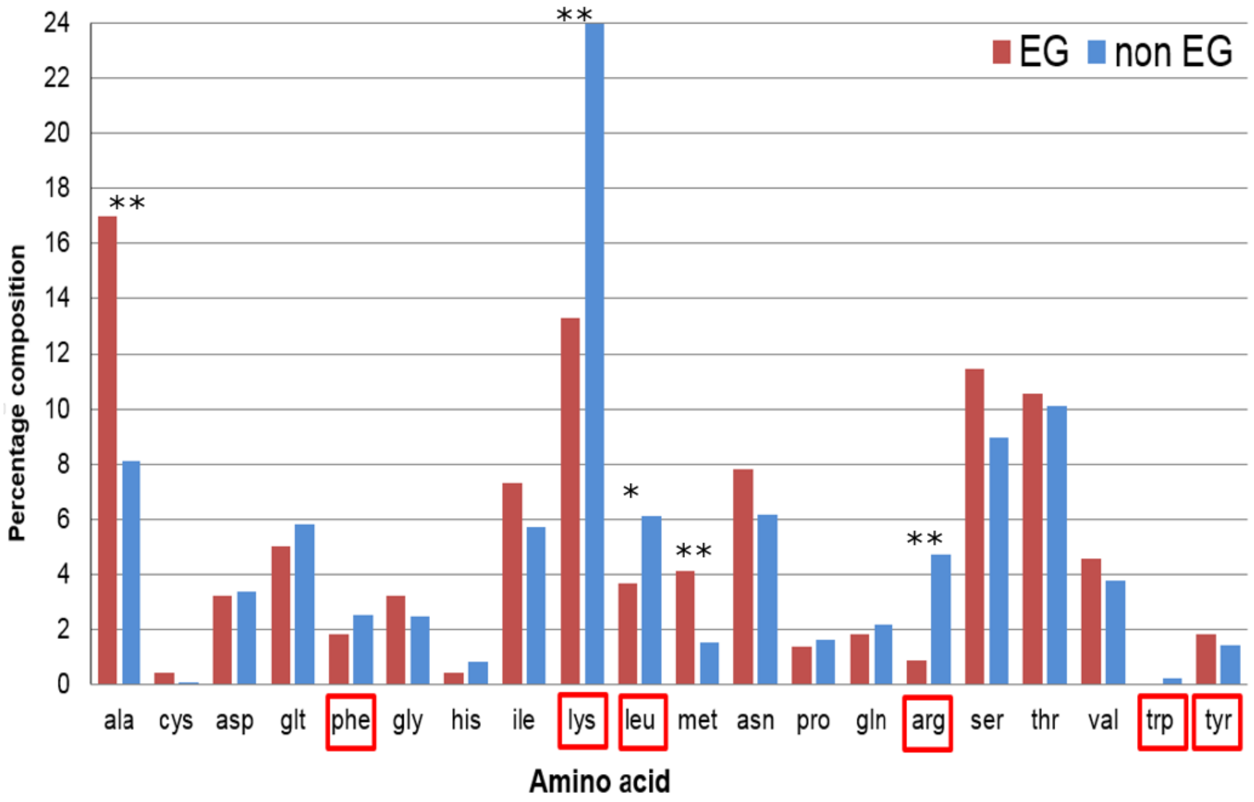
We also investigated the application of the N-end rule on the predicted half-lives of essential and non-essential proteins (Fig. 11). Essential proteins showed to have less degradation-prone amino acids at their N-terminal positions, although some of these degradation-prone amino acids (arg and lys) seem to be more enriched in essential proteins than in non-essential, but not in the N-terminal position.



EG
non EG
Percentage composition
Amino acid
0
1
2
3
4
5
6
7
8
9
10
11
ala
cys
asp
glt
phe
gly
his
ile
lys
leu
met
asn
pro
gln
arg
ser
thr
val
trp
tyr

Figure 10. Percentage composition of every amino acid of essential and non-essential proteins. Measurements were done using Biopython scripts. Green stars show the amino acids biased to essential proteins.

a)


Percentage composition
24
22
20
18
16
14
12
10
8
6
4
2
0
EG
non EG
**
**
*
**
**
ala
cys
asp
glt
phe
gly
his
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met
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arg
ser
thr
val
trp
tyr
Amino acid

b)

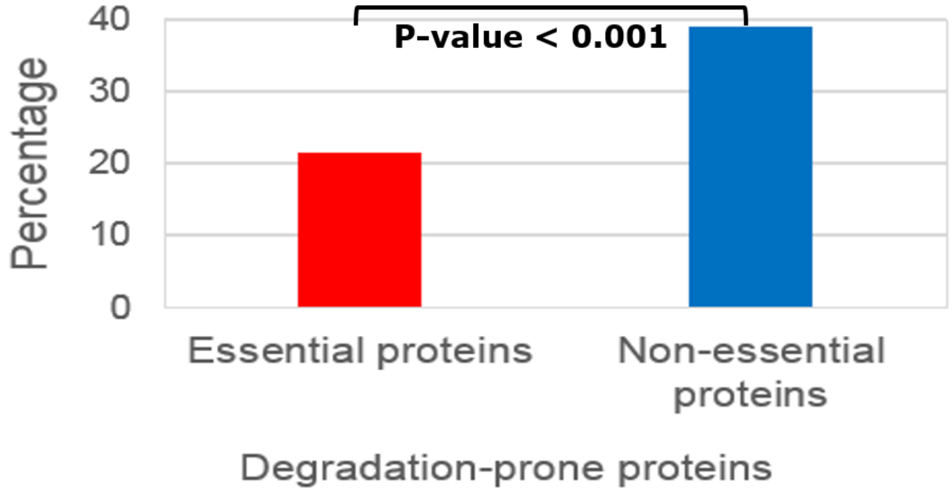
Percentage
40
30
20
10
0
P-value < 0.001
Essential proteins
Non-essential proteins
Degradation-prone proteins

Figure 11. Percentage composition amino acids at the N-terminal position in essential and non-essential proteins. a) Measurements were done using Biopython scripts. Red squares show the degradation-prone amino acids biased to essential proteins. One asterisk indicates a P-value <0.05. Two asterisks indicate a P-value <0.001 b) Total percentages of essential and non-essential proteins that have predicted short-half lives based on the localization of degradation-prone amino acids (phe, lys, leu, arg, trp, tyr) at N-terminal position.

Phenylalanyl-tRNA synthetase β-subunit (SSA_0914) was slightly increased across the three time points, while the α-subunit (SSA_0912) was severely down-regulated, indicating perhaps a general decrease in translational activity. Phenylalanine is a major component of the non-essential proteins than of the essential proteins (Fig. 10), but it contributes to a longer protein half-life and hence it composes 4.05% of *S. sanguinis* essential proteins. The same applies to isoleucine and threonine, which compose a slightly higher percentage of non-essential proteins than essential and they promote protein longevity.

Glycolysis. Glycolysis represents a fundamental source of energy production and supplier of products for many anabolic pathways (Fig. 7). In ampicillin-treated cells, a significant transcriptional up-regulation of essential genes involved in conversion of UDP-glucose to 3-phospho-D-glycerate (SSA_2169, SSA_2183, SSA_1992, SSA_2108, SSA_0302), is seen with the remaining 3 enzymes leading to pyruvate production being transcriptionally down-regulated (SSA_0688, SSA_0886, SSA_0848) across all three time points. In heat-shocked cells, mRNA levels of genes encoding glycolytic enzymes were severely down-regulated and perhaps the up-regulation of gene encoding PTS components compensated for that through importing of metabolic products for sugar storage.

Transcriptomic analysis of glycolytic essential genes is a challenging task, given the moonlighting behavior of these enzymes in multiple pathways as findings in *S. pneumoniae* have classified many glycolytic enzymes as virulence factors, such as enolase [203] and pyruvate oxidase [204]. Many of these enzymes, such as glucose 6-phosphate isomerase, phosphoglycerate kinase, and glyceraldehyde-3-phosphate dehydrogenase, have been described as adhesion factors as they were associated with the cell surface of *Streptococcus agalactiae* [205].

Cell wall biosynthesis. Terpenoid, peptidoglycan, amino sugar, glycerophospholipid and phosphatidyl glycerol biosynthesis pathways converge to produce the cell wall in *S. sanguinis* (Fig. 7). In both types of stressed cells, all transcriptomic data across the three time points showed a general down-regulation of most essential genes encompassed in the amino sugar, phosphatidyl glycerol, glycerophospholipid, and peptidoglycan biosynthetic pathways across the three time points, with minor exceptions. A major exception was the terpenoid biosynthesis pathway: four genes involved in the terpenoid pathway (SSA_0334, SSA_0335, SSA_0336, SSA_0337) were transcriptionally up-regulated at all three time points, although the enzyme of rate limiting reaction in the pathway was significantly down-regulated at the time point measurements in ampicillin-treated cells. In heat-treated cells, the data was inconclusive for the terpenoid pathway as the statistical significance was low regarding the mRNA readings across the three time points.

Nucleic acid biosynthesis. Transcriptomic analysis of genes involved in the pentose phosphate pathway, RNA and DNA biosynthesis showed a general down-regulation among the majority of genes within these pathways. In heat-treated cells, there was remarkable transcriptional down-regulation of genes related to RNA polymerase, amino sugar metabolism, and DNA replication, with one gene (SSA_1452) encoding a helicase involved in homologous recombination being transcriptionally up-regulated at later time points, T_{20} and T_{30}.

Discussion

Despite the previous studies conducted on heat-shocked bacterial models and the tremendous clinical significance of deciphering the impact of sub-inhibitory concentrations of commonly prescribed drugs against *S. sanguinis*, the oral commensal, early colonizer that initiates oral biofilms, and opportunistic etiologic agent of infective endocarditis, this is the first study to address comprehensively the transcriptomic dynamics of stressed essential genes in *S. sanguinis* on a temporal basis. The complex response of *S. sanguinis* to stress is indispensable for survival through adaptive transcription, necessitating the use of a systems biology approach through RNA-seq to decipher globally the dynamics of mRNA levels at different time points.

Adopting the pathway-dependent approach (Fig. 7) facilitated the task of elucidating functional essentiality through reading the transcriptomic findings. Functional enrichment of many genes (Table 7) provided hints about general functional clusters, but lacked topological relatedness and pathways' connectedness through visualization. The temporal factor integrated into our experimental design highlighted the chronological cascade of events, where genes exhibited an immediate stringent stress response against ampicillin at T_{10} through adaptive regulation and mRNA expression, while heat-shocked cells down-regulated totally mRNA levels of ribosomal proteins, which reduced significantly the growth rate of the stressed bacterial cells.

Upon exposure to sub-inhibitory concentration of ampicillin or heat, transition to slow growth rate was observed (Fig. 3) accompanied by extensive reprogramming of gene expression across all major essential pathways, including glycolysis, purine and pyrimidine synthesis, cell wall biosynthesis, transcription and translation. Although we haven't solidified our findings with a metabolomic experiment, we postulate that amino acids are in demand differentially based on their composition of essential proteins, with cysteine as the least abundant constituent and leucine the most. It seems that stressed bacteria favor the amino acids that extend the half-life of the proteins the most, and hence transcriptomic bias is noticed in this direction.

A major drawback in our analysis was the lack of experimentally established transcription regulatory networks that provide biological insights about the differential regulation of a transcription factor in *S. sanguinis* with respect to its target operon/gene. In this sense, two-component systems are fundamental in bridging environmental signals to transcriptional responses. Current knowledge relies majorly on phylogenetically relevant species in inferring knowledge regarding transcriptional networks in *S. sanguinis* [206]. The impact of temperature on transcriptional regulatory networks has been studied elsewhere using other bacterial models and provided invaluable findings: BvgA has been shown to differentially regulate toxin and T3SS expression in *B. pertussis* under temperature effect [207] while H-NS regulates expression of *E. coli* hemolysin also by temperature [208,209]. In *S. sanguinis*, response regulator SSA_1565 (component of two-component system) was experimentally proven to be essential [162] and future studies focusing on delineating the targets of this transcription factor will help better understand the link between essential genes and transcriptional responses to environmental signals.

Taken together, this work is the first global study that monitors time-dependent changes of essential genes encountering antibiotic stress or heat on temporal basis in *S. sanguinis* and reveals crucial switches for the adaptation of metabolic, cell wall biosynthesis, and genetic information processing pathways.

Chapter Three

A Proteomic Analysis of Essential Genes Under Stress in *Streptococcus sanguinis*

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Fadi E. El-Rami performed the proteomic assays, analysis, and preparation of manuscript. Kristina Nelson conducted the mass spectrometry experiments. Ping Xu and Todd Kitten supervised the whole work as an advisor and a co-advisor respectively.

Background

Decoding the bacterial behavior urges dissecting its transcriptomic and proteomic profiles during different growth conditions [210]. With the unprecedented technological advances in transcriptomics that globally cover the genome and measure its mRNA transcript counts even in a single cell, the need for proteomic studies to match this transcriptomic advancement through investigating the maximal number of proteins is overwhelmingly huge. However, proteomic studies have proven more challenging, given the multi-step process that is challenged by many pitfalls at every stage, from protein extraction to high resolution quantification and extensive data analysis [211-213]. Adding to the already complex situation is the diversity of proteomics techniques adopted by different labs for every step, impacting the comparison of results [214,215]. After sequencing the genome of *S. sanguinis* SK36 [19] and identifying experimentally its essential genes, we took the challenge of applying proteomics to our transcriptomic findings and bioinformatics analyses, hoping to decode the proteome dynamics, especially the essential proteins, under different stress conditions that mimic clinical situations, and define "pathogenesis signatures" as promising therapeutic targets.

Proteomic studies have been insightful in analyzing the proteomic dynamics in other bacterial models exposed to different stress factors. Ampicillin-resistant *Fusobacterium nucleatum* isolates collected from 22 dental plaque samples were investigated for significantly changed proteins using MALDI-TOF/TOF mass spectrometry [216]. Elevated expression of beta-lactamase enzyme (29 kDa), ATP-binding protein as a subunit of an ABC transporter (37 kDa), and enolase (46 kDa) were reported. With respect to ampicillin resistant *E. coli* strains, proteomic studies showed elevated expression of 8 outer membrane proteins: 3 previously identified antibiotic resistance determinants (*TolC*, *OmpC* and *YhiU*) and 5 newly identified antibiotic resistance determinants (*LamB*, *Tsx*, *YfiO*, *OmpW*, and *NlpB*) [217]. Among the 167 significantly expressed proteins in *S. mutans* exposed to acidic growth conditions (pH 5.0), the majority (106 proteins) were associated with energy production (glycolysis and branched amino acid biosynthesis) while the rest (61 proteins) were involved in genetic information processing (DNA replication, transcription, and translation) and stress associated pathways (protein folding and proteolysis) [218]. This study was the first to identify 5 upregulated proteins in acid stress conditions: a single-stranded DNA-binding protein (*Ssb*), the transcription elongation factor (*GreA*), an RNA exonuclease, polyribonucleotide nucleotidyltransferase (*PnpA*), and two proteinases (*Clp* and *PepD*). Staphylococcus aureus exposed to cold stress conditions (4 ^{o}C) have shown significantly elevated levels of 9 ribosomal proteins (30S ribosomal protein S1, 30S ribosomal protein S7, 30S ribosomal protein S8, 50S ribosomal protein L3, 50S ribosomal protein L5, 50S ribosomal protein L10, 50S ribosomal protein L24, 50S ribosomal protein L25, 50S ribosomal protein L30) and genetic information processing components (transcriptional regulator *sarA* and cell division protein) in comparison to cells grown at 37 ^{o}C [219]. Coping with the reduced need for growth under stress, significantly reduced proteins included 3 enzymes involved in glycolysis (fructose-bisphosphate aldolase, pyruvate dehydrogenase E1 component subunit-beta, and lactate dehydrogenase) and cell wall biosynthesis components (N-acetylmuramoyl-L-alanine amidase, serine-aspartate repeat-containing protein D, and immunodominant staphylococcal antigen A precursor).

With advent of technology, it became possible to conduct proteomic analysis of stressed bacteria on a temporal basis. Glucose-starved *S. aureus* COL samples were subjected to proteomic and metabolomic investigations at time points 1, 3, 5, 7, 9, 13, 19, 24 hours [220]. Unsurprisingly, an increase of enzymes of TCC and gluconeogenesis (such as *PckA* and *GapA2*) was reported in starved cells, while enzymes involved in branched-chain amino acid biosynthesis (*IlvB, IlvD*), glycolysis (*GapA1, Pgi, Pgk*), purine metabolism (*NrdF, PurF*) and a ribosomal protein (*RplJ*) were strikingly downregulated in starved cells. Another mass spectrometry temporal-based study investigated the proteomic changes in *Mycobacterium smegmatis*, a non-pathogenic model for *M. tuberculosis*, exposed to sub-lethal concentrations of rifampicin at time-points that resemble early response (30 minutes post-drug treatment), onset of bacteriostasis (255 minutes post-drug treatment) and early recovery phases (300 minutes post-drug treatment) [221]. Although few proteins were significantly upregulated at first time point (Probable nicotinate-nucleotide adenylyltransferase, *Clp* protease, Coenzyme F420-dependent N5, N10-methylene tetrahydromethanopterin), second time point (Zinc metalloprotease Rip1), and third time point (a putative helicase), the majority of proteins were significantly downregulated: at first time point (TetR-family protein transcriptional regulator, HpcH/HpaI aldolase/citrate lyase family protein, and succinate dehydrogenase hydrophobic membrane anchor protein *SdhD*), second time point (Peptidase S1 and S6, chymotrypsin/Hap, cytochrome D ubiquinol oxidase subunit 1, and hydrogenase assembly chaperone *HypC/HupF*), and third time point (Peptidase S1 and S6, chymotrypsin/Hap, cytochrome D ubiquinol oxidase subunit 1, and ribonucleoside-diphosphate reductase subunit alpha 1/alpha 2).

All in all, if a genome is considered by many to be the “blueprint of life”, then the proteins encoded and expressed bring this genome to life. Proteins are the main players in any biological phenomenon, and elucidating the dynamics of bacterial proteins, especially the essential proteins at stressful conditions has paved the way for drug discovery and understanding further microbial behavior in health and disease.

Materials and Methods

Bacterial strains, media and growth conditions. *S. sanguinis* SK36 samples were routinely grown in brain heart infusion (BHI) broth (BD, San Jose, CA) under micro-aerobic conditions (7.2% H_2, 7.2% CO_2, 79.6% N_2, and 6% O_2) at 37°C as previously described [194].

Reagents and Buffers. All buffers and solutions were prepared using ultrapure water and analytical grade reagents. All prepared reagents were stored at room temperature unless indicated otherwise. Protease Inhibitor Cocktail Set II (Calbiochem, EMD Millipore, cat # 539132) was prepared as a stock solution by adding to each vial of lyophilized protease inhibitor cocktail 1 ml of DMSO first then add 4 ml of ultrapure water. Stock solution stored at -20 ^{o}C. DL-Dithiothreitol (Sigma, cat # D9779 SIGMA) was prepared as 1 M stock solution and stored at 4 ^{o}C. Incomplete lysis buffer was prepared as follows: 50 mM Tris (pH 7.4), 150 mM NaCl, SDS 0.1% (w/v). Before usage directly, 1 ml of complete lysis buffer for each sample was prepared by mixing 100 μL of reconstituted protease inhibitors solution, 1 μL of 1 M DTT (stock), and 900 μL incomplete lysis buffer. The complete lysis buffer was stored on ice.

Protein Extraction. Frozen bacteria (glycerol stock at -80 °C) were inoculated into 3 ml BHI and incubated at 37^{o}C overnight in anoxomat jars adjusted to microaerophilic conditions (6% O_2, 7.2% CO_2, 7.2% H_2, and 79.6% N_2). 400 μL of overnight grown bacteria were added into 40 ml BHI and incubated 5-5.5 hours until late log phase at the OD_{600} reading was ~ 0.8. Bacterial samples were exposed to stress for 10, 20, and 30 minutes in triplicates. One triplicate sample was left untreated as control. After centrifugation, the pellet was mixed with 1 ml of freshly prepared complete lysis buffer and

incubated on ice for 30 minutes. Afterwards, samples were sonicated as follows: Amplitude 35%, 5 sec ON, 10 sec OFF, for a total sonication time of 1 minute. The sonication efficiency was measured by detecting the absorbance of solution at 260 nm (A_{260}) and quantifying the released DNA from the lysed cells. Tubes were centrifuged at 13,000 rpm for 15 minutes at 4°C and supernatants were stored at -80 °C or moved directly to protein quantification.

Protein Quantification. Protein was quantified using Pierce BCA Protein Assay Kit (Thermo Scientific, cat # 23227) as recommended by the manufacturer. Briefly, the BCA Working Reagent (WR) was prepared by mixing 50 parts of BCA Reagent A with 1 part of BCA Reagent B (Reagent A:B ratio = 50:1). 25µL of each BCA Standard or sample was pipetted into a microplate well (Greiner Bio-one, cat # 655090) and then 200µL of the WR was added to each well. Plate was placed on a plate shaker for 30 seconds and incubated at 37°C for 30 minutes. The absorbance of each sample was measured at 562nm on a plate reader (Synergy H1 Hybrid, BioTek, United States).

Sample Preparation for Quantitative Mass Spectrometry. Four volumes of cold (-20°C) acetone were added to each protein sample and incubated for 60 minutes at -20°C.

After centrifugation for 10 minutes at 13,000 ×g, supernatant was decanted and the acetone was allowed to evaporate from the uncapped tube at room temperature for 30 minutes. RapiGest SF working solution was reconstituted by adding 1 mg RapiGest SF powder in 50 mM Ammonium Bicarbonate (NH_4HCO_3) to achieve a 0.1% (w/v) solution. Every protein pellet was resuspended in 100 µL RapiGest SF working solution and vortexed thoroughly to dissolve the protein pellet. Samples were reduced with 4 µL of 10 mM dithiothreitol (DTT) in 0.1 M ammonium bicarbonate at room temperature for 30 minutes, then the samples were alkylated with 4 µL 50 mM iodoacetamide in 0.1 M ammonium bicarbonate at room temperature for 30 minutes. Finally, samples were digested with 1 µg trypsin overnight and then quenched with 5% (v:v) glacial acetic acid.

Proteomic Analysis by Quantitative Mass Spectrometry. Samples were analyzed by a Waters Synapt G2Si mass spectrometer system with a nanospray ion source interfaced to a Waters M-Class C18 reversed-phase capillary column. MSE scout runs were performed on each sample with spiked internal standards to determine the amount of protein on column. The injection volume was adjusted to achieve 200 ng protein on column for each analysis using ion mobility separation. Each sample was run in triplicate using this technique.

Results

Quantification of differentially expressed proteins under different stressors. Differentially expressed genes with statistical significance were counted (Table 8). More proteins were differentially expressed in ampicillin treated cells than the heat shocked cells at all three time points. In addition, the pattern of protein abundance was strikingly different with the ampicillin treated cells being down-regulated at all three measured time points, while the heat-shocked cells we up-regulated at first time point (T_{10}) and down-regulated at later time points.

Table 8. Quantification of differentially expressed proteins in counts and percentages under different stress factors in *S. sanguinis*. Statistically significant differential regulations in *S. sanguinis* proteins were measured after 10, 20, and 30 minutes of ampicillin or heat stress at T_{10}, T_{20}, and T_{30} respectively.

	Ampicillin-treated cells		
	T_{10}	T_{20}	T_{30}
Up-regulated	20 (7%)	46 (17%)	18 (9%)
Same	0	0	0
Down-regulated	249 (93%)	222 (83%)	184 (91%)
Total	**269**	**268**	**202**
	Heat-shocked cells		
Up-regulated	70 (74%)	8 (16%)	18 (31%)
Same	0	0	0
Down-regulated	24 (26%)	41(84%)	40 (69%)
Total	**94**	**49**	**58**

Furthermore, we conducted a functional enrichment analysis of all differentially expressed proteins (Table 9). Besides the variable protein inventory measured on a temporal basis, a functional annotation analysis of these detected proteins using DAVID Gene Functional Annotation Clustering tool identified the following top overrepresented functional groups in ampicillin-treated cells among the up-regulated proteins: At T_{10}, “phosphorylation”; at T_{20}, “ribosomal biogenesis”; at T_{30}, “purine nucleoside binding”. Top overrepresented functional groups among the down-regulated proteins at all time points were “ribosomal biogenesis”, “glycolysis”, and “aminoacyl-tRNA biosynthesis” (Table 9). The 9.5-fold up-regulation of RelA enzyme, a major (p)ppGpp synthase [74,75], at T_{20} revealed the orchestration of a stringent response that impacted growth and persistence under stressful conditions by controlling sugar metabolism, ribosomal biogenesis, and cell wall biosynthesis.

Regarding heat-shocked cells, the reduced protein inventory showed in the up-regulated proteins a dominant functional group attributed to ribosomal biogenesis, followed by translation elongation at T_{10}, reflecting a translational surge as a stress response. Later on, ribosomal biogenesis became the top ranked functional group enriched with down-regulated proteins at T_{20} and T_{30}, in addition to glycolysis, thus reflecting a proteomic manifestation of the reduced growth rate observed with stressed cells. Comparing the enriched functional group in cells affected by the stressors, it is evident that ribosomal biogenesis and glycolysis are prominent markers of the cell homeostasis that correlate well with the general population’s growth rate.

Table 9. Functional enrichment and clustering of differentially regulated genes under impact of ampicillin and mild heat shock.

		Ampicillin-treated cells		Heat-shocked cells	
		Functional category	P-value	Functional category	P-value
T_{10}	**Up-regulated**	Phosphorylation	0.071	Ribosomal biogenesis	8.7E-26
				Translation elongation	0.005
	Down-regulated	Ribosomal biogenesis	2.7E-30	Ribosomal biogenesis	0.0001
		Glycolysis	1.2E-06	Glycolysis	0.002
		Aminoacyl-tRNA biosynthesis	4.6E-05		
		Protein folding	0.0022		
T_{20}	**Up-regulated**	Ribosomal biogenesis	8.9E-05	Not enough proteins detected	
	Down-regulated	Ribosomal biogenesis	9.5E-24	Ribosomal biogenesis	3.10E-11
		Glycolysis	1.0E-05	Glycolysis	2.67E-04
		Aminoacyl-tRNA biosynthesis	1.3E-05		
		Protein folding	1.4E-04		
		Oxidoreductase activity	0.034		
T_{30}	**Up-regulated**	Purine nucleoside binding	0.0962	Not enough proteins detected	
	Down-regulated	Ribosomal biogenesis	1.8E-29	Ribosomal biogenesis	2.2E-11
		Glycolysis	1.5E-07	Glycolysis	0.0019
		Aminoacyl-tRNA biosynthesis	9.3E-05		
		Cell division	0.0101		
		RNA polymerase	0.0142		
		Translational elongation	0.0349		

Pathway-dependent interpretation of proteomic profiles of essential proteins.

Ribosomal biogenesis. Proteomic findings in ampicillin-treated cells showed the reduction in 29 ribosomal protein levels at all the time points. Five ribosomal proteins (SSA_1105, *rplL,*50S ribosomal protein L7/L12; SSA_0110, *rplB,* 50S ribosomal protein L2; SSA_1104, rplJ, 50S ribosomal protein L10; SSA_1265, *rplS*, 50S ribosomal protein L19; SSA_0113, *rpsC*, 30S ribosomal protein S3) were up-regulated only at T_{20}, and two ribosomal proteins (SSA_0108, *rplD*, 50S ribosomal protein L4; SSA_0117, *rplN*, 50S ribosomal protein L14) were up-regulated only at T_{30}. For heat treated cells, the opposite scenario was observed: 21 proteins were up-regulated at T_{10} and only 5 down-regulated. In addition to their major role in protein synthesis, ribosomes have been implicated in pleiotropic functions, ranging from antibiotic adaptation [77] to fatty acid biosynthesis [78], in which we postulate that these exceptionally regulated ribosomal proteins may be involved. These findings provide "proteomic signatures" of different stress treatments that are phenotypically demonstrated in different growth patterns (Fig. 8).

Amino acid biosynthesis. Our findings show that most proteins involved in translation were down-regulated, with some interesting exceptions. Although elongation factors Ts (SSA_2202) and G (SSA_2109) were down-regulated in ampicillin-treated cells at all time points, the opposite result was recorded for elongation factor Tu (SSA_1520) at T_{20}. It is beneficial to mention that EF-Tu has been shown to mimic the chaperone activity of *DnaK* in *E. coli* [79,80] and act as an adhesion factor in *Mycoplasma pneumonia*e [81]. Another exception is peptide deformylase (SSA_2061), whose protein levels have been elevated 6.3-fold at T_{10} only, reflecting an early stress response that assists in the formation of methionyl peptides that lead protein synthesis of early stress response proteins. This provides new hints for the ongoing efforts to design anti-peptide deformylase drugs [82,83]. As far as heat-treated cells are concerned, the three essential elongation factors Ts (SSA_2202), G (SSA_2109), and Tu (SSA_1520) were up-regulated at $T_{10,}$ to aid the ribosomes in bolstering the translational potency as an early stress response.

We found previously that essential proteins contain less of the "degradation-prone" amino acids than non-essential proteins, except for arginine. We further investigated the top 10% of essential proteins that contain arginine most and least, and we found in both cases ribosomal proteins are the most abundant in both groups, indicating perhaps a need for faster regulation in response to a sudden stressor. In heat-stressed cells, we noticed an up-regulation of histidyl-tRNA synthetase, feeding up the translational machinery for synthesis of essential proteome.

One interesting exception worth mentioning is the significant up-regulation of mRNA and protein levels of cysteine-tRNA synthetase. Cysteine is the least abundant component of essential proteins in comparison to all other amino acids and perhaps the abundance of cysteine-tRNA synthetase was to secure the recruitment of this amino acid to essential proteins during stressful conditions. Another interpretation to be suggested is that cysteine abundance can help resist an ampicillin-induced oxidative stress, as a similar role has been attributed to cysteine in diamide-stressed *B. subtilis* and *S. aureus* [84].

Previously, we have shown that enzymes involved in amino acid biosynthesis would be essential if chemically defined medium (CDM) was used instead of the nutritionally enriched BHI medium [85]. We investigated the biosynthesis pathways of all amino acids in ampicillin-treated cells using the KEGG maps and identified a proteomic down-regulation of most amino acids biosynthesis enzymes with two exceptions at T_{10}: the strategically positioned *IlvE* enzyme

(SSA_1225) at the rate-determining step of the biosynthetic pathways for valine, leucine, and isoleucine was elevated 3.5-fold; *glnA* enzyme (SSA_0307) responsible for interconversion between glutamate and glutamine was up-regulated 3-fold. Interestingly, valine and glutamate are more abundant among the essential proteome than among the non-essential one, and this may be a contributor to their biosynthesis at times of energy scarcity. However, the import of ready-made amino acids due to the up-regulation of peptide ABC transporter ATPase 15.5-fold at T_{20}, the non-essential protein SSA_1531, and the proteolytic activity of the 5.8-fold up-regulated zinc-dependent peptidase, the non-essential protein SSA_2371, may have supplied the cell with ready-made amino acids that saved the cell the energy for biosynthesis at stressful settings and perhaps compensated for the intracellular biosynthetic activity. No amino acid biosynthesis enzymes were measured in heat-treated cells.

Glycolysis. Glycolysis represents a fundamental source of energy production and supplier of products for many anabolic pathways (Fig. 7). Proteomic findings revealed down-regulation of 8 glycolytic enzymes across all time points, except for SSA_0688 showing a slight protein increase at T_{20}. However, in heat-treated cells, we noticed a general down-regulation of glycolytic enzymes except for fba (SSA_1992), gpmA (SSA_0688), and pgk (SSA_0302) at T_{10}, and enolase (SSA_0886) at T_{30}. These enzymes catalyze bi-directional reactions and may be involved in gluconeogenesis pathway, as implied by functional enrichment analysis.

Cell wall biosynthesis. Terpenoid, peptidoglycan, amino sugar, glycerophospholipid and phosphatidyl glycerol biosynthesis pathways converge to produce the cell wall in *S. sanguinis* (Fig. 7). In ampicillin-treated cells, proteomic findings showed complete down-regulation of measured proteins belonging to the peptidoglycan, amino sugar, and glycerophospholipid biosynthesis. Unfortunately, no proteins of the terpenoid biosynthesis pathway were measured. In heat-treated cells, the scarcity of total detected proteins led to total absence of proteins involved in any pathway contributing to cell wall biosynthesis.

Nucleic acid biosynthesis. In ampicillin-treated cells, proteomic analysis of proteins involved in the pentose phosphate pathway, RNA and DNA biosynthesis showed a general down-regulation among majority of genes within these pathways except for an up-regulation of RNA polymerase subunit β (SSA_0176) at T_{30} and RNA polymerase subunit α (SSA_0132) at T_{20}, probably in response to elevated protein levels of the transcriptional regulators *RipR* (SSA_0081, 5.64-folds) at T_{10}, Spx (SSA_2244, 2.1-folds) at T_{20}, and TetR (SSA_0927, 11.8-folds) at T_{30}. The ortholog of RpiR in *E. coli* has been shown to repress ribose phosphate isomerase B (*rpiB*), blocking the production of ribose 5-phosphate and down-regulating the pentose phosphate pathway [89], an observation recorded in ampicillin-stressed *S. sanguinis* cells. *TetR* repressor has been linked to antibiotics resistance [90,91] and Spx regulators have been known to bind to the RNA polymerase subunit α (SSA_0132), where both are concurrently up-regulated at T_{20}, and enhancing or repressing transcription initiation [92,93]. In heat-treated cells, proteomic analysis showed a down-regulation of proteins involved in nucleic acid biosynthesis pathways, except for DNA polymerase III subunit delta (SSA_1721) and adenylate kinase (SSA_0218) at T_{10}, coping with the abrupt protein biosynthesis observed at T_{10} as an early stress response mechanism.

Correlation between transcriptome and proteome. Using high throughput approaches for the identification of differentially expressed genes and proteins enabled the identification of transcriptomic and proteomic dynamics in response to sub-inhibitory ampicillin concentration and heat at three time points. We calculated the correlation between the mRNA and protein levels of every gene and protein, respectively, which displayed statistically significant expression (Table 10). In both ampicillin and heat-stressed cells, the mRNA/protein correlation was higher among the essential genes/proteins than among their non-essential counterparts, although both groups were stressed at early response phase (T_{10}). This may be explained through the chronological frame of events where transcription precedes translation and protein synthesis, added to the fact that bacterial mRNA on average has a half-life less than 10 minutes [94] while proteins enjoy more longevity, although dependent on post-translational modifications, protein folding and degradation machinery [95]. After going through the early stress shock (after T_{10}), correlation was enhanced more in essential than non-essential ratios. It is noteworthy to emphasize that with essential ratios in ampicillin-treated cells, the mRNA/protein non-correlation percentage never offset the correlation ratios, a scenario that happened during T_{10} with the non-essential setting. Moreover, with both stressors, the essential correlation percentages at T_{20} and T_{30} were much higher than the essential non-correlation percentages, peaking at T_{30}, unlike those in non-essential setting at T_{20} and T_{30} were the margin of difference was smaller, and even the balance was tipped off in heat-treated samples at T_{30}.

Table 10. Correlation analysis between differential expression of mRNA and proteins of essential and non-essential genes and proteins in two stressed populations. Transcriptional and proteomic profiles of all genes and proteins were measured at time points T_{10}, T_{20}, T_{30} corresponding to 10, 20, and 30 minutes post-treatment of exponentially growing *S. sanguinis* SK36 samples with sub-inhibitory dose of ampicillin or heat. All expression values of mRNAs and proteins at different time points were normalized to untreated *S. sanguinis* SK36 samples. The correlation at every time point is expressed as a count and percentage of mRNA/protein pairs' match.

		Ampicillin-treated cells		
		T_{10} / T_0	T_{20} / T_0	T_{30} / T_0
Essential gene/protein	Count of correlated mRNA/protein expressions (%)	111 (50%)	131 (59%)	117 (66%)
	Count of non-correlated mRNA/protein expressions (%)	111 (50%)	90 (41%)	60 (34%)
		T_{10}/T_0	T_{20}/T_0	T_{30}/T_0
Non-essential gene/protein	Count of correlated mRNA/protein expressions (%)	59 (43%)	73 (52.5%)	60 (57%)
	Count of non-correlated mRNA/protein expressions (%)	79 (57%)	66 (47.5%)	45 (43%)

		Heat-shocked cells		
		T_{10} / T_0	T_{20} / T_0	T_{30} / T_0
Essential gene/protein	Count of correlated mRNA/protein expressions (%)	14 (30%)	23 (82%)	22 (69%)
	Count of non-correlated mRNA/protein expressions (%)	32 (70%)	5 (18%)	10 (31%)
		T_{10}/T_0	T_{20}/T_0	T_{30}/T_0
Non-essential gene/protein	Count of correlated mRNA/protein expressions (%)	7 (33%)	6 (67%)	5 (38%)
	Count of non-correlated mRNA/protein expressions (%)	14 (67%)	3 (33%)	8 (62%)

Discussion

Coping with transcriptomic advances through global proteomic studies is a challenging task that provides tremendous clinical significance. We provide hereby the first study to address comprehensively the proteomic dynamics of essential proteins on a temporal basis in *S. sanguinis* under impact of two clinically-relevant stress factors, namely high temperature and sub-inhibitory concentration of ampicillin.

Combining transcriptomic and proteomic analysis under the same cultivation conditions and same time points aimed at correlating our protein abundance findings with their corresponding transcriptional profiles, providing an insightful endeavor that sheds light on the biological intricacies of transcription, translation, mRNA stability, and protein degradation [222,223], and drawing a global framework for gene/protein regulation that can be therapeutically targeted. Although bacteria lack the complex regulatory mechanisms harnessed by eukaryotic systems, such as poly-ubiquitination and proteasomes, it has been shown that bacteria have lower mRNA/protein correlations [224-226] in comparison to eukaryotic models [227,228]. Interestingly, using the functional pathways approach, it was shown that kinases, cell cycle genes, signaling and metabolic proteins display the highest mRNA/protein correlations in the yeast *Schizosaccharomyces pombe*. We hypothesized that since these proteins are conducting essential functions, it is worth testing the essential mRNA/protein correlation in our bacterial model under stress where essential functions are in utmost demand. Moreover, codon usage has been linked to higher mRNA/protein correlation [224], and since essential genes have optimized their codon usage for a high sustainable expression, we expected this factor to enhance our mRNA/protein ratios. Our findings support this rationale as essential genes exhibited better mRNA/protein ratios than non-essential genes at all time point measurements (Table 4), and it improved with time as the bacteria adjusted to the antibiotic shock. The correlation was not perfect for many reasons: the proteome was not completely measured and almost half of the essential proteins were covered. In addition, recent findings in *E. coli* and other bacterial models stressed the role of mRNA secondary structure, more than codon usage, in modulating gene expression [229-232]. Further investigation is needed for a better understanding of this biological equation.

Our proteomic findings along the integrated temporal factor highlighted the chronological cascade of events, where proteins differentially expressed at T_{10} demonstrated an immediate stress response, while protein changes at T_{20} and T_{30} demonstrated the time lag between transcription and adaptive production of translated proteins as bacterial cells were undergoing replication. Bioinformatics analyses suggested that the immediate transcriptomic responses correlate with short-lived transcripts while the “slower” protein responses correlate with a more persistent and conserved response, as exemplified through findings in yeast [233] and *Caenorhabditis elegans* [234]. Comparing conservation of *S. sanguinis* essential proteins of transcription versus translation (Fig. 5), we have shown that translation is more enriched in essential and conserved proteins than transcription. Moreover, the measured stress response essential proteins, especially the ones involved in translation, demonstrated to a large degree a high conservation rate across species (Fig. 5), highlighting further the reliability of translation essential proteins as “proteomic signatures” that dictate the cell’s physiology and even the energy status, especially that it was shown earlier that translation proteins consume more than 70% of the cellular ATP pool [199]. Whether the pattern of differentially expressed *S. sanguinis* proteins during stress response is conserved across other bacterial species is currently speculative and worth further investigation, because if it holds true for bacterial models, then essential proteins’ behavior in response to stress will provide a wealth of proteomic signatures that may serve as potential therapeutic targets and open doors wide for synthetic biology engineering as well as evolutionary studies.

Upon exposure to stress, transition to slow growth rate was observed (Fig. 8) accompanied by extensive reprogramming of proteome across all major essential pathways, including glycolysis, purine and pyrimidine synthesis, cell wall biosynthesis, transcription and translation. We postulated that essential proteins tend to favor the less “degradation-prone” amino acids as demonstrated by the N-rule as this enhances their persistence and functional dynamics (Fig. 10). This may explain in part the up-regulation of biosynthetic enzymes for valine (branched amino acids), glutamine and glutamate, where the ampicillin-stressed cells seem not to rely solely on the recycling of degraded proteins nor peptide import through ABC transporters to satisfy their need for building blocks of essential proteome. The need for branched amino acids has been demonstrated in acid-stressed *S. mutans* [218] and *S. suis* isolated from porcine cerebrospinal fluid [235] as well, showing promise for establishing a potential “stress proteomic signature” based on amino acids’ composition of essential proteome.

Taken together, this work is the first global study that monitors time-dependent changes of essential proteins encountering antibiotic stress and heat, revealing crucial switches for the adaptation of metabolic, cell wall biosynthesis, and genetic information processing pathways.

Appendix

Supplemental Table 1. Comparison of predicted and experimentally verified essential genes. The experimentally defined list of essential genes (experimental EG) for every bacterial strain is shown and compared to our predicted list (predicted EG) of essential genes. DEG codes were extracted from the database of essential genes. Gene symbols, loci, COG annotations, and gene products were extracted from NCBI.

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rpmH	BSU41060	-	50S ribosomal protein L34	DEG10010271	BSU41060	BSU41060	Bacillus subtilis 168
rnpA	BSU41050	COG0594J	ribonuclease P protein component	DEG10010270	BSU41050	BSU41050	Bacillus subtilis 168
rpsF	BSU40910	COG0360J	30S ribosomal protein S6	DEG10010269	BSU40910	BSU40910	Bacillus subtilis 168
ssbA	BSU40900	COG0629L	single-stranded DNA-binding protein	DEG10010268	BSU40900	BSU40900	Bacillus subtilis 168
rpsR	BSU40890	COG0238J	30S ribosomal protein S18	DEG10010267	BSU40890	BSU40890	Bacillus subtilis 168
ppaC	BSU40550	COG1227C	manganese-dependent inorganic pyrophosphatase	DEG10010266	BSU40550	BSU40550	Bacillus subtilis 168
rplI	BSU40500	COG0359J	50S ribosomal protein L9	DEG10010265	BSU40500	BSU40500	Bacillus subtilis 168
dnaC	BSU40440	COG0305L	replicative DNA helicase	DEG10010264	BSU40440	BSU40440	Bacillus subtilis 168
walR	BSU40410	COG0745TK	transcriptional regulator	DEG10010263	BSU40410	BSU40410	Bacillus subtilis 168
walK	BSU40400	COG5002T	sensor histidine kinase	DEG10010262	BSU40400	BSU40400	Bacillus subtilis 168
menA	BSU38490	COG1575H	1,4-dihydroxy-2-naphthoate octaprenyltransferase	DEG10010261	BSU38490	BSU38490	Bacillus subtilis 168
rodA	BSU38120	COG0772D	rod shape-determining protein RodA	DEG10010260	BSU38120	BSU38120	Bacillus subtilis 168
argS	BSU37330	COG0018J	arginine--tRNA ligase	DEG10010259	BSU37330	BSU37330	Bacillus subtilis 168
pyrG	BSU37150	COG0504F	CTP synthase	DEG10010258	BSU37150	BSU37150	Bacillus subtilis 168
fbaA	BSU37120	COG0191G	fructose-bisphosphate aldolase	DEG10010257	BSU37120	BSU37120	Bacillus subtilis 168
rpmE	BSU37070	COG0254J	50S ribosomal protein L31	DEG10010256	BSU37070	BSU37070	Bacillus subtilis 168
prfA	BSU37010	COG0216J	peptide chain release factor 1	DEG10010255	BSU37010	BSU37010	Bacillus subtilis 168
ywlC	BSU36950	COG0009J	tRNA threonylcarbamoyladenosine biosynthesis protein YwlC	DEG10010254	BSU36950	BSU36950	Bacillus subtilis 168
glyA	BSU36900	COG0112E	serine hydroxymethyltransferase	DEG10010253	BSU36900	BSU36900	Bacillus subtilis 168
murAA	BSU36760	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	DEG10010252	BSU36760	BSU36760	Bacillus subtilis 168
tagB	BSU35760	COG1887M	CDP-glycerol:glycerophosphate glycerophosphotransferase	DEG10010251	BSU35760	BSU35760	Bacillus subtilis 168
tagA	BSU35750	COG1922M	N-acetylmannosaminyltransferase	DEG10010250	BSU35750	BSU35750	Bacillus subtilis 168
tagD	BSU35740	COG0615MI	glycerol-3-phosphate cytidylyltransferase	DEG10010249	BSU35740	BSU35740	Bacillus subtilis 168
tagF	BSU35720	COG1887M	CDP-glycerol:poly	DEG10010248	BSU35720	BSU35720	Bacillus subtilis 168
tagG	BSU35710	COG1682GM	teichoic acid translocation permease protein TagG	DEG10010247	BSU35710	BSU35710	Bacillus subtilis 168
tagH	BSU35700	COG1134GM	teichoic acids export ATP-binding protein TagH	DEG10010246	BSU35700	BSU35700	Bacillus subtilis 168
mnaA	BSU35660	COG0381M	UDP-N-acetylglucosamine 2-epimerase	DEG10010245	BSU35660	BSU35660	Bacillus subtilis 168
tagO	BSU35530	COG0472M	undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase	DEG10010244	BSU35530	BSU35530	Bacillus subtilis 168
secA	BSU35300	COG0653U	protein translocase subunit SecA	DEG10010243	BSU35300	BSU35300	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
prfB	BSU35290	COG1186J	peptide chain release factor 2	DEG10010242	BSU35290	BSU35290	Bacillus subtilis 168
trxB	BSU34790	COG0492O	thioredoxin	DEG10010241	BSU34790	BSU34790	Bacillus subtilis 168
pgk	BSU33930	COG0126G	phosphoglycerate kinase	DEG10010240	BSU33930	BSU33930	Bacillus subtilis 168
tpiA	BSU33920	COG0149G	triosephosphate isomerase	DEG10010239	BSU33920	BSU33920	Bacillus subtilis 168
pgm	BSU33910	COG0696G	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	DEG10010238	BSU33910	BSU33910	Bacillus subtilis 168
eno	BSU33900	COG0148G	enolase	DEG10010237	BSU33900	BSU33900	Bacillus subtilis 168
sufC	BSU32710	COG0396O	vegetative protein 296	DEG10010236	BSU32710		Bacillus subtilis 168
sufD	BSU32700	COG0719O	FeS cluster assembly protein SufD	DEG10010235	BSU32700	BSU32700	Bacillus subtilis 168
sufS	BSU32690	COG0520E	cysteine desulfurase	DEG10010234	BSU32690	BSU32690	Bacillus subtilis 168
iscU	BSU32680	COG0822C	NifU-like protein	DEG10010233	BSU32680		Bacillus subtilis 168
sufB	BSU32670	COG0719O	FeS cluster assembly protein SufB	DEG10010232	BSU32670	BSU32670	Bacillus subtilis 168
dapF	BSU32170	COG0253E	diaminopimelate epimerase	DEG10010231	BSU32170	BSU32170	Bacillus subtilis 168
yumC	BSU32110	COG0492O	ferredoxin--NADP reductase 2	DEG10010230	BSU32110	BSU32110	Bacillus subtilis 168
yueK	BSU31750	COG1488H	nicotinate phosphoribosyltransferase	DEG10010229	BSU31750	BSU31750	Bacillus subtilis 168
mrpF	BSU31650	COG2212P	Na(+)/H(+) antiporter subunit F	DEG10010228	BSU31650		Bacillus subtilis 168
mrpD	BSU31630	COG0651CP	Na(+)/H(+) antiporter subunit D	DEG10010227	BSU31630		Bacillus subtilis 168
mrpC	BSU31620	COG1006P	Na(+)/H(+) antiporter subunit C	DEG10010226	BSU31620		Bacillus subtilis 168
mrpB	BSU31610	COG2111P	Na(+)/H(+) antiporter subunit B	DEG10010225	BSU31610		Bacillus subtilis 168
mrpA	BSU31600	COG1009CP	Na(+)/H(+) antiporter subunit A	DEG10010224	BSU31600		Bacillus subtilis 168
menD	BSU30820	COG1165H	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	DEG10010223	BSU30820	BSU30820	Bacillus subtilis 168
menB	BSU30800	COG0447H	1,4-dihydroxy-2-naphthoyl-CoA synthase	DEG10010222	BSU30800	BSU30800	Bacillus subtilis 168
menE	BSU30790	COG0318IQ	2-succinylbenzoate--CoA ligase	DEG10010221	BSU30790	BSU30790	Bacillus subtilis 168
menC	BSU30780	COG4948MR	o-succinylbenzoate synthase	DEG10010220	BSU30780	BSU30780	Bacillus subtilis 168
metK	BSU30550	COG0192H	S-adenosylmethionine synthase	DEG10010219	BSU30550	BSU30550	Bacillus subtilis 168
leuS	BSU30320	COG0495J	leucine--tRNA ligase	DEG10010218	BSU30320	BSU30320	Bacillus subtilis 168
murC	BSU29790	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10010217	BSU29790	BSU29790	Bacillus subtilis 168
tyrS	BSU29670	COG0162J	tyrosine--tRNA ligase 1	DEG10010216	BSU29670	BSU29670	Bacillus subtilis 168
rpsD	BSU29660	COG0522J	30S ribosomal protein S4	DEG10010215	BSU29660	BSU29660	Bacillus subtilis 168
dnaE	BSU29230	COG0587L	DNA polymerase III subunit alpha	DEG10010214	BSU29230	BSU29230	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
accD	BSU29210	COG0777I	acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	DEG10010213	BSU29210	BSU29210	Bacillus subtilis 168
accA	BSU29200	COG0825I	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	DEG10010212	BSU29200	BSU29200	Bacillus subtilis 168
pfkA	BSU29190	COG0205G	6-phosphofructokinase	DEG10010211	BSU29190	BSU29190	Bacillus subtilis 168
coaE	BSU29060	COG0237H	dephospho-CoA kinase	DEG10010210	BSU29060	BSU29060	Bacillus subtilis 168
dnaB	BSU28990	COG3611L	replication initiation and membrane attachment protein	DEG10010209	BSU28990	BSU28990	Bacillus subtilis 168
dnaI	BSU28980	COG1484L	primosomal protein DnaI	DEG10010208	BSU28980	BSU28980	Bacillus subtilis 168
infC	BSU28870	COG0290J	translation initiation factor IF-3	DEG10010207	BSU28870	BSU28870	Bacillus subtilis 168
rpmI	BSU28860	COG0291J	50S ribosomal protein L35	DEG10010206	BSU28860	BSU28860	Bacillus subtilis 168
rplT	BSU28850	COG0292J	50S ribosomal protein L20	DEG10010205	BSU28850	BSU28850	Bacillus subtilis 168
pheS	BSU28640	COG0016J	phenylalanine--tRNA ligase alpha subunit	DEG10010204	BSU28640	BSU28640	Bacillus subtilis 168
pheT	BSU28630	COG0072J	phenylalanine--tRNA ligase beta subunit	DEG10010203	BSU28630	BSU28630	Bacillus subtilis 168
trxA	BSU28500	COG3118O	thioredoxin	DEG10010202	BSU28500	BSU28500	Bacillus subtilis 168
racE	BSU28390	COG0796M	glutamate racemase	DEG10010201	BSU28390	BSU28390	Bacillus subtilis 168
engB	BSU28190	COG0218R	GTP-binding protein EngB	DEG10010200	BSU28190	BSU28190	Bacillus subtilis 168
valS	BSU28090	COG0525J	valine--tRNA ligase	DEG10010199	BSU28090	BSU28090	Bacillus subtilis 168
mreB	BSU28030	COG1077D	rod shape-determining protein MreB	DEG10010198	BSU28030	BSU28030	Bacillus subtilis 168
mreC	BSU28020	COG1792M	cell shape-determining protein MreC	DEG10010197	BSU28020	BSU28020	Bacillus subtilis 168
rplU	BSU27960	COG0261J	50S ribosomal protein L21	DEG10010196	BSU27960	BSU27960	Bacillus subtilis 168
rpmA	BSU27940	COG0211J	50S ribosomal protein L27	DEG10010195	BSU27940	BSU27940	Bacillus subtilis 168
obgE	BSU27920	COG0536R	GTPase ObgE	DEG10010194	BSU27920	BSU27920	Bacillus subtilis 168
hisS	BSU27560	COG0124J	histidine--tRNA ligase	DEG10010193	BSU27560	BSU27560	Bacillus subtilis 168
aspS	BSU27550	COG0173J	aspartate--tRNA ligase	DEG10010192	BSU27550	BSU27550	Bacillus subtilis 168
iscS	BSU27510	COG1104E	cysteine desulfurase IscS 1	DEG10010191	BSU27510		Bacillus subtilis 168
mnmA	BSU27500	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10010190	BSU27500		Bacillus subtilis 168
alaS	BSU27410	COG0013J	alanine--tRNA ligase	DEG10010189	BSU27410	BSU27410	Bacillus subtilis 168
yqeH	BSU25670	COG1161R	hypothetical protein	DEG10010188	BSU25670	BSU25670	Bacillus subtilis 168
yqeI	BSU25650	COG1534J	RNA-binding protein YqeI	DEG10010187	BSU25650	BSU25650	Bacillus subtilis 168
nadD	BSU25640	COG1057H	nicotinate-nucleotide adenylyltransferase	DEG10010186	BSU25640	BSU25640	Bacillus subtilis 168
holA	BSU25560	COG1466L	hypothetical protein	DEG10010185	BSU25560	BSU25560	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rpsT	BSU25550	COG0268J	30S ribosomal protein S20	DEG10010184	BSU25550	BSU25550	Bacillus subtilis 168
rpsU	BSU25410	-	30S ribosomal protein S21	DEG10010183	BSU25410	BSU25410	Bacillus subtilis 168
era	BSU25290	COG1159R	GTPase Era	DEG10010182	BSU25290	BSU25290	Bacillus subtilis 168
glyQ	BSU25270	COG0752J	glycine--tRNA ligase alpha subunit	DEG10010181	BSU25270	BSU25270	Bacillus subtilis 168
glyS	BSU25260	COG0751J	glycine--tRNA ligase beta subunit	DEG10010180	BSU25260	BSU25260	Bacillus subtilis 168
dnaG	BSU25210	COG0358L	DNA primase	DEG10010179	BSU25210	BSU25210	Bacillus subtilis 168
sigA	BSU25200	COG0568K	RNA polymerase sigma factor RpoD	DEG10010178	BSU25200	BSU25200	Bacillus subtilis 168
ispH	BSU25160	COG0761IM	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	DEG10010177	BSU25160	BSU25160	Bacillus subtilis 168
ispG	BSU25070	COG0821I	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	DEG10010176	BSU25070	BSU25070	Bacillus subtilis 168
rpmG	BSU24900	COG0267J	50S ribosomal protein L33 1	DEG10010175	BSU24900	BSU24900	Bacillus subtilis 168
accB	BSU24350	COG0511I	biotin carboxyl carrier protein of acetyl-CoA carboxylase	DEG10010174	BSU24350	BSU24350	Bacillus subtilis 168
accC	BSU24340	COG0439I	biotin carboxylase 1	DEG10010173	BSU24340	BSU24340	Bacillus subtilis 168
folD	BSU24310	COG0190H	bifunctional protein FolD	DEG10010172	BSU24310	BSU24310	Bacillus subtilis 168
ispA	BSU24280	COG0142H	farnesyl diphosphate synthase	DEG10010171	BSU24280	BSU24280	Bacillus subtilis 168
dxs	BSU24270	COG1154HI	1-deoxy-D-xylulose-5-phosphate synthase	DEG10010170	BSU24270	BSU24270	Bacillus subtilis 168
yqjK	BSU23840	COG1234R	ribonuclease Z	DEG10010169	BSU23840	BSU23840	Bacillus subtilis 168
scpA	BSU23220	COG1354S	segregation and condensation protein A	DEG10010168	BSU23220		Bacillus subtilis 168
spcB	BSU23210	COG1386K	segregation and condensation protein B	DEG10010167	BSU23210		Bacillus subtilis 168
resA	BSU23150	COG1225O	thiol-disulfide oxidoreductase ResA	DEG10010166	BSU23150	BSU23150	Bacillus subtilis 168
resB	BSU23140	COG1333O	cytochrome c biogenesis protein ResB	DEG10010165	BSU23140	BSU23140	Bacillus subtilis 168
resC	BSU23130	COG0755O	cytochrome c biogenesis protein ResC	DEG10010164	BSU23130	BSU23130	Bacillus subtilis 168
cmk	BSU22890	COG0283F	cytidylate kinase	DEG10010163	BSU22890	BSU22890	Bacillus subtilis 168
engA	BSU22840	COG1160R	GTPase Der	DEG10010162	BSU22840	BSU22840	Bacillus subtilis 168
gpsA	BSU22830	COG0240C	glycerol-3-phosphate dehydrogenase	DEG10010161	BSU22830	BSU22830	Bacillus subtilis 168
hbs	BSU22790	COG0776L	DNA-binding protein HU 1	DEG10010160	BSU22790	BSU22790	Bacillus subtilis 168
hepS	BSU22760	-	heptaprenyl diphosphate synthase component 1	DEG10010159	BSU22760	BSU22760	Bacillus subtilis 168
ubiE	BSU22750	COG2226H	demethylmenaquinone methyltransferase	DEG10010158	BSU22750	BSU22750	Bacillus subtilis 168
hepT	BSU22740	COG0142H	heptaprenyl diphosphate synthase component 2	DEG10010157	BSU22740	BSU22740	Bacillus subtilis 168
dapB	BSU22490	COG0289E	4-hydroxy-tetrahydrodipicolinate reductase	DEG10010156	BSU22490	BSU22490	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
cca	BSU22450	COG0617J	CCA-adding enzyme	DEG10010155	BSU22450	BSU22450	Bacillus subtilis 168
birA	BSU22440	COG0340H	bifunctional protein BirA	DEG10010154	BSU22440	BSU22440	Bacillus subtilis 168
asnC	BSU22360	COG0017J	asparagine--tRNA ligase	DEG10010153	BSU22360	BSU22360	Bacillus subtilis 168
dnaD	BSU22350	COG3935L	DNA replication protein DnaD	DEG10010152	BSU22350	BSU22350	Bacillus subtilis 168
dfrA	BSU21810	COG0262H	dihydrofolate reductase	DEG10010151	BSU21810	BSU21810	Bacillus subtilis 168
odhB	BSU19360	COG0508C	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	DEG10010150	BSU19360		Bacillus subtilis 168
yobD	BSU18850	COG1396K	XRE family transcriptional regulator	DEG10070160	BSU18850	BSU18850	Bacillus subtilis 168
parC	BSU18100	COG0188L	DNA topoisomerase 4 subunit A	DEG10010149	BSU18100	BSU18100	Bacillus subtilis 168
parE	BSU18090	COG0187L	DNA topoisomerase 4 subunit B	DEG10010148	BSU18090	BSU18090	Bacillus subtilis 168
yneS	BSU18070	COG0344S	glycerol-3-phosphate acyltransferase	DEG10010147	BSU18070	BSU18070	Bacillus subtilis 168
tkt	BSU17890	COG0021G	transketolase	DEG10010146	BSU17890	BSU17890	Bacillus subtilis 168
nrdF	BSU17390	COG0208F	ribonucleoside-diphosphate reductase subunit beta	DEG10010145	BSU17390	BSU17390	Bacillus subtilis 168
nrdE	BSU17380	COG0209F	ribonucleoside-diphosphate reductase subunit alpha	DEG10010144	BSU17380	BSU17380	Bacillus subtilis 168
nrdI	BSU17370	COG1780F	ribonucleotide reductase stimulatory protein NrdI	DEG10010143	BSU17370	BSU17370	Bacillus subtilis 168
ymdA	BSU16960	COG1418R	ribonuclease Y	DEG10010142	BSU16960	BSU16960	Bacillus subtilis 168
pgsA	BSU16920	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	DEG10010141	BSU16920	BSU16920	Bacillus subtilis 168
dapA	BSU16770	COG0329EM	4-hydroxy-tetrahydrodipicolinate synthase	DEG10010140	BSU16770	BSU16770	Bacillus subtilis 168
asd	BSU16750	COG0136E	aspartate-semialdehyde dehydrogenase	DEG10010139	BSU16750	BSU16750	Bacillus subtilis 168
rpsO	BSU16680	COG0184J	30S ribosomal protein S15	DEG10010138	BSU16680	BSU16680	Bacillus subtilis 168
infB	BSU16630	COG0532J	translation initiation factor IF-2	DEG10010137	BSU16630	BSU16630	Bacillus subtilis 168
nusA	BSU16600	COG0195K	transcription termination/antitermination protein NusA	DEG10010136	BSU16600	BSU16600	Bacillus subtilis 168
polC	BSU16580	COG2176L	DNA polymerase III PolC-type	DEG10010135	BSU16580	BSU16580	Bacillus subtilis 168
proS	BSU16570	COG0442J	proline--tRNA ligase	DEG10010134	BSU16570	BSU16570	Bacillus subtilis 168
dxr	BSU16550	COG0743I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	DEG10010133	BSU16550	BSU16550	Bacillus subtilis 168
cdsA	BSU16540	COG0575I	phosphatidate cytidylyltransferase	DEG10010132	BSU16540	BSU16540	Bacillus subtilis 168
frr	BSU16520	COG0233J	ribosome-recycling factor	DEG10010131	BSU16520	BSU16520	Bacillus subtilis 168
tsf	BSU16500	COG0264J	elongation factor Ts	DEG10010130	BSU16500	BSU16500	Bacillus subtilis 168
rpsB	BSU16490	COG0052J	30S ribosomal protein S2	DEG10010129	BSU16490	BSU16490	Bacillus subtilis 168
topA	BSU16120	COG0550L	DNA topoisomerase 1	DEG10010128	BSU16120	BSU16120	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rbgA	BSU16050	COG1161R	ribosome biogenesis GTPase A	DEG10010127	BSU16050	BSU16050	Bacillus subtilis 168
rplS	BSU16040	COG0335J	50S ribosomal protein L19	DEG10010126	BSU16040	BSU16040	Bacillus subtilis 168
trmD	BSU16030	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10010125	BSU16030	BSU16030	Bacillus subtilis 168
rpsP	BSU15990	COG0228J	30S ribosomal protein S16	DEG10010124	BSU15990	BSU15990	Bacillus subtilis 168
ffh	BSU15980	COG0541U	signal recognition particle protein	DEG10010123	BSU15980	BSU15980	Bacillus subtilis 168
ftsY	BSU15950	COG0552U	signal recognition particle receptor FtsY	DEG10010122	BSU15950	BSU15950	Bacillus subtilis 168
smc	BSU15940	COG1196D	chromosome partition protein Smc	DEG10010121	BSU15940	BSU15940	Bacillus subtilis 168
rnc	BSU15930	COG0571K	ribonuclease 3	DEG10010120	BSU15930	BSU15930	Bacillus subtilis 168
acpP	BSU15920	COG0236IQ	acyl carrier protein	DEG10010119	BSU15920	BSU15920	Bacillus subtilis 168
fabG	BSU15910	COG1028IQR	3-oxoacyl-[acyl-carrier-protein] reductase FabG	DEG10010118	BSU15910	BSU15910	Bacillus subtilis 168
fabD	BSU15900	COG0331I	malonyl CoA-acyl carrier protein transacylase	DEG10010117	BSU15900	BSU15900	Bacillus subtilis 168
plsX	BSU15890	COG0416I	phosphate acyltransferase	DEG10010116	BSU15890	BSU15890	Bacillus subtilis 168
rpmB	BSU15820	COG0227J	50S ribosomal protein L28	DEG10010115	BSU15820	BSU15820	Bacillus subtilis 168
yloQ	BSU15780	COG1162R	ribosome biogenesis GTPase RsgA	DEG10010114	BSU15780	BSU15780	Bacillus subtilis 168
fmt	BSU15730	COG0223J	methionyl-tRNA formyltransferase	DEG10010113	BSU15730	BSU15730	Bacillus subtilis 168
priA	BSU15710	COG1198L	primosomal protein N'	DEG10010112	BSU15710	BSU15710	Bacillus subtilis 168
gmk	BSU15680	COG0194F	guanylate kinase	DEG10010111	BSU15680	BSU15680	Bacillus subtilis 168
ileS	BSU15430	COG0060J	isoleucine--tRNA ligase	DEG10010110	BSU15430	BSU15430	Bacillus subtilis 168
ftsZ	BSU15290	COG0206D	cell division protein FtsZ	DEG10010109	BSU15290	BSU15290	Bacillus subtilis 168
ftsA	BSU15280	COG0849D	cell division protein FtsA	DEG10010108	BSU15280	BSU15280	Bacillus subtilis 168
divIB	BSU15240	COG1589M	cell division protein DivIB	DEG10010107	BSU15240	BSU15240	Bacillus subtilis 168
murB	BSU15230	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10010106	BSU15230	BSU15230	Bacillus subtilis 168
murG	BSU15220	COG0707M	pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	DEG10010105	BSU15220	BSU15220	Bacillus subtilis 168
murD	BSU15200	COG0771M	UDP-N-acetylmuramoylalanine--D-glutamate ligase	DEG10010104	BSU15200	BSU15200	Bacillus subtilis 168
mraY	BSU15190	COG0472M	phospho-n-acetylmuramoyl-pentapeptide-transferase	DEG10010103	BSU15190	BSU15190	Bacillus subtilis 168
murE	BSU15180	COG0769M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	DEG10010102	BSU15180	BSU15180	Bacillus subtilis 168
pbpB	BSU15160	COG0768M	penicillin-binding protein 2B	DEG10010101	BSU15160	BSU15160	Bacillus subtilis 168
ftsL	BSU15150	COG4839D	cell division protein FtsL	DEG10010100	BSU15150	BSU15150	Bacillus subtilis 168
rpmF	BSU15080	COG0333J	50S ribosomal protein L32	DEG10010099	BSU15080	BSU15080	Bacillus subtilis 168
ftsW	BSU14850	COG0772D	lipid II flippase FtsW	DEG10010098	BSU14850	BSU14850	Bacillus subtilis 168
ylaN	BSU14840	COG4838S	hypothetical protein	DEG10010097	BSU14840		Bacillus subtilis 168
pdhA	BSU14580	COG1071C	pyruvate dehydrogenase E1 component subunit alpha	DEG10010096	BSU14580	BSU14580	Bacillus subtilis 168
rnjA	BSU14530	COG0595R	ribonuclease J 1	DEG10010095	BSU14530	BSU14530	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
dapL	BSU14190	COG1473R	N-acetyldiaminopimelate deacetylase	DEG10010094	BSU14190	BSU14190	Bacillus subtilis 168
dapH	BSU14180	COG2171E	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	DEG10010093	BSU14180	BSU14180	Bacillus subtilis 168
yjcK	BSU11890	COG1670J	ribosomal-protein-alanine acetyltransferase	DEG10030610	BSU11890	BSU11890	Bacillus subtilis 168
ppnK	BSU11610	COG0061G	inorganic polyphosphate/ATP-NAD kinase 1	DEG10010092	BSU11610	BSU11610	Bacillus subtilis 168
trpS	BSU11420	COG0180J	tryptophan--tRNA ligase	DEG10010091	BSU11420	BSU11420	Bacillus subtilis 168
fabF	BSU11340	COG0304IQ	3-oxoacyl-[acyl-carrier-protein] synthase 2	DEG10010090	BSU11340	BSU11340	Bacillus subtilis 168
prsA	BSU09950	COG0760O	foldase protein PrsA	DEG10010089	BSU09950	BSU09950	Bacillus subtilis 168
plsC	BSU09540	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	DEG10010088	BSU09540	BSU09540	Bacillus subtilis 168
yhdL	BSU09510	-	anti-sigma-M factor YhdL	DEG10010087	BSU09510	BSU09510	Bacillus subtilis 168
cspR	BSU08930	COG0219J	tRNA (cytidine(34)-2'-O)-methyltransferase	DEG10010086	BSU08930	BSU08930	Bacillus subtilis 168
yerQ	BSU06720	COG1597IR	diacylglycerol kinase	DEG10010085	BSU06720		Bacillus subtilis 168
gatB	BSU06690	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10010084	BSU06690	BSU06690	Bacillus subtilis 168
gatA	BSU06680	COG0154J	glutamyl-tRNA(Gln) amidotransferase subunit A	DEG10010083	BSU06680	BSU06680	Bacillus subtilis 168
gatC	BSU06670	COG0721J	glutamyl-tRNA(Gln) amidotransferase subunit C	DEG10010082	BSU06670	BSU06670	Bacillus subtilis 168
ligA	BSU06620	COG0272L	DNA ligase	DEG10010081	BSU06620	BSU06620	Bacillus subtilis 168
pcrA	BSU06610	COG0210L	ATP-dependent DNA helicase PcrA	DEG10010080	BSU06610	BSU06610	Bacillus subtilis 168
ydiP	BSU06070	COG0270L	BsuMI modification methylase subunit YdiP	DEG10010079	BSU06070	BSU06070	Bacillus subtilis 168
ydiO	BSU06060	COG0270L	BsuMI modification methylase subunit YdiO	DEG10010078	BSU06060	BSU06060	Bacillus subtilis 168
groEL	BSU06030	COG0459O	60 kDa chaperonin	DEG10010077	BSU06030	BSU06030	Bacillus subtilis 168
groES	BSU06020	COG0234O	10 kDa chaperonin	DEG10010076	BSU06020	BSU06020	Bacillus subtilis 168
gcp	BSU05940	COG0533O	tRNA threonylcarbamoyladenosine biosynthesis protein Gcp	DEG10010075	BSU05940	BSU05940	Bacillus subtilis 168
ydiC	BSU05920	COG1214O	hypothetical protein	DEG10010074	BSU05920		Bacillus subtilis 168
ydiB	BSU05910	COG0802R	UPF0079 ATP-binding protein YdiB	DEG10010073	BSU05910	BSU05910	Bacillus subtilis 168
alrA	BSU04640	COG0787M	alanine racemase 1	DEG10010072	BSU04640	BSU04640	Bacillus subtilis 168
acpS	BSU04620	COG0736I	holo-[acyl-carrier-protein] synthase	DEG10010071	BSU04620	BSU04620	Bacillus subtilis 168
murF	BSU04570	COG0770M	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	DEG10010070	BSU04570	BSU04570	Bacillus subtilis 168
ddl	BSU04560	COG1181M	D-alanine--D-alanine ligase	DEG10010069	BSU04560	BSU04560	Bacillus subtilis 168
nadE	BSU03130	COG0171H	NH(3)-dependent NAD(+) synthetase	DEG10010068	BSU03130	BSU03130	Bacillus subtilis 168
glmS	BSU01780	COG0449M	glutamine--fructose-6-phosphate aminotransferase	DEG10010067	BSU01780	BSU01780	Bacillus subtilis 168
glmM	BSU01770	COG1109G	phosphoglucosamine mutase	DEG10010066	BSU01770	BSU01770	Bacillus subtilis 168
rpsI	BSU01500	COG0103J	30S ribosomal protein S9	DEG10010065	BSU01500	BSU01500	Bacillus subtilis 168
rplM	BSU01490	COG0102J	50S ribosomal protein L13	DEG10010064	BSU01490	BSU01490	Bacillus subtilis 168
rplQ	BSU01440	COG0203J	50S ribosomal protein L17	DEG10010063	BSU01440	BSU01440	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rpoA	BSU01430	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10010062	BSU01430	BSU01430	Bacillus subtilis 168
rpsK	BSU01420	COG0100J	30S ribosomal protein S11	DEG10010061	BSU01420	BSU01420	Bacillus subtilis 168
rpsM	BSU01410	COG0099J	30S ribosomal protein S13	DEG10010060	BSU01410	BSU01410	Bacillus subtilis 168
rpmJ	BSU01400	COG0257J	50S ribosomal protein L36	DEG10010059	BSU01400	BSU01400	Bacillus subtilis 168
infA	BSU01390	COG0361J	translate initiation factor IF-1	DEG10010058	BSU01390	BSU01390	Bacillus subtilis 168
mapA	BSU01380	COG0024J	methionine aminopeptidase	DEG10010057	BSU01380	BSU01380	Bacillus subtilis 168
adk	BSU01370	COG0563F	adenylate kinase	DEG10010056	BSU01370	BSU01370	Bacillus subtilis 168
secY	BSU01360	COG0201U	protein translocase subunit SecY	DEG10010055	BSU01360	BSU01360	Bacillus subtilis 168
rplO	BSU01350	COG0200J	50S ribosomal protein L15	DEG10010054	BSU01350	BSU01350	Bacillus subtilis 168
rpmD	BSU01340	COG1841J	50S ribosomal protein L30	DEG10010053	BSU01340	BSU01340	Bacillus subtilis 168
rpsE	BSU01330	COG0098J	30S ribosomal protein S5	DEG10010052	BSU01330	BSU01330	Bacillus subtilis 168
rplR	BSU01320	COG0256J	50S ribosomal protein L18	DEG10010051	BSU01320	BSU01320	Bacillus subtilis 168
rplF	BSU01310	COG0097J	50S ribosomal protein L6	DEG10010050	BSU01310	BSU01310	Bacillus subtilis 168
rpsH	BSU01300	COG0096J	30S ribosomal protein S8	DEG10010049	BSU01300	BSU01300	Bacillus subtilis 168
rpsN	BSU01290	COG0199J	30S ribosomal protein S14	DEG10010048	BSU01290	BSU01290	Bacillus subtilis 168
rplE	BSU01280	COG0094J	50S ribosomal protein L5	DEG10010047	BSU01280	BSU01280	Bacillus subtilis 168
rplX	BSU01270	COG0198J	50S ribosomal protein L24	DEG10010046	BSU01270	BSU01270	Bacillus subtilis 168
rplN	BSU01260	COG0093J	50S ribosomal protein L14	DEG10010045	BSU01260	BSU01260	Bacillus subtilis 168
rpsQ	BSU01250	COG0186J	30S ribosomal protein S17	DEG10010044	BSU01250	BSU01250	Bacillus subtilis 168
rpmC	BSU01240	COG0255J	50S ribosomal protein L29	DEG10010043	BSU01240	BSU01240	Bacillus subtilis 168
rplP	BSU01230	COG0197J	50S ribosomal protein L16	DEG10010042	BSU01230	BSU01230	Bacillus subtilis 168
rpsC	BSU01220	COG0092J	30S ribosomal protein S3	DEG10010041	BSU01220	BSU01220	Bacillus subtilis 168
rplV	BSU01210	COG0091J	50S ribosomal protein L22	DEG10010040	BSU01210	BSU01210	Bacillus subtilis 168
rpsS	BSU01200	COG0185J	30S ribosomal protein S19	DEG10010039	BSU01200	BSU01200	Bacillus subtilis 168
rplB	BSU01190	COG0090J	50S ribosomal protein L2	DEG10010038	BSU01190	BSU01190	Bacillus subtilis 168
rplW	BSU01180	COG0089J	50S ribosomal protein L23	DEG10010037	BSU01180	BSU01180	Bacillus subtilis 168
rplD	BSU01170	COG0088J	50S ribosomal protein L4	DEG10010036	BSU01170	BSU01170	Bacillus subtilis 168
rplC	BSU01160	COG0087J	50S ribosomal protein L3	DEG10010035	BSU01160	BSU01160	Bacillus subtilis 168
rpsJ	BSU01150	COG0051J	30S ribosomal protein S10	DEG10010034	BSU01150	BSU01150	Bacillus subtilis 168
tufA	BSU01130	COG0050J	elongation factor Tu	DEG10010033	BSU01130	BSU01130	Bacillus subtilis 168
fusA	BSU01120	COG0480J	elongation factor G	DEG10010032	BSU01120	BSU01120	Bacillus subtilis 168
rpsG	BSU01110	COG0049J	30S ribosomal protein S7	DEG10010031	BSU01110	BSU01110	Bacillus subtilis 168
rpsL	BSU01100	COG0048J	30S ribosomal protein S12	DEG10010030	BSU01100	BSU01100	Bacillus subtilis 168
rpoC	BSU01080	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10010029	BSU01080	BSU01080	Bacillus subtilis 168
rpoB	BSU01070	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10010028	BSU01070	BSU01070	Bacillus subtilis 168
rplL	BSU01050	COG0222J	50S ribosomal protein L7/L12	DEG10010027	BSU01050	BSU01050	Bacillus subtilis 168
rplJ	BSU01040	COG0244J	50S ribosomal protein L10	DEG10010026	BSU01040	BSU01040	Bacillus subtilis 168
rplA	BSU01030	COG0081J	50S ribosomal protein L1	DEG10010025	BSU01030	BSU01030	Bacillus subtilis 168
secE	BSU01000	COG0690U	preprotein translocase subunit SecE	DEG10010024	BSU01000	BSU01000	Bacillus subtilis 168
rpmG	BSU00990	COG0267J	50S ribosomal protein L33 2	DEG10010023	BSU00990	BSU00990	Bacillus subtilis 168
cysS	BSU00940	COG0215J	cysteine--tRNA ligase	DEG10010022	BSU00940	BSU00940	Bacillus subtilis 168
gltX	BSU00920	COG0008J	glutamate--tRNA ligase	DEG10010021	BSU00920	BSU00920	Bacillus subtilis 168
ispF	BSU00910	COG0245I	2-D-methyl-D-erythritol 2,4-cyclodiphosphate synthase	DEG10010020	BSU00910	BSU00910	Bacillus subtilis 168
ispD	BSU00900	COG1211I	2-D-methyl-D-erythritol 4-phosphate cytidylyltransferase	DEG10010019	BSU00900	BSU00900	Bacillus subtilis 168
lysS	BSU00820	COG1190J	lysine--tRNA ligase	DEG10010018	BSU00820	BSU00820	Bacillus subtilis 168

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
hprT	BSU00680	COG0634F	hypoxanthine-guanine phosphoribosyltransferase	DEG10010017	BSU00680	BSU00680	Bacillus subtilis 168
tilS	BSU00670	COG0037D	tRNA(ile)-lysidine synthase	DEG10010016	BSU00670	BSU00670	Bacillus subtilis 168
divIC	BSU00620	COG2919D	cell division protein DivIC	DEG10010015	BSU00620	BSU00620	Bacillus subtilis 168
pth	BSU00530	COG0193J	peptidyl-tRNA hydrolase	DEG10010014	BSU00530	BSU00530	Bacillus subtilis 168
prs	BSU00510	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10010013	BSU00510	BSU00510	Bacillus subtilis 168
glmU	BSU00500	COG1207M	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	DEG10010012	BSU00500	BSU00500	Bacillus subtilis 168
ipk	BSU00460	COG1947I	4-diphosphocytidyl-2-c-methyl-d-erythritol kinase	DEG10010011	BSU00460	BSU00460	Bacillus subtilis 168
metS	BSU00380	COG0143J	methionine--tRNA ligase	DEG10010010	BSU00380	BSU00380	Bacillus subtilis 168
holB	BSU00310	COG0470L	DNA polymerase III subunit delta'	DEG10010009	BSU00310	BSU00310	Bacillus subtilis 168
tmk	BSU00280	COG0125F	thymidylate kinase	DEG10010008	BSU00280	BSU00280	Bacillus subtilis 168
dnaX	BSU00190	COG2812L	DNA polymerase III subunit gamma/tau	DEG10010007	BSU00190	BSU00190	Bacillus subtilis 168
serS	BSU00130	COG0172J	serine--tRNA ligase	DEG10010006	BSU00130	BSU00130	Bacillus subtilis 168
guaB	BSU00090	COG0516F	inosine-5'-monophosphate dehydrogenase	DEG10010005	BSU00090	BSU00090	Bacillus subtilis 168
gyrA	BSU00070	COG0188L	DNA gyrase subunit A	DEG10010004	BSU00070	BSU00070	Bacillus subtilis 168
gyrB	BSU00060	COG0187L	DNA gyrase subunit B	DEG10010003	BSU00060	BSU00060	Bacillus subtilis 168
dnaN	BSU00020	COG0592L	DNA polymerase III subunit beta	DEG10010002	BSU00020	BSU00020	
dnaA	BSU00010	COG0593L	chromosomal replication initiator protein DnaA	DEG10010001	BSU00010	BSU00010	
spoIIIJ	BSU41040	COG0706U	membrane protein insertase MisCA			BSU41040	
tyrZ	BSU38460	COG0162J	tyrosine--tRNA ligase 2			BSU38460	
thrZ	BSU37560	COG0441J	threonine--tRNA ligase 2			BSU37560	
murAB	BSU37100	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2			BSU37100	
tdk	BSU37060	COG1435F	thymidine kinase			BSU37060	
ywlF	BSU36920	COG0698G	sugar phosphate isomerase YwlF			BSU36920	
atpB	BSU36870	COG0356C	ATP synthase subunit a			BSU36870	
atpE	BSU36860	COG0636C	ATP synthase subunit c			BSU36860	
atpF	BSU36850	COG0711C	ATP synthase subunit b			BSU36850	
atpH	BSU36840	COG0712C	ATP synthase subunit delta			BSU36840	
atpA	BSU36830	COG0056C	ATP synthase subunit alpha			BSU36830	
atpG	BSU36820	COG0224C	ATP synthase gamma chain			BSU36820	
atpD	BSU36810	COG0055C	ATP synthase subunit beta			BSU36810	
fabZ	BSU36370	COG0764I	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ			BSU36370	
ssbB	BSU36310	COG0629L	single-stranded DNA-binding protein SsbB			BSU36310	
ftsE	BSU35260	COG2884D	cell division ATP-binding protein FtsE			bsu35260	

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
gapA	BSU33940	COG0057G	glyceraldehyde-3-phosphate dehydrogenase 1			BSU33940	
secG	BSU33630	COG1314U	protein-export membrane protein SecG			bsu33630	
pucE	BSU32470	COG2080C	xanthine dehydrogenase subunit E			bsu32470	
dhbC	BSU31990	COG1169HQ	isochorismate synthase DhbC			BSU31990	
pgi	BSU31350	COG0166G	glucose-6-phosphate isomerase			BSU31350	
menF	BSU30830	COG1169HQ	menaquinone-specific isochorismate synthase			BSU30830	
ytxM	BSU30810	COG0596R	esterase			BSU30810	
rpmE2	BSU30700	COG0254J	50S ribosomal protein L31 type B			bsu30700	
asnB	BSU30540	COG0367E	asparagine synthetase 1			BSU30540	
ppnK	BSU29540	COG0061G	inorganic polyphosphate/ATP-NAD kinase 2			BSU29540	
fabG	BSU29420	COG1028IQR	oxidoreductase			bsu29420	
pyk	BSU29180	COG0469G	pyruvate kinase			BSU29180	
polA	BSU29090	COG0749L	DNA polymerase I			BSU29090	
gapB	BSU29020	COG0057G	glyceraldehyde-3-phosphate dehydrogenase 2			BSU29020	
rnhC	BSU28620	COG1039L	ribonuclease HIII			BSU28620	
lcfA	BSU28560	COG0318IQ	long-chain-fatty-acid--CoA ligase			BSU28560	
ruvB	BSU27730	COG2255L	holliday junction ATP-dependent DNA helicase RuvB			BSU27730	
yajC	BSU27700	COG1862U	preprotein translocase subunit YajC			bsu27700	
secDF	BSU27650	COG0342U	protein translocase subunit SecDF			bsu27650	
yrrC	BSU27480	COG0507L	hypothetical protein			bsu27480	
pbpI	BSU27310	COG0768M	penicillin-binding protein 4B			BSU27310	
yrpC	BSU26810	COG0796M	glutamate racemase			BSU26810	
comEB	BSU25580	COG2131F	ComE operon protein 2			bsu25580	
dnaK	BSU25470	COG0443O	chaperone protein DnaK			bsu25470	
lpdV	BSU24060	COG1249C	dihydrolipoyl dehydrogenase			BSU24060	
yqjG	BSU23890	COG0706U	membrane protein insertase MisCB			bsu23890	
pupG	BSU23490	COG0005F	purine nucleoside phosphorylase 1			BSU23490	
rpsA	BSU22880	COG0539J	30S ribosomal protein S1 homolog			bsu22880	
fni	BSU22870	COG1304C	isopentenyl-diphosphate delta-isomerase			BSU22870	

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
ndk	BSU22730	COG0105F	nucleoside diphosphate kinase			BSU22730	
ypdQ	BSU21990	COG0328L	14.7 kDa ribonuclease H-like protein			BSU21990	
ypeP	BSU21970	COG0328L	hypothetical protein			BSU21970	
thyA	BSU21820	COG0207F	thymidylate synthase			bsu21820	
yonN	BSU21050	COG0776L	DNA-binding protein HU 2			BSU21050	
yorL	BSU20340	COG0587L	DNA polymerase YorL			BSU20340	
nrdEB	BSU20060	COG0209F	ribonucleoside-diphosphate reductase NrdEB subunit alpha			bsu20060	
nrdF	BSU20040	COG0208F	ribonucleoside-diphosphate reductase subunit beta			BSU20040	
deoD	BSU19630	COG0813F	purine nucleoside phosphorylase DeoD-type			BSU19630	
thyA	BSU17680	COG0207F	thymidylate synthase			bsu17680	
alrB	BSU17640	COG0787M	alanine racemase 2			BSU17640	
hfq	BSU17340	COG1923R	RNA-binding protein Hfq			BSU17340	
recA	BSU16940	COG0468L	recombinase RecA			BSU16940	
cinA	BSU16930	COG1058R	competence-damage inducible protein			BSU16930	
fabG	BSU16870	COG1028IQR	oxidoreductase			BSU16870	
rnjB	BSU16780	COG0595R	ribonuclease J 2			BSU16780	
pnpA	BSU16690	COG1185J	polyribonucleotide nucleotidyltransferase			bsu16690	
pyrH	BSU16510	COG0528F	uridylate kinase			BSU16510	
flhF	BSU16400	COG1419N	flagellar biosynthesis protein FlhF			BSU16400	
rnhB	BSU16060	COG0164L	ribonuclease HII			BSU16060	
recG	BSU15870	COG1200LK	ATP-dependent DNA helicase RecG			bsu15870	
rpe	BSU15790	COG0036G	ribulose-phosphate 3-epimerase			BSU15790	
def	BSU15720	COG0242J	peptide deformylase			BSU15720	
spoVE	BSU15210	COG0772D	stage V sporulation protein E			BSU15210	
coaD	BSU15020	COG0669H	phosphopantetheine adenylyltransferase			BSU15020	
ylaM	BSU14830	COG2066E	glutaminase			bsu14830	
pdhD	BSU14610	COG1249C	dihydrolipoyl dehydrogenase			BSU14610	
pdhC	BSU14600	COG0508C	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex			BSU14600	
adeC	BSU14520	COG1001F	adenine deaminase			bsu14520	
ispA	BSU13190	COG1404O	major intracellular serine protease			BSU13190	
metE	BSU13180	COG0620E	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase			BSU13180	
fabI	BSU11720	COG0623I	enoyl-ACP reductase			BSU11720	
yitJ	BSU11010	COG0646E	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase			BSU11010	

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
yhfL	BSU10270	COG0318IQ	long-chain-fatty-acid--CoA ligase			BSU10270	
dat	BSU09670	COG0115EH	D-alanine aminotransferase			BSU09670	
pgcA	BSU09310	COG1109G	phosphoglucomutase			BSU09310	
yhcV	BSU09230	COG0517R	CBS domain-containing protein YhcV			BSU09230	
rpsN	BSU08880	COG0199J	alternate 30S ribosomal protein S14			bsu08880	
fabL	BSU08650	COG1028IQR	enoyl-[acyl-carrier-protein] reductase [NADPH] FabL			BSU08650	
acoL	BSU08090	COG1249C	dihydrolipoyl dehydrogenase			BSU08090	
acoC	BSU08080	COG0508C	dihydrolipoyllysine-residue acetyltransferase component of acetoin cleaving system			BSU08080	
yfkN	BSU07840	COG0737F	nucleotide phosphoesterase			BSU07840	
yflG	BSU07690	COG0024J	methionine aminopeptidase 2			BSU07690	
yerA	BSU06560	COG1001F	adenine deaminase YerA			bsu06560	
purH	BSU06520	COG0138F	bifunctional purine biosynthesis protein PurH			BSU06520	
purN	BSU06510	COG0299F	phosphoribosylglycinamide formyltransferase			bsu06510	
guaA	BSU06360	COG0519F	GMP synthase			bsu06360	
ycgT	BSU03270	COG0492O	ferredoxin--NADP reductase 1			BSU03270	
ybgJ	BSU02430	COG2066E	glutaminase 1			BSU02430	
mmuM	BSU02410	COG2040E	homocysteine S-methyltransferase YbgG			BSU02410	
purT	BSU02230	COG0027F	phosphoribosylglycinamide formyltransferase			bsu02230	
ybxF	BSU01090	COG1358J	ribosome-associated protein L7Ae-like			BSU01090	
rplK	BSU01020	COG0080J	50S ribosomal protein L11			bsu01020	
folB	BSU00780	COG1539H	dihydroneopterin aldolase			BSU00780	
sul	BSU00770	COG0294H	dihydropteroate synthase			BSU00770	
ctc	BSU00520	COG1825J	general stress protein CTC			bsu00520	

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rpsT	MG_522	COG0268J	30S ribosomal protein S20	DEG10060298	MG_522	MG_522	Mycoplasma genitalium G37
acpS	MG_482	COG0736I	4'-phosphopantetheinyl transferase	DEG10060180	MG_482	MG_482	Mycoplasma genitalium G37
rpsU	MG_481	-	30S ribosomal protein S21	DEG10060178	MG_481	MG_481	Mycoplasma genitalium G37
secG	MG_476	COG1314U	preprotein translocase subunit SecG	DEG10060084	MG_476	MG_476	Mycoplasma genitalium G37
rpmG	MG_473	COG0267J	50S ribosomal protein L33	DEG10060042	MG_473	MG_473	Mycoplasma genitalium G37
dnaA	MG_469	COG0593L	chromosomal replication initiation protein	DEG10060380	MG_469	MG_469	Mycoplasma genitalium G37
rpmH	MG_466	COG0230J	50S ribosomal protein L34	DEG10060376	MG_466	MG_466	Mycoplasma genitalium G37
-	MG_464	COG0706U	inner membrane protein translocase component YidC	DEG10060374	MG_464	MG_464	Mycoplasma genitalium G37
gltX	MG_462	COG0008J	glutamyl-tRNA synthetase	DEG10060373	MG_462	MG_462	Mycoplasma genitalium G37
hpt	MG_458	COG0634F	hypoxanthine phosphoribosyltransferase	DEG10060370	MG_458	MG_458	Mycoplasma genitalium G37
ftsH	MG_457	COG0465O	ATP-dependent metalloprotease FtsH	DEG10060369	MG_457	MG_457	Mycoplasma genitalium G37
tyrS	MG_455	COG0162J	tyrosyl-tRNA synthetase	DEG10060368	MG_455	MG_455	Mycoplasma genitalium G37
gtaB	MG_453	COG1210M	UTP-glucose-1-phosphate uridylyltransferase	DEG10060367	MG_453	MG_453	Mycoplasma genitalium G37
rpsP	MG_446	COG0228J	30S ribosomal protein S16	DEG10060362	MG_446	MG_446	Mycoplasma genitalium G37
trmD	MG_445	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10060361	MG_445	MG_445	Mycoplasma genitalium G37
rplS	MG_444	COG0335J	50S ribosomal protein L19	DEG10060360	MG_444	MG_444	Mycoplasma genitalium G37
rbgA	MG_442	COG1161R	ribosomal biogenesis GTPase	DEG10060358	MG_442	MG_442	Mycoplasma genitalium G37
pyrH	MG_434	COG0528F	uridylate kinase	DEG10060353	MG_434	MG_434	Mycoplasma genitalium G37
tpiA	MG_431	COG0149G	triosephosphate isomerase	DEG10060350	MG_431	MG_431	Mycoplasma genitalium G37
pgm	MG_430	COG0696G	phosphoglyceromutase	DEG10060349	MG_430	MG_430	Mycoplasma genitalium G37
ptsI	MG_429	COG1080G	phosphoenolpyruvate-protein phosphotransferase	DEG10060348	MG_429	MG_429	Mycoplasma genitalium G37
rpmB	MG_426	COG0227J	50S ribosomal protein L28	DEG10060346	MG_426	MG_426	Mycoplasma genitalium G37
rpsO	MG_424	COG0184J	30S ribosomal protein S15	DEG10060344	MG_424	MG_424	Mycoplasma genitalium G37
-	MG_423	COG0595R	hypothetical protein	DEG10060343	MG_423	MG_423	Mycoplasma genitalium G37
uvrA	MG_421	COG0178L	excinuclease ABC subunit A	DEG10060341	MG_421	MG_421	Mycoplasma genitalium G37
-	MG_419	COG2812L	DNA polymerase III subunits gamma/tau	DEG10060340	MG_419	MG_419	Mycoplasma genitalium G37
rplM	MG_418	COG0102J	50S ribosomal protein L13	DEG10060339	MG_418	MG_418	Mycoplasma genitalium G37
rpsI	MG_417	COG0103J	30S ribosomal protein S9	DEG10060338	MG_417	MG_417	Mycoplasma genitalium G37
eno	MG_407	COG0148G	phosphopyruvate hydratase	DEG10060336	MG_407	MG_407	Mycoplasma genitalium G37
atpB	MG_405	COG0356C	F0F1 ATP synthase subunit A	DEG10060334	MG_405	MG_405	Mycoplasma genitalium G37
atpE	MG_404	COG0636C	F0F1 ATP synthase subunit C	DEG10060333	MG_404	MG_404	Mycoplasma genitalium G37
atpF	MG_403	COG0711C	F0F1 ATP synthase subunit B	DEG10060332	MG_403	MG_403	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
atpH	MG_402	COG0712C	F0F1 ATP synthase subunit delta	DEG10060331	MG_402	MG_402	Mycoplasma genitalium G37
atpA	MG_401	COG0056C	F0F1 ATP synthase subunit alpha	DEG10060330	MG_401	MG_401	Mycoplasma genitalium G37
atpG	MG_400	COG0224C	F0F1 ATP synthase subunit gamma	DEG10060329	MG_400	MG_400	Mycoplasma genitalium G37
atpD	MG_399	COG0055C	F0F1 ATP synthase subunit beta	DEG10060328	MG_399	MG_399	Mycoplasma genitalium G37
atpC	MG_398	COG0355C	F0F1 ATP synthase subunit epsilon			MG_398	Mycoplasma genitalium G37
-	MG_396	COG0698G	ribose-5-phosphate isomerase B	DEG10060327	MG_396	MG_396	Mycoplasma genitalium G37
glyA	MG_394	COG0112E	serine hydroxymethyltransferase	DEG10060325	MG_394	MG_394	Mycoplasma genitalium G37
groES	MG_393	COG0234O	co-chaperonin GroES	DEG10060324	MG_393	MG_393	Mycoplasma genitalium G37
groEL	MG_392	COG0459O	chaperonin GroEL	DEG10060323	MG_392	MG_392	Mycoplasma genitalium G37
-	MG_391	COG0260E	leucyl aminopeptidase	DEG10060322	MG_391	MG_391	Mycoplasma genitalium G37
era	MG_387	COG1159R	GTP-binding protein Era	DEG10060319	MG_387	MG_387	Mycoplasma genitalium G37
obgE	MG_384	COG0536R	GTPase ObgE	DEG10060316	MG_384	MG_384	Mycoplasma genitalium G37
-	MG_383	COG0171H	NH(3)-dependent NAD+ synthetase	DEG10060315	MG_383	MG_383	Mycoplasma genitalium G37
udk	MG_382	COG0572F	uridine kinase	DEG10060314	MG_382	MG_382	Mycoplasma genitalium G37
argS	MG_378	COG0018J	arginyl-tRNA synthetase	DEG10060311	MG_378	MG_378	Mycoplasma genitalium G37
thrS	MG_375	COG0441J	threonyl-tRNA synthetase	DEG10060308	MG_375	MG_375	Mycoplasma genitalium G37
plsX	MG_368	COG0416I	glycerol-3-phosphate acyltransferase PlsX	DEG10060302	MG_368	MG_368	Mycoplasma genitalium G37
fmt	MG_365	COG0223J	methionyl-tRNA formyltransferase	DEG10060300	MG_365	MG_365	Mycoplasma genitalium G37
rpmF	MG_363	COG0333J	50S ribosomal protein L32	DEG10060297	MG_363	MG_363	Mycoplasma genitalium G37
rplL	MG_362	COG0222J	50S ribosomal protein L7/L12	DEG10060296	MG_362	MG_362	Mycoplasma genitalium G37
rplJ	MG_361	COG0244J	50S ribosomal protein L10	DEG10060295	MG_361	MG_361	Mycoplasma genitalium G37
ruvB	MG_359	COG2255L	Holliday junction DNA helicase RuvB			MG_359	Mycoplasma genitalium G37
ruvA	MG_358	COG0632L	Holliday junction DNA helicase RuvA			MG_358	Mycoplasma genitalium G37
ackA	MG_357	COG0282C	acetate kinase	DEG10060294	MG_357	MG_357	Mycoplasma genitalium G37
ppa	MG_351	COG0221C	inorganic pyrophosphatase	DEG10060290	MG_351	MG_351	Mycoplasma genitalium G37
-	MG_347	COG0220R	tRNA (guanine-N(7)-)-methyltransferase	DEG10060285	MG_347	MG_347	Mycoplasma genitalium G37
ileS	MG_345	COG0060J	isoleucyl-tRNA synthetase	DEG10060284	MG_345	MG_345	Mycoplasma genitalium G37
rpoB	MG_341	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10060281	MG_341	MG_341	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
rpoC	MG_340	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10060280	MG_340	MG_340	Mycoplasma genitalium G37
recA	MG_339	COG0468L	recombinase A			MG_339	Mycoplasma genitalium G37
nifS	MG_336	COG0520E	aminotransferase, class V	DEG10060277	MG_336	MG_336	Mycoplasma genitalium G37
valS	MG_334	COG0525J	valyl-tRNA synthetase	DEG10060273	MG_334	MG_334	Mycoplasma genitalium G37
cmk	MG_330	COG0283F	cytidylate kinase	DEG10060269	MG_330	MG_330	Mycoplasma genitalium G37
engA	MG_329	COG1160R	GTP-binding protein EngA	DEG10060268	MG_329	MG_329	Mycoplasma genitalium G37
rpmG	MG_325	COG0267J	50S ribosomal protein L33	DEG10060265	MG_325	MG_325	Mycoplasma genitalium G37
-	MG_315	COG1466L	DNA polymerase III subunit delta			MG_315	Mycoplasma genitalium G37
rpsD	MG_311	COG0522J	30S ribosomal protein S4	DEG10060252	MG_311	MG_311	Mycoplasma genitalium G37
dnaK	MG_305	COG0443O	molecular chaperone DnaK	DEG10060246	MG_305	MG_305	Mycoplasma genitalium G37
-	MG_304	COG1122P	metal ABC transporter ATP-binding protein	DEG10060245	MG_304	MG_304	Mycoplasma genitalium G37
-	MG_303	COG1122P	metal ABC transporter ATP-binding protein	DEG10060244	MG_303	MG_303	Mycoplasma genitalium G37
-	MG_302	COG0619P	metal ABC transporter permease	DEG10060243	MG_302	MG_302	Mycoplasma genitalium G37
gap	MG_301	COG0057G	glyceraldehyde-3-phosphate dehydrogenase	DEG10060242	MG_301	MG_301	Mycoplasma genitalium G37
pgk	MG_300	COG0126G	phosphoglycerate kinase	DEG10060241	MG_300	MG_300	Mycoplasma genitalium G37
eutD	MG_299	COG0280C	phosphotransacetylase	DEG10060240	MG_299	MG_299	Mycoplasma genitalium G37
ftsY	MG_297	COG0552U	signal recognition particle-docking protein FtsY	DEG10060239	MG_297	MG_297	Mycoplasma genitalium G37
mnmA	MG_295	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10060237	MG_295	MG_295	Mycoplasma genitalium G37
alaS	MG_292	COG0013J	alanyl-tRNA synthetase	DEG10060236	MG_292	MG_292	Mycoplasma genitalium G37
proS	MG_283	COG0442J	prolyl-tRNA synthetase	DEG10060233	MG_283	MG_283	Mycoplasma genitalium G37
greA	MG_282	COG0782K	transcription elongation factor GreA	DEG10060232	MG_282	MG_282	Mycoplasma genitalium G37
-	MG_277	-	hypothetical protein	DEG10060230	MG_277	MG_277	Mycoplasma genitalium G37
-	MG_276	COG0503F	adenine phosphoribosyltransferase	DEG10060229	MG_276	MG_276	Mycoplasma genitalium G37
nox	MG_275	COG0446R	NADH oxidase	DEG10060228	MG_275	MG_275	Mycoplasma genitalium G37
pdhA	MG_274	COG1071C	pyruvate dehydrogenase component E1, alpha subunit	DEG10060227	MG_274	MG_274	Mycoplasma genitalium G37
pdhB	MG_273	COG0022C	pyruvate dehydrogenase component E1, beta subunit	DEG10060226	MG_273	MG_273	Mycoplasma genitalium G37
pdhC	MG_272	COG0508C	branched-chain alpha-keto acid dehydrogenase subunit E2	DEG10060225	MG_272	MG_272	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
lplA	MG_270	COG0095H	lipoyltransferase/lipoate-protein ligase	DEG10060224	MG_270	MG_270	Mycoplasma genitalium G37
leuS	MG_266	COG0495J	leucyl-tRNA synthetase	DEG10060222	MG_266	MG_266	Mycoplasma genitalium G37
-	MG_262	COG0258L	5'-3' exonuclease	DEG10060219	MG_262	MG_262	Mycoplasma genitalium G37
polC-2	MG_261	COG0587L	DNA polymerase III subunit alpha	DEG10060218	MG_261	MG_261	Mycoplasma genitalium G37
prfA	MG_258	COG0216J	peptide chain release factor 1	DEG10060216	MG_258	MG_258	Mycoplasma genitalium G37
rpmE	MG_257	COG0254J	50S ribosomal protein L31	DEG10060215	MG_257	MG_257	Mycoplasma genitalium G37
-	MG_254	COG0272L	DNA ligase, NAD-dependent	DEG10060214	MG_254	MG_254	Mycoplasma genitalium G37
cysS	MG_253	COG0215J	cysteinyl-tRNA synthetase	DEG10060213	MG_253	MG_253	Mycoplasma genitalium G37
-	MG_251	COG0423J	glycyl-tRNA synthetase	DEG10060212	MG_251	MG_251	Mycoplasma genitalium G37
dnaE	MG_250	COG0358L	DNA primase	DEG10060211	MG_250	MG_250	Mycoplasma genitalium G37
rpoD	MG_249	COG0568K	RNA polymerase sigma factor	DEG10060210	MG_249	MG_249	Mycoplasma genitalium G37
-	MG_247	COG0344S	glycerol-3-phosphate acyltransferase PlsY	DEG10060209	MG_247	MG_247	Mycoplasma genitalium G37
-	MG_245	COG0212H	5-formyltetrahydrofolate cyclo-ligase	DEG10060207	MG_245	MG_245	Mycoplasma genitalium G37
nadD	MG_240	COG1713H	nicotinate-nucleotide adenylyltransferase	DEG10060203	MG_240	MG_240	Mycoplasma genitalium G37
-	MG_235	COG0648L	apurinic endonuclease (APN1)	DEG10060200	MG_235	MG_235	Mycoplasma genitalium G37
rpmA	MG_234	COG0211J	50S ribosomal protein L27	DEG10060199	MG_234	MG_234	Mycoplasma genitalium G37
rplU	MG_232	COG0261J	50S ribosomal protein L21	DEG10060197	MG_232	MG_232	Mycoplasma genitalium G37
nrdE	MG_231	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10060196	MG_231	MG_231	Mycoplasma genitalium G37
nrdF	MG_229	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10060194	MG_229	MG_229	Mycoplasma genitalium G37
dhfR	MG_228	COG0262H	dihydrofolate reductase	DEG10060193	MG_228	MG_228	Mycoplasma genitalium G37
ftsZ	MG_224	COG0206D	cell division protein FtsZ	DEG10060191	MG_224	MG_224	Mycoplasma genitalium G37
-	MG_221	COG2001S	cell division protein MraZ	DEG10060188	MG_221	MG_221	Mycoplasma genitalium G37
pyk	MG_216	COG0469G	pyruvate kinase	DEG10060183	MG_216	MG_216	Mycoplasma genitalium G37
pfkA	MG_215	COG0205G	6-phosphofructokinase	DEG10060182	MG_215	MG_215	Mycoplasma genitalium G37
plsC	MG_212	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	DEG10060181	MG_212	MG_212	Mycoplasma genitalium G37
uvrC	MG_206	COG0322L	excinuclease ABC, C subunit	DEG10060174	MG_206	MG_206	Mycoplasma genitalium G37
parC	MG_204	COG0188L	DNA topoisomerase IV, A subunit	DEG10060172	MG_204	MG_204	Mycoplasma genitalium G37
parE	MG_203	COG0187L	DNA topoisomerase IV, B subunit	DEG10060171	MG_203	MG_203	Mycoplasma genitalium G37
grpE	MG_201	COG0576O	co-chaperone GrpE	DEG10060169	MG_201	MG_201	Mycoplasma genitalium G37
rplT	MG_198	COG0292J	50S ribosomal protein L20	DEG10060166	MG_198	MG_198	Mycoplasma genitalium G37
rpmI	MG_197	COG0291J	50S ribosomal protein L35	DEG10060165	MG_197	MG_197	Mycoplasma genitalium G37
infC	MG_196	COG0290J	translation initiation factor IF-3	DEG10060164	MG_196	MG_196	Mycoplasma genitalium G37
pheT	MG_195	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10060163	MG_195	MG_195	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
pheS	MG_194	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10060162	MG_194	MG_194	Mycoplasma genitalium G37
-	MG_187	COG3839G	ABC transporter ATP-binding protein	DEG10060156	MG_187	MG_187	Mycoplasma genitalium G37
-	MG_181	COG0619P	metal ABC transporter permease	DEG10060152	MG_181	MG_181	Mycoplasma genitalium G37
cbiO	MG_180	COG1122P	cobalt transporter ATP-binding subunit	DEG10060151	MG_180	MG_180	Mycoplasma genitalium G37
cbiO	MG_179	COG1122P	cobalt transporter ATP-binding subunit	DEG10060150	MG_179	MG_179	Mycoplasma genitalium G37
rplQ	MG_178	COG0203J	50S ribosomal protein L17	DEG10060149	MG_178	MG_178	Mycoplasma genitalium G37
rpoA	MG_177	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10060148	MG_177	MG_177	Mycoplasma genitalium G37
rpS11	MG_176	COG0100J	30S ribosomal protein S11	DEG10060147	MG_176	MG_176	Mycoplasma genitalium G37
rpsM	MG_175	COG0099J	30S ribosomal protein S13	DEG10060146	MG_175	MG_175	Mycoplasma genitalium G37
rpmJ	MG_174	-	50S ribosomal protein L36	DEG10060145	MG_174	MG_174	Mycoplasma genitalium G37
infA	MG_173	COG0361J	translation initiation factor IF-1	DEG10060144	MG_173	MG_173	Mycoplasma genitalium G37
adk	MG_171	COG0563F	adenylate kinase	DEG10060142	MG_171	MG_171	Mycoplasma genitalium G37
secY	MG_170	COG0201U	preprotein translocase subunit SecY	DEG10060141	MG_170	MG_170	Mycoplasma genitalium G37
rplO	MG_169	COG0200J	50S ribosomal protein L15	DEG10060140	MG_169	MG_169	Mycoplasma genitalium G37
rpsE	MG_168	COG0098J	30S ribosomal protein S5	DEG10060139	MG_168	MG_168	Mycoplasma genitalium G37
rplR	MG_167	COG0256J	50S ribosomal protein L18	DEG10060138	MG_167	MG_167	Mycoplasma genitalium G37
rplF	MG_166	COG0097J	50S ribosomal protein L6	DEG10060137	MG_166	MG_166	Mycoplasma genitalium G37
rpsH	MG_165	COG0096J	30S ribosomal protein S8	DEG10060136	MG_165	MG_165	Mycoplasma genitalium G37
rpsN	MG_164	COG0199J	30S ribosomal protein S14	DEG10060135	MG_164	MG_164	Mycoplasma genitalium G37
rplE	MG_163	COG0094J	50S ribosomal protein L5	DEG10060134	MG_163	MG_163	Mycoplasma genitalium G37
rplX	MG_162	COG0198J	50S ribosomal protein L24	DEG10060133	MG_162	MG_162	Mycoplasma genitalium G37
rplN	MG_161	COG0093J	50S ribosomal protein L14	DEG10060132	MG_161	MG_161	Mycoplasma genitalium G37
rpsQ	MG_160	COG0186J	30S ribosomal protein S17	DEG10060131	MG_160	MG_160	Mycoplasma genitalium G37
rpmC	MG_159	COG0255J	50S ribosomal protein L29	DEG10060130	MG_159	MG_159	Mycoplasma genitalium G37
rplP	MG_158	COG0197J	50S ribosomal protein L16	DEG10060129	MG_158	MG_158	Mycoplasma genitalium G37
rpsC	MG_157	COG0092J	30S ribosomal protein S3	DEG10060128	MG_157	MG_157	Mycoplasma genitalium G37
rplV	MG_156	COG0091J	50S ribosomal protein L22	DEG10060127	MG_156	MG_156	Mycoplasma genitalium G37
rpsS	MG_155	COG0185J	30S ribosomal protein S19	DEG10060126	MG_155	MG_155	Mycoplasma genitalium G37
rplB	MG_154	COG0090J	50S ribosomal protein L2	DEG10060125	MG_154	MG_154	Mycoplasma genitalium G37
rplW	MG_153	COG0089J	50S ribosomal protein L23	DEG10060124	MG_153	MG_153	Mycoplasma genitalium G37
rplD	MG_152	COG0088J	50S ribosomal protein L4	DEG10060123	MG_152	MG_152	Mycoplasma genitalium G37
rplC	MG_151	COG0087J	50S ribosomal protein L3	DEG10060122	MG_151	MG_151	Mycoplasma genitalium G37
rpsJ	MG_150	COG0051J	30S ribosomal protein S10	DEG10060121	MG_150	MG_150	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MG_145	COG0196H	riboflavin biosynthesis protein RibF	DEG10060117	MG_145	MG_145	Mycoplasma genitalium G37
infB	MG_142	COG0532J	translation initiation factor IF-2	DEG10060114	MG_142	MG_142	Mycoplasma genitalium G37
nusA	MG_141	COG0195K	transcription elongation factor NusA	DEG10060112	MG_141	MG_141	Mycoplasma genitalium G37
-	MG_139	COG0595R	metallo-beta-lactamase superfamily protein	DEG10060111	MG_139	MG_139	Mycoplasma genitalium G37
glf	MG_137	COG0562M	UDP-galactopyranose mutase	DEG10060110	MG_137	MG_137	Mycoplasma genitalium G37
lysS	MG_136	COG1190J	lysyl-tRNA synthetase	DEG10060109	MG_136	MG_136	Mycoplasma genitalium G37
-	MG_130	COG1418R	hypothetical protein	DEG10060105	MG_130	MG_130	Mycoplasma genitalium G37
ppnK	MG_128	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10060103	MG_128	MG_128	Mycoplasma genitalium G37
trpS	MG_126	COG0180J	tryptophanyl-tRNA synthetase	DEG10060101	MG_126	MG_126	Mycoplasma genitalium G37
trxA	MG_124	COG3118O	thioredoxin	DEG10060099	MG_124	MG_124	Mycoplasma genitalium G37
topA	MG_122	COG0550L	DNA topoisomerase I	DEG10060097	MG_122	MG_122	Mycoplasma genitalium G37
galE	MG_118	COG1087M	UDP-glucose 4-epimerase	DEG10060094	MG_118	MG_118	Mycoplasma genitalium G37
asnC	MG_113	COG0017J	asparaginyl-tRNA synthetase	DEG10060092	MG_113	MG_113	Mycoplasma genitalium G37
pgi	MG_111	COG0166G	glucose-6-phosphate isomerase	DEG10060091	MG_111	MG_111	Mycoplasma genitalium G37
gmk	MG_107	COG0194F	guanylate kinase	DEG10060088	MG_107	MG_107	Mycoplasma genitalium G37
def	MG_106	COG0242J	peptide deformylase	DEG10060087	MG_106	MG_106	Mycoplasma genitalium G37
vacB	MG_104	COG0557K	ribonuclease R	DEG10060085	MG_104	MG_104	Mycoplasma genitalium G37
trxB	MG_102	COG0492O	thioredoxin-disulfide reductase	DEG10060083	MG_102	MG_102	Mycoplasma genitalium G37
gatB	MG_100	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10060081	MG_100	MG_100	Mycoplasma genitalium G37
gatA	MG_099	COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A	DEG10060080	MG_099	MG_099	Mycoplasma genitalium G37
ung	MG_097	COG0692L	uracil-DNA glycosylase	DEG10060078	MG_097	MG_097	Mycoplasma genitalium G37
dnaB	MG_094	COG0305L	replicative DNA helicase	DEG10060076	MG_094	MG_094	Mycoplasma genitalium G37
rplI	MG_093	COG0359J	50S ribosomal protein L9	DEG10060075	MG_093	MG_093	Mycoplasma genitalium G37
rpsR	MG_092	COG0238J	30S ribosomal protein S18	DEG10060074	MG_092	MG_092	Mycoplasma genitalium G37
ssb	MG_091	COG0629L	single-strand binding protein family	DEG10060073	MG_091	MG_091	Mycoplasma genitalium G37
rpsF	MG_090	COG0360J	30S ribosomal protein S6	DEG10060072	MG_090	MG_090	Mycoplasma genitalium G37
fus	MG_089	COG0480J	elongation factor G	DEG10060071	MG_089	MG_089	Mycoplasma genitalium G37
rpS7	MG_088	COG0049J	30S ribosomal protein S7	DEG10060070	MG_088	MG_088	Mycoplasma genitalium G37
rpsL	MG_087	COG0048J	30S ribosomal protein S12	DEG10060069	MG_087	MG_087	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
pth	MG_083	COG0193J	peptidyl-tRNA hydrolase	DEG10060065	MG_083	MG_083	Mycoplasma genitalium G37
rplA	MG_082	COG0081J	50S ribosomal protein L1	DEG10060064	MG_082	MG_082	Mycoplasma genitalium G37
rplK	MG_081	COG0080J	50S ribosomal protein L11	DEG10060063	MG_081	MG_081	Mycoplasma genitalium G37
oppF	MG_080	COG4608E	peptide ABC transporter ATP-binding protein	DEG10060062	MG_080	MG_080	Mycoplasma genitalium G37
oppD	MG_079	COG0444EP	peptide ABC transporter ATP-binding protein	DEG10060061	MG_079	MG_079	Mycoplasma genitalium G37
oppC	MG_078	COG1173EP	peptide ABC transporter permease	DEG10060060	MG_078	MG_078	Mycoplasma genitalium G37
oppB	MG_077	COG0601EP	peptide ABC transporter permease	DEG10060059	MG_077	MG_077	Mycoplasma genitalium G37
uvrB	MG_073	COG0556L	excinuclease ABC subunit B	DEG10060055	MG_073	MG_073	Mycoplasma genitalium G37
secA	MG_072	COG0653U	preprotein translocase subunit SecA	DEG10060054	MG_072	MG_072	Mycoplasma genitalium G37
rpsB	MG_070	COG0052J	30S ribosomal protein S2	DEG10060052	MG_070	MG_070	Mycoplasma genitalium G37
ptsG	MG_069	COG2190G	PTS system, glucose-specific IIABC component	DEG10060051	MG_069	MG_069	Mycoplasma genitalium G37
-	MG_060	COG0463M	glycosyl transferase, group 2 family protein	DEG10060047	MG_060	MG_060	Mycoplasma genitalium G37
prs	MG_058	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10060045	MG_058	MG_058	Mycoplasma genitalium G37
secE	MG_055	COG0690U	preprotein translocase subunit SecE	DEG10060041	MG_055	MG_055	Mycoplasma genitalium G37
manB	MG_053	COG1109G	phosphoglucomutase/phosphomannomutase	DEG10060039	MG_053	MG_053	Mycoplasma genitalium G37
cdd	MG_052	COG0295F	cytidine deaminase	DEG10060038	MG_052	MG_052	Mycoplasma genitalium G37
-	MG_050	COG0274F	deoxyribose-phosphate aldolase	DEG10060037	MG_050	MG_050	Mycoplasma genitalium G37
deoD	MG_049	COG0813F	purine nucleoside phosphorylase	DEG10060036	MG_049	MG_049	Mycoplasma genitalium G37
ffh	MG_048	COG0541U	signal recognition particle protein	DEG10060035	MG_048	MG_048	Mycoplasma genitalium G37
metX	MG_047	COG0192H	S-adenosylmethionine synthetase	DEG10060034	MG_047	MG_047	Mycoplasma genitalium G37
-	MG_045	COG0687E	spermidine/putrescine ABC transporter spermidine/putrescine binding protein	DEG10060032	MG_045	MG_045	Mycoplasma genitalium G37
potC	MG_044	COG1177E	spermidine/putrescine ABC transporter permease	DEG10060031	MG_044	MG_044	Mycoplasma genitalium G37
potB	MG_043	COG1176E	spermidine/putrescine ABC transporter permease	DEG10060030	MG_043	MG_043	Mycoplasma genitalium G37
potA	MG_042	COG3842E	spermidine/putrescine ABC transporter ATP-binding protein	DEG10060029	MG_042	MG_042	Mycoplasma genitalium G37
glpK	MG_038	COG0554C	glycerol kinase	DEG10060027	MG_038	MG_038	Mycoplasma genitalium G37
-	MG_037	COG1488H	nicotinate phosphoribosyltransferase	DEG10060026	MG_037	MG_037	Mycoplasma genitalium G37
aspS	MG_036	COG0173J	aspartyl-tRNA synthetase	DEG10060025	MG_036	MG_036	Mycoplasma genitalium G37
hisS	MG_035	COG0124J	histidyl-tRNA synthetase	DEG10060024	MG_035	MG_035	Mycoplasma genitalium G37
tdk	MG_034	COG1435F	thymidine kinase	DEG10060023	MG_034	MG_034	Mycoplasma genitalium G37
polC	MG_031	COG2176L	DNA polymerase III PolC	DEG10060022	MG_031	MG_031	Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
upp	MG_030	COG0035F	uracil phosphoribosyltransferase	DEG10060021	MG_030	MG_030	Mycoplasma genitalium G37
efp	MG_026	COG0231J	elongation factor P	DEG10060017	MG_026	MG_026	Mycoplasma genitalium G37
-	MG_025	COG0463M	glycosyl transferase, group 2 family protein	DEG10060016	MG_025	MG_025	Mycoplasma genitalium G37
-	MG_024	COG0012J	GTP-dependent nucleic acid-binding protein EngD			MG_024	Mycoplasma genitalium G37
fba	MG_023	COG0191G	fructose-1,6-bisphosphate aldolase, class II	DEG10060015	MG_023	MG_023	Mycoplasma genitalium G37
rpoE	MG_022	COG3343K	DNA-directed RNA polymerase subunit delta	DEG10060014	MG_022	MG_022	Mycoplasma genitalium G37
metS	MG_021	COG0143J	methionyl-tRNA synthetase	DEG10060013	MG_021	MG_021	Mycoplasma genitalium G37
dnaJ	MG_019	COG0484O	chaperone protein DnaJ	DEG10060011	MG_019	MG_019	Mycoplasma genitalium G37
folD	MG_013	COG0190H	methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase	DEG10060008	MG_013	MG_013	Mycoplasma genitalium G37
-	MG_007	COG0470L	DNA polymerase III subunit delta'	DEG10060006	MG_007	MG_007	Mycoplasma genitalium G37
tmk	MG_006	COG0125F	thymidylate kinase	DEG10060005	MG_006	MG_006	Mycoplasma genitalium G37
serS	MG_005	COG0172J	seryl-tRNA synthetase	DEG10060004	MG_005	MG_005	Mycoplasma genitalium G37
gyrA	MG_004	COG0188L	DNA gyrase subunit A	DEG10060003	MG_004	MG_004	Mycoplasma genitalium G37
gyrB	MG_003	COG0187L	DNA gyrase subunit B	DEG10060002	MG_003	MG_003	Mycoplasma genitalium G37
dnaN	MG_001	COG0592L	DNA polymerase III subunit beta	DEG10060001	MG_001	MG_001	Mycoplasma genitalium G37
-	MG_526	COG1136V	ABC transporter ATP-binding protein	DEG10060379	MG_526		Mycoplasma genitalium G37
-	MG_524	-	hypothetical protein	DEG10060317	MG_524		Mycoplasma genitalium G37
-	MG_521	-	hypothetical protein	DEG10060289	MG_521		Mycoplasma genitalium G37
-	MG_517	COG0463M	glycosyl transferase, group 2 family protein	DEG10060276	MG_517		Mycoplasma genitalium G37
-	MG_516	COG3763S	hypothetical protein	DEG10060275	MG_516		Mycoplasma genitalium G37
-	MG_515	-	hypothetical protein	DEG10060263	MG_515		Mycoplasma genitalium G37
-	MG_505	COG0816L	hypothetical protein	DEG10060235	MG_505		Mycoplasma genitalium G37
-	MG_491	-	hypothetical protein	DEG10060186	MG_491		Mycoplasma genitalium G37
-	MG_480	-	hypothetical protein	DEG10060177	MG_480		Mycoplasma genitalium G37
-	MG_477	COG2740K	hypothetical protein	DEG10060113	MG_477		Mycoplasma genitalium G37
-	MG_474	-	hypothetical protein	DEG10060043	MG_474		Mycoplasma genitalium G37
soj	MG_470	COG1192D	CobQ/CobB/MinD/ParA nucleotide binding domain-containing protein	DEG10060381	MG_470		Mycoplasma genitalium G37
-	MG_468	-	ABC transporter permease	DEG10060378	MG_468		Mycoplasma genitalium G37
-	MG_467	COG1136V	ABC transporter ATP-binding protein	DEG10060377	MG_467		Mycoplasma genitalium G37
rnpA	MG_465	COG0594J	ribonuclease P protein component	DEG10060375	MG_465		Mycoplasma genitalium G37
-	MG_461	COG1078R	HD domain-containing protein	DEG10060372	MG_461		Mycoplasma genitalium G37
-	MG_459	COG0245I	hypothetical protein	DEG10060371	MG_459		Mycoplasma genitalium G37
tuf	MG_451	COG0050J	elongation factor Tu	DEG10060366	MG_451		Mycoplasma genitalium G37
-	MG_450	COG1307S	degV family protein	DEG10060365	MG_450		Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MG_448	COG0229O	methionine sulfoxide reductase B	DEG10060364	MG_448		Mycoplasma genitalium G37
-	MG_447	COG0534V	hypothetical protein	DEG10060363	MG_447		Mycoplasma genitalium G37
-	MG_443	COG1284S	hypothetical protein	DEG10060359	MG_443		Mycoplasma genitalium G37
-	MG_441	-	hypothetical protein	DEG10060357	MG_441		Mycoplasma genitalium G37
-	MG_440	-	lipoprotein	DEG10060356	MG_440		Mycoplasma genitalium G37
-	MG_439	-	lipoprotein	DEG10060355	MG_439		Mycoplasma genitalium G37
frr	MG_435	COG0233J	ribosome recycling factor	DEG10060354	MG_435		Mycoplasma genitalium G37
tsf	MG_433	COG0264J	elongation factor Ts	DEG10060352	MG_433		Mycoplasma genitalium G37
-	MG_432	COG1284S	hypothetical protein	DEG10060351	MG_432		Mycoplasma genitalium G37
-	MG_427	COG1765O	OsmC-like protein	DEG10060347	MG_427		Mycoplasma genitalium G37
deaD	MG_425	COG0513LKJ	DEAD-box ATP dependent DNA helicase	DEG10060345	MG_425		Mycoplasma genitalium G37
-	MG_422	-	hypothetical protein	DEG10060342	MG_422		Mycoplasma genitalium G37
-	MG_409	COG0704P	phosphate transport system regulatory protein PhoU	DEG10060337	MG_409		Mycoplasma genitalium G37
-	MG_406	-	hypothetical protein	DEG10060335	MG_406		Mycoplasma genitalium G37
-	MG_395	-	lipoprotein	DEG10060326	MG_395		Mycoplasma genitalium G37
-	MG_389	-	hypothetical protein	DEG10060321	MG_389		Mycoplasma genitalium G37
-	MG_388	COG0319R	hypothetical protein	DEG10060320	MG_388		Mycoplasma genitalium G37
-	MG_386	-	hypothetical protein	DEG10060318	MG_386		Mycoplasma genitalium G37
-	MG_381	-	hypothetical protein	DEG10060313	MG_381		Mycoplasma genitalium G37
gidA	MG_379	COG0445D	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	DEG10060312	MG_379		Mycoplasma genitalium G37
-	MG_377	-	hypothetical protein	DEG10060310	MG_377		Mycoplasma genitalium G37
-	MG_376	-	hypothetical protein	DEG10060309	MG_376		Mycoplasma genitalium G37
-	MG_374	-	hypothetical protein	DEG10060307	MG_374		Mycoplasma genitalium G37
-	MG_373	-	hypothetical protein	DEG10060306	MG_373		Mycoplasma genitalium G37
guaA	MG_372	COG0301H	thiamine biosynthesis protein	DEG10060305	MG_372		Mycoplasma genitalium G37
-	MG_371	COG0618R	DHH family protein	DEG10060304	MG_371		Mycoplasma genitalium G37
-	MG_369	COG1461R	DAK2 domain-containing protein	DEG10060303	MG_369		Mycoplasma genitalium G37
-	MG_366	-	hypothetical protein	DEG10060301	MG_366		Mycoplasma genitalium G37
-	MG_364	-	hypothetical protein	DEG10060299	MG_364		Mycoplasma genitalium G37
-	MG_356	COG0510M	choline/ethanolamine kinase	DEG10060293	MG_356		Mycoplasma genitalium G37
-	MG_354	-	hypothetical protein	DEG10060292	MG_354		Mycoplasma genitalium G37
-	MG_353	COG0776L	DNA-binding protein HU	DEG10060291	MG_353		Mycoplasma genitalium G37
-	MG_350	-	hypothetical protein	DEG10060288	MG_350		Mycoplasma genitalium G37
-	MG_349	COG3611L	hypothetical protein	DEG10060287	MG_349		Mycoplasma genitalium G37
-	MG_348	-	lipoprotein	DEG10060286	MG_348		Mycoplasma genitalium G37
-	MG_344	COG0596R	alpha/beta fold family hydrolase	DEG10060283	MG_344		Mycoplasma genitalium G37
-	MG_342	COG0431R	NADPH-dependent FMN reductase domain-containing protein	DEG10060282	MG_342		Mycoplasma genitalium G37
-	MG_338	-	lipoprotein	DEG10060279	MG_338		Mycoplasma genitalium G37
-	MG_337	COG0822C	hypothetical protein	DEG10060278	MG_337		Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
engB	MG_335	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10060274	MG_335		Mycoplasma genitalium G37
-	MG_332	COG0217S	hypothetical protein	DEG10060271	MG_332		Mycoplasma genitalium G37
-	MG_331	-	hypothetical protein	DEG10060270	MG_331		Mycoplasma genitalium G37
-	MG_327	COG0596R	alpha/beta fold family hydrolase	DEG10060267	MG_327		Mycoplasma genitalium G37
-	MG_326	COG1307S	degV family protein	DEG10060266	MG_326		Mycoplasma genitalium G37
pepP	MG_324	COG0006E	M24 family metallopeptidase	DEG10060264	MG_324		Mycoplasma genitalium G37
-	MG_323	COG0569P	TrkA family potassium uptake protein	DEG10060262	MG_323		Mycoplasma genitalium G37
-	MG_322	COG0168P	TrkH family potassium uptake protein	DEG10060261	MG_322		Mycoplasma genitalium G37
-	MG_321	-	lipoprotein	DEG10060260	MG_321		Mycoplasma genitalium G37
-	MG_320	-	hypothetical protein	DEG10060259	MG_320		Mycoplasma genitalium G37
-	MG_319	-	hypothetical protein	DEG10060258	MG_319		Mycoplasma genitalium G37
-	MG_318	-	P32 adhesin	DEG10060257	MG_318		Mycoplasma genitalium G37
hmw3	MG_317	-	HMW3 cytadherence accessory protein	DEG10060256	MG_317		Mycoplasma genitalium G37
-	MG_314	-	hypothetical protein	DEG10060255	MG_314		Mycoplasma genitalium G37
-	MG_313	-	hypothetical protein	DEG10060254	MG_313		Mycoplasma genitalium G37
hmw1	MG_312	-	HMW1 cytadherence accessory protein	DEG10060253	MG_312		Mycoplasma genitalium G37
-	MG_310	COG0596R	alpha/beta fold family hydrolase	DEG10060251	MG_310		Mycoplasma genitalium G37
-	MG_309	-	lipoprotein	DEG10060250	MG_309		Mycoplasma genitalium G37
-	MG_308	COG0513LKJ	DEAD-box ATP dependent DNA helicase	DEG10060249	MG_308		Mycoplasma genitalium G37
-	MG_307	-	lipoprotein	DEG10060248	MG_307		Mycoplasma genitalium G37
-	MG_306	COG0392S	hypothetical protein	DEG10060247	MG_306		Mycoplasma genitalium G37
-	MG_296	-	hypothetical protein	DEG10060238	MG_296		Mycoplasma genitalium G37
-	MG_287	COG0236IQ	acyl carrier protein	DEG10060234	MG_287		Mycoplasma genitalium G37
relA	MG_278	COG0317TK	GTP pyrophosphokinase	DEG10060231	MG_278		Mycoplasma genitalium G37
-	MG_267	-	hypothetical protein	DEG10060223	MG_267		Mycoplasma genitalium G37
-	MG_265	COG0561R	Cof-like hydrolase	DEG10060221	MG_265		Mycoplasma genitalium G37
-	MG_263	COG0561R	Cof-like hydrolase	DEG10060220	MG_263		Mycoplasma genitalium G37
-	MG_259	COG2890J	HemK family modification methylase	DEG10060217	MG_259		Mycoplasma genitalium G37
-	MG_246	COG1692S	serine/threonine protein phosphatase	DEG10060208	MG_246		Mycoplasma genitalium G37
-	MG_242	-	hypothetical protein	DEG10060205	MG_242		Mycoplasma genitalium G37
-	MG_241	-	hypothetical protein	DEG10060204	MG_241		Mycoplasma genitalium G37
lon	MG_239	COG0466O	ATP-dependent protease La	DEG10060202	MG_239		Mycoplasma genitalium G37
-	MG_236	COG0735P	hypothetical protein	DEG10060201	MG_236		Mycoplasma genitalium G37
-	MG_233	COG2868J	hypothetical protein	DEG10060198	MG_233		Mycoplasma genitalium G37
nrdI	MG_230	COG1780F	ribonucleotide reductase stimulatory protein	DEG10060195	MG_230		Mycoplasma genitalium G37
-	MG_225	COG0531E	amino acid-polyamine-organocation (APC) permease family protein	DEG10060192	MG_225		Mycoplasma genitalium G37
-	MG_223	-	hypothetical protein	DEG10060190	MG_223		Mycoplasma genitalium G37
mraW	MG_222	COG0275M	S-adenosyl-methyltransferase MraW	DEG10060189	MG_222		Mycoplasma genitalium G37
-	MG_219	-	hypothetical protein	DEG10060187	MG_219		Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
hmw2	MG_218	COG1196D	HMW2 cytadherence accessory protein	DEG10060185	MG_218		Mycoplasma genitalium G37
-	MG_217	-	proline-rich P65 protein	DEG10060184	MG_217		Mycoplasma genitalium G37
-	MG_211	-	hypothetical protein	DEG10060179	MG_211		Mycoplasma genitalium G37
-	MG_209	COG0564J	RluA family pseudouridine synthase	DEG10060176	MG_209		Mycoplasma genitalium G37
-	MG_208	COG1214O	glycoprotease	DEG10060175	MG_208		Mycoplasma genitalium G37
hrcA	MG_205	COG1420K	heat-inducible transcription repressor	DEG10060173	MG_205		Mycoplasma genitalium G37
-	MG_202	-	hypothetical protein	DEG10060170	MG_202		Mycoplasma genitalium G37
-	MG_200	COG0484O	DnaJ domain-containing protein	DEG10060168	MG_200		Mycoplasma genitalium G37
mgpC	MG_192	-	hypothetical protein	DEG10060161	MG_192		Mycoplasma genitalium G37
mgpB	MG_191	-	MgPa adhesin	DEG10060160	MG_191		Mycoplasma genitalium G37
mgpA	MG_190	COG0618R	DHH family phosphoesterase	DEG10060159	MG_190		Mycoplasma genitalium G37
-	MG_189	COG0395G	ABC transporter permease	DEG10060158	MG_189		Mycoplasma genitalium G37
-	MG_188	COG1175G	ABC transporter permease	DEG10060157	MG_188		Mycoplasma genitalium G37
-	MG_186	COG1525L	nuclease-like protein	DEG10060155	MG_186		Mycoplasma genitalium G37
-	MG_184	-	adenine-specific DNA modification methylase	DEG10060154	MG_184		Mycoplasma genitalium G37
truA	MG_182	COG0101J	tRNA pseudouridine synthase A	DEG10060153	MG_182		Mycoplasma genitalium G37
map	MG_172	COG0024J	methionine aminopeptidase, type I	DEG10060143	MG_172		Mycoplasma genitalium G37
-	MG_148	COG4487S	hypothetical protein	DEG10060120	MG_148		Mycoplasma genitalium G37
-	MG_147	-	hypothetical protein	DEG10060119	MG_147		Mycoplasma genitalium G37
-	MG_146	COG1253R	hypothetical protein	DEG10060118	MG_146		Mycoplasma genitalium G37
-	MG_144	-	hypothetical protein	DEG10060116	MG_144		Mycoplasma genitalium G37
-	MG_143	COG0858J	ribosome-binding factor A	DEG10060115	MG_143		Mycoplasma genitalium G37
-	MG_135	-	hypothetical protein	DEG10060108	MG_135		Mycoplasma genitalium G37
-	MG_133	-	hypothetical protein	DEG10060107	MG_133		Mycoplasma genitalium G37
-	MG_132	COG0537FGR	HIT domain-containing protein	DEG10060106	MG_132		Mycoplasma genitalium G37
-	MG_129	COG1264G	hypothetical protein	DEG10060104	MG_129		Mycoplasma genitalium G37
-	MG_127	COG1393P	Spx subfamily protein	DEG10060102	MG_127		Mycoplasma genitalium G37
-	MG_125	COG0561R	Cof-like hydrolase	DEG10060100	MG_125		Mycoplasma genitalium G37
-	MG_123	-	hypothetical protein	DEG10060098	MG_123		Mycoplasma genitalium G37
-	MG_120	COG4603R	ABC transporter permease	DEG10060096	MG_120		Mycoplasma genitalium G37
mglA	MG_119	COG3845R	ABC transporter ATP-binding protein	DEG10060095	MG_119		Mycoplasma genitalium G37
-	MG_117	-	hypothetical protein	DEG10060093	MG_117		Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MG_109	COG0515RTKL	serine/threonine protein kinase	DEG10060090	MG_109		Mycoplasma genitalium G37
-	MG_108	COG0631T	protein phosphatase 2C	DEG10060089	MG_108		Mycoplasma genitalium G37
-	MG_105	COG1624S	hypothetical protein	DEG10060086	MG_105		Mycoplasma genitalium G37
-	MG_101	COG2188K	hypothetical protein	DEG10060082	MG_101		Mycoplasma genitalium G37
-	MG_098	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10060079	MG_098		Mycoplasma genitalium G37
-	MG_095	-	lipoprotein	DEG10060077	MG_095		Mycoplasma genitalium G37
lgt	MG_086	COG0682M	prolipoprotein diacylglyceryl transferase	DEG10060068	MG_086		Mycoplasma genitalium G37
ser	MG_085	COG1493T	HPr kinase/phosphorylase	DEG10060067	MG_085		Mycoplasma genitalium G37
-	MG_084	COG0037D	tRNA(Ile)-lysidine synthetase	DEG10060066	MG_084		Mycoplasma genitalium G37
-	MG_076	-	hypothetical protein	DEG10060058	MG_076		Mycoplasma genitalium G37
-	MG_075	-	hypothetical protein	DEG10060057	MG_075		Mycoplasma genitalium G37
-	MG_074	-	hypothetical protein	DEG10060056	MG_074		Mycoplasma genitalium G37
-	MG_071	COG0474P	ATPase P	DEG10060053	MG_071		Mycoplasma genitalium G37
-	MG_068	-	lipoprotein	DEG10060050	MG_068		Mycoplasma genitalium G37
-	MG_065	COG1136V	ABC transporter ATP-binding protein	DEG10060049	MG_065		Mycoplasma genitalium G37
-	MG_064	-	ABC transporter permease	DEG10060048	MG_064		Mycoplasma genitalium G37
smpB	MG_059	COG0691O	SsrA-binding protein	DEG10060046	MG_059		Mycoplasma genitalium G37
-	MG_057	COG1658L	small primase-like protein	DEG10060044	MG_057		Mycoplasma genitalium G37
-	MG_054	COG0250K	transcription antitermination protein NusG	DEG10060040	MG_054		Mycoplasma genitalium G37
-	MG_046	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10060033	MG_046		Mycoplasma genitalium G37
ptsH	MG_041	COG1925G	phosphocarrier protein HPr	DEG10060028	MG_041		Mycoplasma genitalium G37
-	MG_029	COG0693R	DJ-1/PfpI family protein	DEG10060020	MG_029		Mycoplasma genitalium G37
-	MG_028	-	hypothetical protein	DEG10060019	MG_028		Mycoplasma genitalium G37
-	MG_027	COG0781K	transcription termination/antitermination protein NusB	DEG10060018	MG_027		Mycoplasma genitalium G37
pip	MG_020	COG0596R	proline iminopeptidase	DEG10060012	MG_020		Mycoplasma genitalium G37
-	MG_015	COG1132V	ABC transporter ATP-binding protein/permease	DEG10060010	MG_015		Mycoplasma genitalium G37
-	MG_014	COG1132V	ABC transporter ATP-binding protein/permease	DEG10060009	MG_014		Mycoplasma genitalium G37
trmE	MG_008	COG0486R	tRNA modification GTPase TrmE	DEG10060007	MG_008		Mycoplasma genitalium G37

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_7820	COG0507L	exodeoxyribonuclease V subunit alpha	DEG10140310	MYPU_7820	MYPU_7820	Mycoplasma pulmonis UAB CTIP
-	MYPU_7810	COG0193J	peptidyl-tRNA hydrolase	DEG10140309	MYPU_7810	MYPU_7810	Mycoplasma pulmonis UAB CTIP
-	MYPU_7790	COG0465O	cell division protein FTSH	DEG10140307	MYPU_7790	MYPU_7790	Mycoplasma pulmonis UAB CTIP
-	MYPU_7740	COG4591M	ABC transporter permease	DEG10140306	MYPU_7740	MYPU_7740	Mycoplasma pulmonis UAB CTIP
-	MYPU_7730	COG1136V	ABC transporter ATP-binding protein	DEG10140305	MYPU_7730	MYPU_7730	Mycoplasma pulmonis UAB CTIP
asnC	MYPU_7710	COG0017J	asparaginyl-tRNA synthetase	DEG10140304	MYPU_7710	MYPU_7710	Mycoplasma pulmonis UAB CTIP
-	MYPU_7680	COG0210L	ATP-dependent helicase PcrA	DEG10140302	MYPU_7680	MYPU_7680	Mycoplasma pulmonis UAB CTIP
-	MYPU_7640	COG1071C	pyruvate dehydrogenase E1 component, alpha subunit	DEG10140299	MYPU_7640	MYPU_7640	Mycoplasma pulmonis UAB CTIP
-	MYPU_7620	COG0508C	dihydrolipoamide acetyltransferase	DEG10140298	MYPU_7620	MYPU_7620	Mycoplasma pulmonis UAB CTIP
-	MYPU_7610	COG1249C	dihydrolipoamide dehydrogenase (E3 component of pyruvate complex)	DEG10140297	MYPU_7610	MYPU_7610	Mycoplasma pulmonis UAB CTIP
thrS	MYPU_7460	COG0441J	threonyl-tRNA synthetase	DEG10140296	MYPU_7460	MYPU_7460	Mycoplasma pulmonis UAB CTIP
-	MYPU_7450	COG0180J	tryptophanyl-tRNA synthetase	DEG10140295	MYPU_7450	MYPU_7450	Mycoplasma pulmonis UAB CTIP
-	MYPU_7420	COG1132V	ABC transporter permease/ATP-binding protein			MYPU_7420	Mycoplasma pulmonis UAB CTIP
-	MYPU_7410	COG1132V	ABC transporter permease/ATP-binding			MYPU_7410	Mycoplasma pulmonis UAB CTIP
-	MYPU_7390	COG0187L	DNA gyrase subunit B	DEG10140293	MYPU_7390	MYPU_7390	Mycoplasma pulmonis UAB CTIP
-	MYPU_7350	COG5160O	lipoprotein			MYPU_7350	Mycoplasma pulmonis UAB CTIP
-	MYPU_7340	COG5271R	lipoprotein			MYPU_7340	Mycoplasma pulmonis UAB CTIP
-	MYPU_7330	COG0484O	molecular chaperone DnaJ	DEG10140291	MYPU_7330	MYPU_7330	Mycoplasma pulmonis UAB CTIP
-	MYPU_7200	COG0258L	DNA polymerase I (POL I)	DEG10140287	MYPU_7200	MYPU_7200	Mycoplasma pulmonis UAB CTIP
dnaE	MYPU_7190	COG0587L	DNA polymerase III DnaE	DEG10140286	MYPU_7190	MYPU_7190	Mycoplasma pulmonis UAB CTIP
rpsD	MYPU_7160	COG0522J	30S ribosomal protein S4	DEG10140283	MYPU_7160	MYPU_7160	Mycoplasma pulmonis UAB CTIP
-	MYPU_7140	COG1196D	ABC transporter ATP-binding protein	DEG10140282	MYPU_7140	MYPU_7140	Mycoplasma pulmonis UAB CTIP
-	MYPU_7130	COG0492O	thioredoxin reductase	DEG10140281	MYPU_7130	MYPU_7130	Mycoplasma pulmonis UAB CTIP
-	MYPU_7070	COG0526OC	thioredoxin	DEG10140277	MYPU_7070	MYPU_7070	Mycoplasma pulmonis UAB CTIP
-	MYPU_7050	COG0595R	ribonuclease J	DEG10140276	MYPU_7050	MYPU_7050	Mycoplasma pulmonis UAB CTIP
-	MYPU_7040	COG0595R	ribonuclease J	DEG10140275	MYPU_7040	MYPU_7040	Mycoplasma pulmonis UAB CTIP
-	MYPU_7020	COG0192H	S-adenosylmethionine synthetase	DEG10140274	MYPU_7020	MYPU_7020	Mycoplasma pulmonis UAB CTIP
-	MYPU_7000	COG0056C	ATP synthase F0F1 subunit alpha			MYPU_7000	Mycoplasma pulmonis UAB CTIP
-	MYPU_6990	COG0055C	ATP synthase F0F1 subunit beta	DEG10140273	MYPU_6990	MYPU_6990	Mycoplasma pulmonis UAB CTIP
-	MYPU_6980	COG0210L	ATP-dependent helicase PcrA			MYPU_6980	Mycoplasma pulmonis UAB CTIP
rpmB	MYPU_6960	COG0227J	50S ribosomal protein L28			MYPU_6960	Mycoplasma pulmonis UAB CTIP
-	MYPU_6890	COG0242J	polypeptide deformylase	DEG10140270	MYPU_6890	MYPU_6890	Mycoplasma pulmonis UAB CTIP
gmk	MYPU_6870	COG0194F	guanylate kinase	DEG10140269	MYPU_6870	MYPU_6870	Mycoplasma pulmonis UAB CTIP
-	MYPU_6860	COG0631T	protein phosphatase	DEG10140268	MYPU_6860	MYPU_6860	Mycoplasma pulmonis UAB CTIP
-	MYPU_6830	COG0036G	ribulose-phosphate 3-epimerase			MYPU_6830	Mycoplasma pulmonis UAB CTIP
gltX	MYPU_6820	COG0008J	glutamyl-tRNA synthetase	DEG10140266	MYPU_6820	MYPU_6820	Mycoplasma pulmonis UAB CTIP
-	MYPU_6810	-	glutamyl-tRNA synthetase			MYPU_6810	Mycoplasma pulmonis UAB CTIP
polC	MYPU_6750	COG2176L	DNA polymerase III PolC	DEG10140265	MYPU_6750	MYPU_6750	Mycoplasma pulmonis UAB CTIP
-	MYPU_6740	COG0552U	cell division protein FTSY	DEG10140264	MYPU_6740	MYPU_6740	Mycoplasma pulmonis UAB CTIP
-	MYPU_6720	COG0858J	ribosome-binding factor A	DEG10140263	MYPU_6720	MYPU_6720	Mycoplasma pulmonis UAB CTIP
-	MYPU_6680	COG0597MU	lipoprotein signal peptidase	DEG10140259	MYPU_6680	MYPU_6680	Mycoplasma pulmonis UAB CTIP
ileS	MYPU_6670	COG0060J	isoleucyl-tRNA synthetase	DEG10140258	MYPU_6670	MYPU_6670	Mycoplasma pulmonis UAB CTIP
pyrG	MYPU_6660	COG0504F	CTP synthetase	DEG10140257	MYPU_6660	MYPU_6660	Mycoplasma pulmonis UAB CTIP
-	MYPU_6650	COG1502I	cardiolipin synthetase	DEG10140256	MYPU_6650	MYPU_6650	Mycoplasma pulmonis UAB CTIP
-	MYPU_6590	COG0342U	bifunctional preprotein translocase subunit SecD/SecF	DEG10140255	MYPU_6590	MYPU_6590	Mycoplasma pulmonis UAB CTIP
ruvB	MYPU_6580	COG2255L	Holliday junction DNA helicase RuvB			MYPU_6580	Mycoplasma pulmonis UAB CTIP
ruvA	MYPU_6570	COG0632L	Holliday junction DNA helicase RuvA			MYPU_6570	Mycoplasma pulmonis UAB CTIP
rpsT	MYPU_6560	COG0268J	30S ribosomal protein S20	DEG10140254	MYPU_6560	MYPU_6560	Mycoplasma pulmonis UAB CTIP
-	MYPU_6540	-	lipoprotein			MYPU_6540	Mycoplasma pulmonis UAB CTIP
-	MYPU_6520	-	lipoprotein			MYPU_6520	Mycoplasma pulmonis UAB CTIP
-	MYPU_6460	COG0213F	thymidine phosphorylase			MYPU_6460	Mycoplasma pulmonis UAB CTIP
-	MYPU_6450	COG0813F	purine nucleoside phosphorylase	DEG10140253	MYPU_6450	MYPU_6450	Mycoplasma pulmonis UAB CTIP
-	MYPU_6410	COG3839G	maltodextrin ABC transporter ATP-binding protein			MYPU_6410	Mycoplasma pulmonis UAB CTIP
-	MYPU_6370	-	lipoprotein			MYPU_6370	Mycoplasma pulmonis UAB CTIP
-	MYPU_6330	COG0366G	oligo-1,6-glucosidase	DEG10140252	MYPU_6330	MYPU_6330	Mycoplasma pulmonis UAB CTIP
-	MYPU_6260	COG1136V	ABC transporter permease/ATP-binding protein			MYPU_6260	Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_6250	COG1136V	ABC transporter permease/ATP-binding protein			MYPU_6250	Mycoplasma pulmonis UAB CTIP
-	MYPU_6230	COG0171H	NH(3)-dependent NAD(+) synthetase	DEG10140251	MYPU_6230	MYPU_6230	Mycoplasma pulmonis UAB CTIP
-	MYPU_6210	COG0648L	endonuclease IV	DEG10140250	MYPU_6210	MYPU_6210	Mycoplasma pulmonis UAB CTIP
-	MYPU_6180	COG4603R	sugar ABC transporter permease			MYPU_6180	Mycoplasma pulmonis UAB CTIP
-	MYPU_6170	COG1079R	sugar ABC transporter permease			MYPU_6170	Mycoplasma pulmonis UAB CTIP
-	MYPU_6150	COG0692L	uracil-DNA glycosylase			MYPU_6150	Mycoplasma pulmonis UAB CTIP
-	MYPU_6120	COG0698G	ribose-5-phosphate isomerase B	DEG10140248	MYPU_6120	MYPU_6120	Mycoplasma pulmonis UAB CTIP
rpsF	MYPU_6110	COG0360J	30S ribosomal protein S6	DEG10140247	MYPU_6110	MYPU_6110	Mycoplasma pulmonis UAB CTIP
-	MYPU_6100	COG0629L	single-strand binding protein (SSB) (helix-destabilizing protein)	DEG10140246	MYPU_6100	MYPU_6100	Mycoplasma pulmonis UAB CTIP
rpsR	MYPU_6090	COG0238J	30S ribosomal protein S18			MYPU_6090	Mycoplasma pulmonis UAB CTIP
-	MYPU_6070	-	lipoprotein			MYPU_6070	Mycoplasma pulmonis UAB CTIP
-	MYPU_6060	-	lipoprotein			MYPU_6060	Mycoplasma pulmonis UAB CTIP
-	MYPU_6050	-	lipoprotein			MYPU_6050	Mycoplasma pulmonis UAB CTIP
-	MYPU_6040	-	lipoprotein			MYPU_6040	Mycoplasma pulmonis UAB CTIP
-	MYPU_6020	COG1080G	PTS	DEG10140244	MYPU_6020	MYPU_6020	Mycoplasma pulmonis UAB CTIP
pfkA	MYPU_6010	COG0205G	6-phosphofructokinase	DEG10140243	MYPU_6010	MYPU_6010	Mycoplasma pulmonis UAB CTIP
-	MYPU_5900	COG0051J	30S ribosomal protein S10	DEG10140242	MYPU_5900	MYPU_5900	Mycoplasma pulmonis UAB CTIP
rplC	MYPU_5890	COG0087J	50S ribosomal protein L3	DEG10140241	MYPU_5890	MYPU_5890	Mycoplasma pulmonis UAB CTIP
rplD	MYPU_5870	COG0088J	50S ribosomal protein L4	DEG10140240	MYPU_5870	MYPU_5870	Mycoplasma pulmonis UAB CTIP
rplW	MYPU_5860	COG0089J	50S ribosomal protein L23	DEG10140239	MYPU_5860	MYPU_5860	Mycoplasma pulmonis UAB CTIP
rplB	MYPU_5850	COG0090J	50S ribosomal protein L2	DEG10140238	MYPU_5850	MYPU_5850	Mycoplasma pulmonis UAB CTIP
rpsS	MYPU_5840	COG0185J	30S ribosomal protein S19	DEG10140237	MYPU_5840	MYPU_5840	Mycoplasma pulmonis UAB CTIP
rplV	MYPU_5830	COG0091J	50S ribosomal protein L22	DEG10140236	MYPU_5830	MYPU_5830	Mycoplasma pulmonis UAB CTIP
rpsC	MYPU_5810	COG0092J	30S ribosomal protein S3	DEG10140235	MYPU_5810	MYPU_5810	Mycoplasma pulmonis UAB CTIP
rplP	MYPU_5800	COG0197J	50S ribosomal protein L16	DEG10140234	MYPU_5800	MYPU_5800	Mycoplasma pulmonis UAB CTIP
-	MYPU_5790	COG0255J	50S ribosomal protein L29	DEG10140233	MYPU_5790	MYPU_5790	Mycoplasma pulmonis UAB CTIP
rpsQ	MYPU_5780	COG0186J	30S ribosomal protein S17	DEG10140232	MYPU_5780	MYPU_5780	Mycoplasma pulmonis UAB CTIP
rplN	MYPU_5770	COG0093J	50S ribosomal protein L14	DEG10140231	MYPU_5770	MYPU_5770	Mycoplasma pulmonis UAB CTIP
rplX	MYPU_5760	COG0198J	50S ribosomal protein L24	DEG10140230	MYPU_5760	MYPU_5760	Mycoplasma pulmonis UAB CTIP
rplE	MYPU_5750	COG0094J	50S ribosomal protein L5	DEG10140229	MYPU_5750	MYPU_5750	Mycoplasma pulmonis UAB CTIP
rpsN	MYPU_5740	COG0199J	30S ribosomal protein S14	DEG10140228	MYPU_5740	MYPU_5740	Mycoplasma pulmonis UAB CTIP
rpsH	MYPU_5730	COG0096J	30S ribosomal protein S8	DEG10140227	MYPU_5730	MYPU_5730	Mycoplasma pulmonis UAB CTIP
rplF	MYPU_5720	COG0097J	50S ribosomal protein L6	DEG10140226	MYPU_5720	MYPU_5720	Mycoplasma pulmonis UAB CTIP
rplR	MYPU_5710	COG0256J	50S ribosomal protein L18	DEG10140225	MYPU_5710	MYPU_5710	Mycoplasma pulmonis UAB CTIP
rpsE	MYPU_5700	COG0098J	30S ribosomal protein S5	DEG10140224	MYPU_5700	MYPU_5700	Mycoplasma pulmonis UAB CTIP
rplO	MYPU_5690	COG0200J	50S ribosomal protein L15	DEG10140223	MYPU_5690	MYPU_5690	Mycoplasma pulmonis UAB CTIP
secY	MYPU_5680	COG0201U	preprotein translocase subunit SecY	DEG10140222	MYPU_5680	MYPU_5680	Mycoplasma pulmonis UAB CTIP
-	MYPU_5670	COG0563F	adenylate kinase	DEG10140221	MYPU_5670	MYPU_5670	Mycoplasma pulmonis UAB CTIP
-	MYPU_5650	COG0361J	translation initiation factor IF-1	DEG10140219	MYPU_5650	MYPU_5650	Mycoplasma pulmonis UAB CTIP
-	MYPU_5640	COG0257J	ribosomal protein L36	DEG10140218	MYPU_5640	MYPU_5640	Mycoplasma pulmonis UAB CTIP
rpsM	MYPU_5630	COG0099J	30S ribosomal protein S13	DEG10140217	MYPU_5630	MYPU_5630	Mycoplasma pulmonis UAB CTIP
-	MYPU_5620	COG0100J	30S ribosomal protein S11	DEG10140216	MYPU_5620	MYPU_5620	Mycoplasma pulmonis UAB CTIP
-	MYPU_5610	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10140215	MYPU_5610	MYPU_5610	Mycoplasma pulmonis UAB CTIP
rplQ	MYPU_5600	COG0203J	50S ribosomal protein L17	DEG10140214	MYPU_5600	MYPU_5600	Mycoplasma pulmonis UAB CTIP
mnmA	MYPU_5580	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10140213	MYPU_5580	MYPU_5580	Mycoplasma pulmonis UAB CTIP
alaS	MYPU_5570	COG0013J	alanyl-tRNA synthetase	DEG10140212	MYPU_5570	MYPU_5570	Mycoplasma pulmonis UAB CTIP
-	MYPU_5530	COG0782K	transcription elongation factor GreA	DEG10140210	MYPU_5530	MYPU_5530	Mycoplasma pulmonis UAB CTIP
-	MYPU_5510	COG0634F	hypoxanthine-guanine phosphoribosyltransferase	DEG10140209	MYPU_5510	MYPU_5510	Mycoplasma pulmonis UAB CTIP
-	MYPU_5480	COG0196H	hypothetical protein	DEG10140207	MYPU_5480	MYPU_5480	Mycoplasma pulmonis UAB CTIP
rpoB	MYPU_5460	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10140206	MYPU_5460	MYPU_5460	Mycoplasma pulmonis UAB CTIP
-	MYPU_5450	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10140205	MYPU_5450	MYPU_5450	Mycoplasma pulmonis UAB CTIP
-	MYPU_5410	COG0209F	ribonucleotide-diphosphate reductase subunit alpha			MYPU_5410	Mycoplasma pulmonis UAB CTIP
nrdF	MYPU_5390	COG0208F	ribonucleotide-diphosphate reductase subunit beta			MYPU_5390	Mycoplasma pulmonis UAB CTIP
thyA	MYPU_5380	COG0207F	thymidylate synthase			MYPU_5380	Mycoplasma pulmonis UAB CTIP
-	MYPU_5370	COG0262H	dihydrofolate reductase	DEG10140203	MYPU_5370	MYPU_5370	Mycoplasma pulmonis UAB CTIP
rpsB	MYPU_5330	COG0052J	30S ribosomal protein S2	DEG10140202	MYPU_5330	MYPU_5330	Mycoplasma pulmonis UAB CTIP
tsf	MYPU_5320	COG0264J	elongation factor Ts	DEG10140201	MYPU_5320	MYPU_5320	Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_5300	COG5271R	lipoprotein			MYPU_5300	Mycoplasma pulmonis UAB CTIP
-	MYPU_5280	-	lipoprotein VSAI			MYPU_5280	Mycoplasma pulmonis UAB CTIP
-	MYPU_5220	-	lipoprotein B			MYPU_5220	Mycoplasma pulmonis UAB CTIP
-	MYPU_5200	-	lipoprotein D			MYPU_5200	Mycoplasma pulmonis UAB CTIP
eno	MYPU_5180	COG0148G	phosphopyruvate hydratase	DEG10140199	MYPU_5180	MYPU_5180	Mycoplasma pulmonis UAB CTIP
rplI	MYPU_5160	COG0359J	50S ribosomal protein L9	DEG10140197	MYPU_5160	MYPU_5160	Mycoplasma pulmonis UAB CTIP
-	MYPU_5150	COG0305L	replicative DNA helicase	DEG10140196	MYPU_5150	MYPU_5150	Mycoplasma pulmonis UAB CTIP
-	MYPU_5130	COG0231J	elongation factor P	DEG10140194	MYPU_5130	MYPU_5130	Mycoplasma pulmonis UAB CTIP
-	MYPU_5110	COG0021G	transketolase	DEG10140193	MYPU_5110	MYPU_5110	Mycoplasma pulmonis UAB CTIP
-	MYPU_5090	-	lipoprotein			MYPU_5090	Mycoplasma pulmonis UAB CTIP
-	MYPU_5080	COG5271R	lipoprotein			MYPU_5080	Mycoplasma pulmonis UAB CTIP
-	MYPU_5040	COG3883S	lipoprotein			MYPU_5040	Mycoplasma pulmonis UAB CTIP
-	MYPU_4990	COG0395G	ABC transporter permease			MYPU_4990	Mycoplasma pulmonis UAB CTIP
-	MYPU_4980	COG1175G	ABC transporter permease			MYPU_4980	Mycoplasma pulmonis UAB CTIP
-	MYPU_4970	COG3839G	ABC transporter ATP-binding protein			MYPU_4970	Mycoplasma pulmonis UAB CTIP
rpsI	MYPU_4960	COG0103J	30S ribosomal protein S9	DEG10140191	MYPU_4960	MYPU_4960	Mycoplasma pulmonis UAB CTIP
rplM	MYPU_4950	COG0102J	50S ribosomal protein L13	DEG10140190	MYPU_4950	MYPU_4950	Mycoplasma pulmonis UAB CTIP
-	MYPU_4940	COG2001S	cell division protein MraZ	DEG10140189	MYPU_4940	MYPU_4940	Mycoplasma pulmonis UAB CTIP
-	MYPU_4910	COG0206D	cell division protein FtsZ	DEG10140186	MYPU_4910	MYPU_4910	Mycoplasma pulmonis UAB CTIP
metG	MYPU_4900	COG0143J	methionyl-tRNA synthetase	DEG10140185	MYPU_4900	MYPU_4900	Mycoplasma pulmonis UAB CTIP
rpmG	MYPU_4890	COG0267J	50S ribosomal protein L33			MYPU_4890	Mycoplasma pulmonis UAB CTIP
-	MYPU_4870	COG5028	lipoprotein			MYPU_4870	Mycoplasma pulmonis UAB CTIP
-	MYPU_4860	COG0073R	phenylalanyl-tRNA synthetase subunit beta	DEG10140183	MYPU_4860	MYPU_4860	Mycoplasma pulmonis UAB CTIP
-	MYPU_4850	COG0162J	tyrosyl-tRNA synthetase	DEG10140182	MYPU_4850	MYPU_4850	Mycoplasma pulmonis UAB CTIP
-	MYPU_4830	COG1488H	nicotinate phosphoribosyltransferase	DEG10140180	MYPU_4830	MYPU_4830	Mycoplasma pulmonis UAB CTIP
-	MYPU_4820	-	lipoprotein			MYPU_4820	Mycoplasma pulmonis UAB CTIP
-	MYPU_4780	-	lipoprotein			MYPU_4780	Mycoplasma pulmonis UAB CTIP
-	MYPU_4740	COG0575I	phosphatidate cytidylyltransferase	DEG10140177	MYPU_4740	MYPU_4740	Mycoplasma pulmonis UAB CTIP
-	MYPU_4710	COG0550L	DNA topoisomerase I	DEG10140176	MYPU_4710	MYPU_4710	Mycoplasma pulmonis UAB CTIP
-	MYPU_4700	COG0221C	inorganic pyrophosphatase	DEG10140175	MYPU_4700	MYPU_4700	Mycoplasma pulmonis UAB CTIP
rpsP	MYPU_4690	COG0228J	30S ribosomal protein S16	DEG10140174	MYPU_4690	MYPU_4690	Mycoplasma pulmonis UAB CTIP
trmD	MYPU_4680	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10140173	MYPU_4680	MYPU_4680	Mycoplasma pulmonis UAB CTIP
rplS	MYPU_4670	COG0335J	50S ribosomal protein L19	DEG10140172	MYPU_4670	MYPU_4670	Mycoplasma pulmonis UAB CTIP
-	MYPU_4650	COG2176L	lipoprotein			MYPU_4650	Mycoplasma pulmonis UAB CTIP
-	MYPU_4620	COG1466L	hypothetical protein	DEG10140171	MYPU_4620	MYPU_4620	Mycoplasma pulmonis UAB CTIP
-	MYPU_4590	COG0696G	phosphoglyceromutase	DEG10140170	MYPU_4590	MYPU_4590	Mycoplasma pulmonis UAB CTIP
tpiA	MYPU_4580	COG0149G	triosephosphate isomerase	DEG10140169	MYPU_4580	MYPU_4580	Mycoplasma pulmonis UAB CTIP
-	MYPU_4550	-	lipoprotein			MYPU_4550	Mycoplasma pulmonis UAB CTIP
-	MYPU_4540	COG0568K	RNA polymerase sigma factor	DEG10140168	MYPU_4540	MYPU_4540	Mycoplasma pulmonis UAB CTIP
-	MYPU_4530	COG0358L	DNA primase	DEG10140167	MYPU_4530	MYPU_4530	Mycoplasma pulmonis UAB CTIP
-	MYPU_4510	COG0423J	glycyl-tRNA synthetase	DEG10140166	MYPU_4510	MYPU_4510	Mycoplasma pulmonis UAB CTIP
-	MYPU_4500	COG0055C	ATP synthase F0F1 subunit beta			MYPU_4500	Mycoplasma pulmonis UAB CTIP
-	MYPU_4490	COG0056C	ATP synthase F0F1 subunit alpha	DEG10140165	MYPU_4490	MYPU_4490	Mycoplasma pulmonis UAB CTIP
-	MYPU_4360	-	lipoprotein			MYPU_4360	Mycoplasma pulmonis UAB CTIP
rpsL	MYPU_4300	COG0048J	30S ribosomal protein S12	DEG10140162	MYPU_4300	MYPU_4300	Mycoplasma pulmonis UAB CTIP
-	MYPU_4290	COG0049J	30S ribosomal protein S7	DEG10140161	MYPU_4290	MYPU_4290	Mycoplasma pulmonis UAB CTIP
-	MYPU_4280	COG0480J	elongation factor G	DEG10140160	MYPU_4280	MYPU_4280	Mycoplasma pulmonis UAB CTIP
-	MYPU_4250	COG3842E	spermidine/putrescine ABC transporter ATP-binding protein	DEG10140159	MYPU_4250	MYPU_4250	Mycoplasma pulmonis UAB CTIP
-	MYPU_4240	COG1176E	spermidine/putrescine ABC transporter permease	DEG10140158	MYPU_4240	MYPU_4240	Mycoplasma pulmonis UAB CTIP
-	MYPU_4230	COG1177E	spermidine/putrescine ABC transporter permease	DEG10140157	MYPU_4230	MYPU_4230	Mycoplasma pulmonis UAB CTIP
-	MYPU_4220	COG0687E	hypothetical protein	DEG10140156	MYPU_4220	MYPU_4220	Mycoplasma pulmonis UAB CTIP
-	MYPU_4190	-	lipoprotein			MYPU_4190	Mycoplasma pulmonis UAB CTIP
-	MYPU_4150	COG4166E	lipoprotein			MYPU_4150	Mycoplasma pulmonis UAB CTIP
-	MYPU_4130	COG1124EP	oligopeptide ABC transporter ATP-binding protein OppF			MYPU_4130	Mycoplasma pulmonis UAB CTIP
-	MYPU_4120	COG0444EP	oligopeptide ABC transporter ATP-binding protein OppD			MYPU_4120	Mycoplasma pulmonis UAB CTIP
-	MYPU_4110	COG1173EP	oligopeptide ABC transporter system permease OPPC			MYPU_4110	Mycoplasma pulmonis UAB CTIP
-	MYPU_4100	COG0601EP	oligopeptide ABC transporter system permease OPPB	DEG10140154	MYPU_4100	MYPU_4100	Mycoplasma pulmonis UAB CTIP
tuf	MYPU_4050	COG0050J	elongation factor Tu	DEG10140150	MYPU_4050	MYPU_4050	Mycoplasma pulmonis UAB CTIP
lysS	MYPU_4020	COG1190J	lysyl-tRNA synthetase			MYPU_4020	Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_4010	COG0272L	DNA ligase (polydeoxyribonucleotide synthase [NAD+]) (fragment)	DEG10140149	MYPU_4010	MYPU_4010	Mycoplasma pulmonis UAB CTIP
lysS	MYPU_3900	COG1190J	lysyl-tRNA synthetase			MYPU_3900	Mycoplasma pulmonis UAB CTIP
-	MYPU_3890	COG0272L	DNA ligase (polydeoxyribonucleotide synthase [NAD+])	DEG10140148	MYPU_3890	MYPU_3890	Mycoplasma pulmonis UAB CTIP
-	MYPU_3880	COG0619P	ABC transporter permease	DEG10140147	MYPU_3880	MYPU_3880	Mycoplasma pulmonis UAB CTIP
-	MYPU_3870	COG1122P	cobalt transporter ATP-binding subunit	DEG10140146	MYPU_3870	MYPU_3870	Mycoplasma pulmonis UAB CTIP
cbiO	MYPU_3860	COG1122P	cobalt transporter ATP-binding subunit	DEG10140145	MYPU_3860	MYPU_3860	Mycoplasma pulmonis UAB CTIP
era	MYPU_3800	COG1159R	GTP-binding protein Era	DEG10140144	MYPU_3800	MYPU_3800	Mycoplasma pulmonis UAB CTIP
-	MYPU_3740	-	lipoprotein	DEG10140143	MYPU_3740	MYPU_3740	Mycoplasma pulmonis UAB CTIP
-	MYPU_3730	COG0188L	DNA topoisomerase IV subunit A	DEG10140142	MYPU_3730	MYPU_3730	Mycoplasma pulmonis UAB CTIP
-	MYPU_3720	COG0187L	topoisomerase IV subunit B	DEG10140141	MYPU_3720	MYPU_3720	Mycoplasma pulmonis UAB CTIP
-	MYPU_3710	-	lipoprotein			MYPU_3710	Mycoplasma pulmonis UAB CTIP
-	MYPU_3690	COG1820G	N-acetylglucosamine-6-phosphate deacetylase			MYPU_3690	Mycoplasma pulmonis UAB CTIP
-	MYPU_3640	COG1263G	PTS system, glucose-specific IIABC component (EIIABC-glc) (glucose-permease IIABC component) (phosphotransferase enzyme II, ABC component) (EII-glc/EIII-glc)	DEG10140140	MYPU_3640	MYPU_3640	Mycoplasma pulmonis UAB CTIP
nagB	MYPU_3620	COG0363G	glucosamine-6-phosphate deaminase			MYPU_3620	Mycoplasma pulmonis UAB CTIP
-	MYPU_3610	COG1263G	PTS system	DEG10140139	MYPU_3610	MYPU_3610	Mycoplasma pulmonis UAB CTIP
-	MYPU_3600	COG0191G	fructose-bisphosphate aldolase			MYPU_3600	Mycoplasma pulmonis UAB CTIP
-	MYPU_3580	COG0236IQ	acyl carrier protein	DEG10140137	MYPU_3580	MYPU_3580	Mycoplasma pulmonis UAB CTIP
obgE	MYPU_3530	COG0536R	GTPase ObgE	DEG10140136	MYPU_3530	MYPU_3530	Mycoplasma pulmonis UAB CTIP
-	MYPU_3510	COG0557K	ribonuclease II			MYPU_3510	Mycoplasma pulmonis UAB CTIP
pheS	MYPU_3480	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10140134	MYPU_3480	MYPU_3480	Mycoplasma pulmonis UAB CTIP
pheT	MYPU_3470	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10140133	MYPU_3470	MYPU_3470	Mycoplasma pulmonis UAB CTIP
-	MYPU_3430	COG4213G	lipoprotein			MYPU_3430	Mycoplasma pulmonis UAB CTIP
-	MYPU_3420	COG0541U	signal recognition particle protein	DEG10140132	MYPU_3420	MYPU_3420	Mycoplasma pulmonis UAB CTIP
glyA	MYPU_3390	COG0112E	serine hydroxymethyltransferase	DEG10140131	MYPU_3390	MYPU_3390	Mycoplasma pulmonis UAB CTIP
-	MYPU_3380	-	lipoprotein			MYPU_3380	Mycoplasma pulmonis UAB CTIP
nadD	MYPU_3350	COG1057H	nicotinate-nucleotide adenylyltransferase	DEG10140130	MYPU_3350	MYPU_3350	Mycoplasma pulmonis UAB CTIP
hisS	MYPU_3330	COG0124J	histidyl-tRNA synthetase	DEG10140129	MYPU_3330	MYPU_3330	Mycoplasma pulmonis UAB CTIP
-	MYPU_3320	COG0173J	aspartyl-tRNA synthetase	DEG10140128	MYPU_3320	MYPU_3320	Mycoplasma pulmonis UAB CTIP
rplU	MYPU_3300	COG0261J	50S ribosomal protein L21	DEG10140127	MYPU_3300	MYPU_3300	Mycoplasma pulmonis UAB CTIP
rpmA	MYPU_3290	COG0211J	50S ribosomal protein L27	DEG10140126	MYPU_3290	MYPU_3290	Mycoplasma pulmonis UAB CTIP
rpsO	MYPU_3280	COG0184J	30S ribosomal protein S15	DEG10140125	MYPU_3280	MYPU_3280	Mycoplasma pulmonis UAB CTIP
-	MYPU_3270	COG1546R	competence-damage protein			MYPU_3270	Mycoplasma pulmonis UAB CTIP
rpmF	MYPU_3240	COG0333J	50S ribosomal protein L32	DEG10140124	MYPU_3240	MYPU_3240	Mycoplasma pulmonis UAB CTIP
-	MYPU_3230	-	lipoprotein	DEG10140123	MYPU_3230	MYPU_3230	Mycoplasma pulmonis UAB CTIP
-	MYPU_3220	COG0503F	adenine phosphoribosyltransferase	DEG10140122	MYPU_3220	MYPU_3220	Mycoplasma pulmonis UAB CTIP
-	MYPU_3200	-	lipoprotein			MYPU_3200	Mycoplasma pulmonis UAB CTIP
-	MYPU_3190	-	lipoprotein			MYPU_3190	Mycoplasma pulmonis UAB CTIP
-	MYPU_3180	-	lipoprotein			MYPU_3180	Mycoplasma pulmonis UAB CTIP
-	MYPU_3160	-	lipoprotein			MYPU_3160	Mycoplasma pulmonis UAB CTIP
upp	MYPU_3150	COG0035F	uracil phosphoribosyltransferase	DEG10140121	MYPU_3150	MYPU_3150	Mycoplasma pulmonis UAB CTIP
-	MYPU_3140	COG0274F	deoxyribose-phosphate aldolase	DEG10140120	MYPU_3140	MYPU_3140	Mycoplasma pulmonis UAB CTIP
-	MYPU_3100	COG0266L	formamidopyrimidine-DNA glycosylase	DEG10140117	MYPU_3100	MYPU_3100	Mycoplasma pulmonis UAB CTIP
rbgA	MYPU_3060	COG1161R	ribosomal biogenesis GTPase	DEG10140116	MYPU_3060	MYPU_3060	Mycoplasma pulmonis UAB CTIP
-	MYPU_3000	COG1039L	ribonuclease HII (RNase HII)	DEG10140112	MYPU_3000	MYPU_3000	Mycoplasma pulmonis UAB CTIP
-	MYPU_2950	COG0344S	hypothetical protein	DEG10140110	MYPU_2950	MYPU_2950	Mycoplasma pulmonis UAB CTIP
-	MYPU_2910	-	lipoprotein			MYPU_2910	Mycoplasma pulmonis UAB CTIP
rplJ	MYPU_2900	COG0244J	50S ribosomal protein L10	DEG10140108	MYPU_2900	MYPU_2900	Mycoplasma pulmonis UAB CTIP
rplL	MYPU_2890	COG0222J	50S ribosomal protein L7/L12	DEG10140107	MYPU_2890	MYPU_2890	Mycoplasma pulmonis UAB CTIP
-	MYPU_2880	-	lipoprotein			MYPU_2880	Mycoplasma pulmonis UAB CTIP
-	MYPU_2860	COG4608E	oligopeptide ABC transporter ATP-binding protein			MYPU_2860	Mycoplasma pulmonis UAB CTIP
-	MYPU_2850	COG0444EP	oligopeptide ABC transporter ATP-binding protein	DEG10140106	MYPU_2850	MYPU_2850	Mycoplasma pulmonis UAB CTIP
-	MYPU_2840	COG1173EP	oligopeptide ABC transporter permease	DEG10140105	MYPU_2840	MYPU_2840	Mycoplasma pulmonis UAB CTIP
-	MYPU_2830	COG0601EP	oligopeptide ABC transporter permease	DEG10140104	MYPU_2830	MYPU_2830	Mycoplasma pulmonis UAB CTIP
-	MYPU_2820	-	lipoprotein	DEG10140103	MYPU_2820	MYPU_2820	Mycoplasma pulmonis UAB CTIP
-	MYPU_2770	COG1015G	phosphopentomutase	DEG10140102	MYPU_2770	MYPU_2770	Mycoplasma pulmonis UAB CTIP
-	MYPU_2720	COG0356C	ATP synthase F0F1 subunit A	DEG10140101	MYPU_2720	MYPU_2720	Mycoplasma pulmonis UAB CTIP
-	MYPU_2710	COG0636C	ATP synthase subunit C	DEG10140100	MYPU_2710	MYPU_2710	Mycoplasma pulmonis UAB CTIP
-	MYPU_2700	COG0711C	ATP synthase subunit B	DEG10140099	MYPU_2700	MYPU_2700	Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_2690	COG0712C	ATP synthase subunit delta	DEG10140098	MYPU_2690	MYPU_2690	Mycoplasma pulmonis UAB CTIP
-	MYPU_2680	COG0056C	ATP synthase F0F1 subunit alpha	DEG10140097	MYPU_2680	MYPU_2680	Mycoplasma pulmonis UAB CTIP
-	MYPU_2670	COG0224C	ATP synthase F0F1 subunit gamma	DEG10140096	MYPU_2670	MYPU_2670	Mycoplasma pulmonis UAB CTIP
-	MYPU_2660	COG0055C	ATP synthase F0F1 subunit beta	DEG10140095	MYPU_2660	MYPU_2660	Mycoplasma pulmonis UAB CTIP
-	MYPU_2650	COG0355C	ATP synthase subunit epsilon			MYPU_2650	Mycoplasma pulmonis UAB CTIP
-	MYPU_2640	COG0579R	glycerol-3-phosphate dehydrogenase			MYPU_2640	Mycoplasma pulmonis UAB CTIP
rplT	MYPU_2610	COG0292J	50S ribosomal protein L20	DEG10140094	MYPU_2610	MYPU_2610	Mycoplasma pulmonis UAB CTIP
rpmI	MYPU_2600	COG0291J	50S ribosomal protein L35	DEG10140093	MYPU_2600	MYPU_2600	Mycoplasma pulmonis UAB CTIP
infC	MYPU_2590	COG0290J	translation initiation factor IF-3	DEG10140092	MYPU_2590	MYPU_2590	Mycoplasma pulmonis UAB CTIP
-	MYPU_2580	COG0190H	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	DEG10140091	MYPU_2580	MYPU_2580	Mycoplasma pulmonis UAB CTIP
valS	MYPU_2570	COG0525J	valyl-tRNA synthetase	DEG10140090	MYPU_2570	MYPU_2570	Mycoplasma pulmonis UAB CTIP
recA	MYPU_2520	COG0468L	recombinase A			MYPU_2520	Mycoplasma pulmonis UAB CTIP
-	MYPU_2460	COG0126G	phosphoglycerate kinase	DEG10140086	MYPU_2460	MYPU_2460	Mycoplasma pulmonis UAB CTIP
-	MYPU_2450	-	lipoprotein			MYPU_2450	Mycoplasma pulmonis UAB CTIP
-	MYPU_2430	COG0018J	arginyl-tRNA synthetase	DEG10140084	MYPU_2430	MYPU_2430	Mycoplasma pulmonis UAB CTIP
-	MYPU_2400	COG0469G	pyruvate kinase	DEG10140083	MYPU_2400	MYPU_2400	Mycoplasma pulmonis UAB CTIP
engB	MYPU_2390	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10140082	MYPU_2390	MYPU_2390	Mycoplasma pulmonis UAB CTIP
-	MYPU_2380	COG0282C	acetate kinase	DEG10140081	MYPU_2380	MYPU_2380	Mycoplasma pulmonis UAB CTIP
eutD	MYPU_2370	COG0280C	phosphotransacetylase	DEG10140080	MYPU_2370	MYPU_2370	Mycoplasma pulmonis UAB CTIP
-	MYPU_2360	COG0055C	ATP synthase F0F1 subunit beta			MYPU_2360	Mycoplasma pulmonis UAB CTIP
-	MYPU_2350	COG0056C	ATP synthase subunit alpha	DEG10140079	MYPU_2350	MYPU_2350	Mycoplasma pulmonis UAB CTIP
-	MYPU_2280	COG1940KG	glucokinase			MYPU_2280	Mycoplasma pulmonis UAB CTIP
-	MYPU_2250	-	lipoprotein ABC transporter substrate -binding protein	DEG10140076	MYPU_2250	MYPU_2250	Mycoplasma pulmonis UAB CTIP
-	MYPU_2240	COG3638P	ABC transporter ATP-binding protein	DEG10140075	MYPU_2240	MYPU_2240	Mycoplasma pulmonis UAB CTIP
dnaK	MYPU_2230	COG0443O	molecular chaperone DnaK	DEG10140074	MYPU_2230	MYPU_2230	Mycoplasma pulmonis UAB CTIP
glpK	MYPU_2210	COG0554C	glycerol kinase			MYPU_2210	Mycoplasma pulmonis UAB CTIP
pyrH	MYPU_2200	COG0528F	uridylate kinase	DEG10140073	MYPU_2200	MYPU_2200	Mycoplasma pulmonis UAB CTIP
-	MYPU_2180	COG3639P	P69-like ABC transporter permease			MYPU_2180	Mycoplasma pulmonis UAB CTIP
-	MYPU_2070	-	lipoprotein			MYPU_2070	Mycoplasma pulmonis UAB CTIP
-	MYPU_2060	COG0810M	lipoprotein			MYPU_2060	Mycoplasma pulmonis UAB CTIP
infB	MYPU_2050	COG0532J	translation initiation factor IF-2	DEG10140071	MYPU_2050	MYPU_2050	Mycoplasma pulmonis UAB CTIP
nusA	MYPU_2030	COG0195K	transcription elongation factor NusA	DEG10140070	MYPU_2030	MYPU_2030	Mycoplasma pulmonis UAB CTIP
gatB	MYPU_2010	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10140069	MYPU_2010	MYPU_2010	Mycoplasma pulmonis UAB CTIP
-	MYPU_2000	COG0154J	amidase	DEG10140068	MYPU_2000	MYPU_2000	Mycoplasma pulmonis UAB CTIP
-	MYPU_1950	-	lipoprotein			MYPU_1950	Mycoplasma pulmonis UAB CTIP
-	MYPU_1940	-	lipoprotein			MYPU_1940	Mycoplasma pulmonis UAB CTIP
-	MYPU_1930	-	lipoprotein			MYPU_1930	Mycoplasma pulmonis UAB CTIP
-	MYPU_1880	COG0389L	DNA-damage repair protein MucB			MYPU_1880	Mycoplasma pulmonis UAB CTIP
-	MYPU_1840	COG3118O	thioredoxin	DEG10140066	MYPU_1840	MYPU_1840	Mycoplasma pulmonis UAB CTIP
-	MYPU_1830	COG0442J	prolyl-tRNA synthetase	DEG10140065	MYPU_1830	MYPU_1830	Mycoplasma pulmonis UAB CTIP
nusG	MYPU_1820	COG0250K	transcription antitermination protein NusG	DEG10140064	MYPU_1820	MYPU_1820	Mycoplasma pulmonis UAB CTIP
rpmG	MYPU_1800	COG0267J	50S ribosomal protein L33	DEG10140063	MYPU_1800	MYPU_1800	Mycoplasma pulmonis UAB CTIP
-	MYPU_1770	COG0215J	cysteinyl-tRNA synthetase	DEG10140062	MYPU_1770	MYPU_1770	Mycoplasma pulmonis UAB CTIP
-	MYPU_1680	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase	DEG10140058	MYPU_1680	MYPU_1680	Mycoplasma pulmonis UAB CTIP
trmB	MYPU_1660	COG0220R	tRNA (guanine-N(7)-)-methyltransferase			MYPU_1660	Mycoplasma pulmonis UAB CTIP
-	MYPU_1650	COG0012J	GTP-dependent nucleic acid-binding protein EngD	DEG10140057	MYPU_1650	MYPU_1650	Mycoplasma pulmonis UAB CTIP
-	MYPU_1620	COG0416I	glycerol-3-phosphate acyltransferase PlsX	DEG10140056	MYPU_1620	MYPU_1620	Mycoplasma pulmonis UAB CTIP
-	MYPU_1590	COG1381L	recombinase protein			MYPU_1590	Mycoplasma pulmonis UAB CTIP
-	MYPU_1580	-	lipoprotein	DEG10140054	MYPU_1580	MYPU_1580	Mycoplasma pulmonis UAB CTIP
rpmH	MYPU_1540	COG0230J	50S ribosomal protein L34	DEG10140052	MYPU_1540	MYPU_1540	Mycoplasma pulmonis UAB CTIP
-	MYPU_1530	COG0594J	ribonuclease P protein component (protein C5) (RNase P)	DEG10140051	MYPU_1530	MYPU_1530	Mycoplasma pulmonis UAB CTIP
-	MYPU_1520	COG0706U	inner membrane protein translocase component YidC	DEG10140050	MYPU_1520	MYPU_1520	Mycoplasma pulmonis UAB CTIP
-	MYPU_1470	COG0188L	DNA gyrase subunit A	DEG10140048	MYPU_1470	MYPU_1470	Mycoplasma pulmonis UAB CTIP
-	MYPU_1450	COG1435F	thymidine kinase			MYPU_1450	Mycoplasma pulmonis UAB CTIP
-	MYPU_1430	COG0576O	heat shock protein GrpE	DEG10140045	MYPU_1430	MYPU_1430	Mycoplasma pulmonis UAB CTIP
-	MYPU_1400	COG0254J	50S ribosomal protein L31	DEG10140043	MYPU_1400	MYPU_1400	Mycoplasma pulmonis UAB CTIP
pgi	MYPU_1310	COG0166G	glucose-6-phosphate isomerase	DEG10140040	MYPU_1310	MYPU_1310	Mycoplasma pulmonis UAB CTIP
-	MYPU_1300	COG0539J	30S ribosomal protein S1			MYPU_1300	Mycoplasma pulmonis UAB CTIP
-	MYPU_1270	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10140039	MYPU_1270	MYPU_1270	Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_1240	COG0240C	glycerol-3-phosphate dehydrogenase	DEG10140038	MYPU_1240	MYPU_1240	Mycoplasma pulmonis UAB CTIP
scpB	MYPU_1160	COG1386K	segregation and condensation protein B	DEG10140034	MYPU_1160	MYPU_1160	Mycoplasma pulmonis UAB CTIP
scpA	MYPU_1150	COG1354S	segregation and condensation protein A	DEG10140033	MYPU_1150	MYPU_1150	Mycoplasma pulmonis UAB CTIP
-	MYPU_1140	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	DEG10140032	MYPU_1140	MYPU_1140	Mycoplasma pulmonis UAB CTIP
-	MYPU_1130	COG0736I	holo-ACP synthase	DEG10140031	MYPU_1130	MYPU_1130	Mycoplasma pulmonis UAB CTIP
-	MYPU_1100	COG0191G	fructose-bisphosphate aldolase	DEG10140030	MYPU_1100	MYPU_1100	Mycoplasma pulmonis UAB CTIP
-	MYPU_1090	COG1284S	ABC transporter permease			MYPU_1090	Mycoplasma pulmonis UAB CTIP
-	MYPU_1080	COG3639P	ABC transporter permease			MYPU_1080	Mycoplasma pulmonis UAB CTIP
-	MYPU_1070	COG3638P	ABC transporter ATP-binding protein			MYPU_1070	Mycoplasma pulmonis UAB CTIP
prfA	MYPU_1050	COG0216J	peptide chain release factor 1	DEG10140028	MYPU_1050	MYPU_1050	Mycoplasma pulmonis UAB CTIP
secA	MYPU_1040	COG0653U	preprotein translocase subunit SecA	DEG10140027	MYPU_1040	MYPU_1040	Mycoplasma pulmonis UAB CTIP
-	MYPU_1030	COG0366G	oligo-1,6-glucosidase	DEG10140026	MYPU_1030	MYPU_1030	Mycoplasma pulmonis UAB CTIP
-	MYPU_1010	COG1175G	sugar ABC transporter permease			MYPU_1010	Mycoplasma pulmonis UAB CTIP
-	MYPU_1000	COG0395G	sugar ABC transporter permease			MYPU_1000	Mycoplasma pulmonis UAB CTIP
-	MYPU_0990	COG3839G	sugar ABC transporter ATP-binding protein			MYPU_0990	Mycoplasma pulmonis UAB CTIP
-	MYPU_0980	COG1653G	sugar ABC transporter			MYPU_0980	Mycoplasma pulmonis UAB CTIP
-	MYPU_0950	COG0122L	methylated-DNA--protein-cysteine methyltransferase			MYPU_0950	Mycoplasma pulmonis UAB CTIP
leuS	MYPU_0930	COG0495J	leucyl-tRNA synthetase	DEG10140025	MYPU_0930	MYPU_0930	Mycoplasma pulmonis UAB CTIP
-	MYPU_0920	COG0810M	lipoprotein			MYPU_0920	Mycoplasma pulmonis UAB CTIP
-	MYPU_0890	COG0283F	cytidylate kinase	DEG10140024	MYPU_0890	MYPU_0890	Mycoplasma pulmonis UAB CTIP
engA	MYPU_0880	COG1160R	GTP-binding protein EngA	DEG10140023	MYPU_0880	MYPU_0880	Mycoplasma pulmonis UAB CTIP
-	MYPU_0870	COG0776L	DNA-binding protein HU	DEG10140022	MYPU_0870	MYPU_0870	Mycoplasma pulmonis UAB CTIP
-	MYPU_0670	-	lipoprotein			MYPU_0670	Mycoplasma pulmonis UAB CTIP
-	MYPU_0660	COG1136V	ABC transporter ATP-binding protein			MYPU_0660	Mycoplasma pulmonis UAB CTIP
-	MYPU_0650	COG4591M	ABC transporter permease			MYPU_0650	Mycoplasma pulmonis UAB CTIP
-	MYPU_0640	COG1136V	ABC transporter ATP-binding protein			MYPU_0640	Mycoplasma pulmonis UAB CTIP
-	MYPU_0570	-	lipoprotein			MYPU_0570	Mycoplasma pulmonis UAB CTIP
-	MYPU_0560	-	lipoprotein			MYPU_0560	Mycoplasma pulmonis UAB CTIP
-	MYPU_0550	COG0737F	5'-nucleotidase			MYPU_0550	Mycoplasma pulmonis UAB CTIP
-	MYPU_0530	COG0470L	DNA polymerase III subunit delta'	DEG10140021	MYPU_0530	MYPU_0530	Mycoplasma pulmonis UAB CTIP
-	MYPU_0520	COG0125F	thymidylate kinase	DEG10140020	MYPU_0520	MYPU_0520	Mycoplasma pulmonis UAB CTIP
recR	MYPU_0510	COG0353L	recombination protein RecR			MYPU_0510	Mycoplasma pulmonis UAB CTIP
-	MYPU_0490	COG2812L	DNA polymerase III subunits gamma and tau	DEG10140019	MYPU_0490	MYPU_0490	Mycoplasma pulmonis UAB CTIP
-	MYPU_0460	COG0057G	glyceraldehyde 3-phosphate dehydrogenase	DEG10140018	MYPU_0460	MYPU_0460	Mycoplasma pulmonis UAB CTIP
-	MYPU_0450	COG0223J	methionyl-tRNA formyltransferase	DEG10140017	MYPU_0450	MYPU_0450	Mycoplasma pulmonis UAB CTIP
-	MYPU_0410	COG2274V	ABC transporter ATP-binding protein			MYPU_0410	Mycoplasma pulmonis UAB CTIP
-	MYPU_0400	COG4987CO	ABC transporter permease			MYPU_0400	Mycoplasma pulmonis UAB CTIP
-	MYPU_0390	COG1132V	ABC transporter ATP-binding protein			MYPU_0390	Mycoplasma pulmonis UAB CTIP
-	MYPU_0340	COG0172J	seryl-tRNA synthetase	DEG10140016	MYPU_0340	MYPU_0340	Mycoplasma pulmonis UAB CTIP
-	MYPU_0280	COG0395G	ABC transporter permease	DEG10140015	MYPU_0280	MYPU_0280	Mycoplasma pulmonis UAB CTIP
-	MYPU_0270	COG1175G	ABC transporter permease	DEG10140014	MYPU_0270	MYPU_0270	Mycoplasma pulmonis UAB CTIP
-	MYPU_0260	COG3839G	ABC transporter ATP-binding protein	DEG10140013	MYPU_0260	MYPU_0260	Mycoplasma pulmonis UAB CTIP
-	MYPU_0250	COG1525L	lipoprotein	DEG10140012	MYPU_0250	MYPU_0250	Mycoplasma pulmonis UAB CTIP
-	MYPU_0240	-	lipoprotein	DEG10140011	MYPU_0240	MYPU_0240	Mycoplasma pulmonis UAB CTIP
-	MYPU_0230	COG0446R	NADH oxidase	DEG10140010	MYPU_0230	MYPU_0230	Mycoplasma pulmonis UAB CTIP
-	MYPU_0210	COG1249C	dihydrolipoamide dehydrogenase			MYPU_0210	Mycoplasma pulmonis UAB CTIP
-	MYPU_0190	-	lipoprotein			MYPU_0190	Mycoplasma pulmonis UAB CTIP
-	MYPU_0170	COG2190G	PTS system, glucose-specific IIABC component			MYPU_0170	Mycoplasma pulmonis UAB CTIP
trmE	MYPU_0130	COG0486R	tRNA modification GTPase TrmE	DEG10140009	MYPU_0130	MYPU_0130	Mycoplasma pulmonis UAB CTIP
rplA	MYPU_0100	COG0081J	50S ribosomal protein L1	DEG10140007	MYPU_0100	MYPU_0100	Mycoplasma pulmonis UAB CTIP
rplK	MYPU_0090	COG0080J	50S ribosomal protein L14	DEG10140006	MYPU_0090	MYPU_0090	Mycoplasma pulmonis UAB CTIP
-	MYPU_0080	COG0537FGR	HIT-like protein (cell cycle regulation)	DEG10140005	MYPU_0080	MYPU_0080	Mycoplasma pulmonis UAB CTIP
-	MYPU_0070	-	lipoprotein	DEG10140004	MYPU_0070	MYPU_0070	Mycoplasma pulmonis UAB CTIP
-	MYPU_0020	COG0592L	DNA polymerase III, beta chain	DEG10140002	MYPU_0020	MYPU_0020	Mycoplasma pulmonis UAB CTIP
dnaA	MYPU_0010	COG0593L	chromosome replication initiator DnaA	DEG10140001	MYPU_0010	MYPU_0010	Mycoplasma pulmonis UAB CTIP
-	MYPU_7800	COG0037D	hypothetical protein	DEG10140308	MYPU_7800		Mycoplasma pulmonis UAB CTIP
-	MYPU_7700	-	glycosyltransferase	DEG10140303	MYPU_7700		Mycoplasma pulmonis UAB CTIP
-	MYPU_7670	-	hypothetical protein	DEG10140301	MYPU_7670		Mycoplasma pulmonis UAB CTIP
-	MYPU_7660	COG1307S	hypothetical protein	DEG10140300	MYPU_7660		Mycoplasma pulmonis UAB CTIP
-	MYPU_7430	-	hypothetical protein	DEG10140294	MYPU_7430		Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	MYPU_7380	COG0534V	hypothetical protein	DEG10140292	MYPU_7380		Mycoplasma pulmonis UAB CTIP
-	MYPU_7260	COG0260E	aminopeptidase	DEG10140290	MYPU_7260		Mycoplasma pulmonis UAB CTIP
-	MYPU_7240	-	hypothetical protein	DEG10140289	MYPU_7240		Mycoplasma pulmonis UAB CTIP
-	MYPU_7220	COG3611L	hypothetical protein	DEG10140288	MYPU_7220		Mycoplasma pulmonis UAB CTIP
-	MYPU_7180	COG0301H	thiamine biosynthesis protein ThiI	DEG10140285	MYPU_7180		Mycoplasma pulmonis UAB CTIP
-	MYPU_7170	-	hypothetical protein	DEG10140284	MYPU_7170		Mycoplasma pulmonis UAB CTIP
-	MYPU_7120	COG0682M	prolipoprotein diacylglyceryl transferase	DEG10140280	MYPU_7120		Mycoplasma pulmonis UAB CTIP
-	MYPU_7110	COG1493T	HPr kinase/phosphorylase	DEG10140279	MYPU_7110		Mycoplasma pulmonis UAB CTIP
-	MYPU_7090	COG1109G	hypothetical protein	DEG10140278	MYPU_7090		Mycoplasma pulmonis UAB CTIP
-	MYPU_6920	COG0618R	hypothetical protein	DEG10140272	MYPU_6920		Mycoplasma pulmonis UAB CTIP
-	MYPU_6900	COG0488R	ABC transporter ATP-binding protein	DEG10140271	MYPU_6900		Mycoplasma pulmonis UAB CTIP
-	MYPU_6850	COG0515RTKL	serine/threonine-protein kinase PKNB	DEG10140267	MYPU_6850		Mycoplasma pulmonis UAB CTIP
-	MYPU_6710	COG1692S	hypothetical protein	DEG10140262	MYPU_6710		Mycoplasma pulmonis UAB CTIP
-	MYPU_6700	-	hypothetical protein	DEG10140261	MYPU_6700		Mycoplasma pulmonis UAB CTIP
-	MYPU_6690	-	hypothetical protein	DEG10140260	MYPU_6690		Mycoplasma pulmonis UAB CTIP
-	MYPU_6130	COG0009J	hypothetical protein	DEG10140249	MYPU_6130		Mycoplasma pulmonis UAB CTIP
-	MYPU_6030	COG1925G	phosphocarrier protein HPr (histidine-containing protein)	DEG10140245	MYPU_6030		Mycoplasma pulmonis UAB CTIP
-	MYPU_5660	COG0024J	methionine aminopeptidase	DEG10140220	MYPU_5660		Mycoplasma pulmonis UAB CTIP
-	MYPU_5560	COG0816L	hypothetical protein	DEG10140211	MYPU_5560		Mycoplasma pulmonis UAB CTIP
-	MYPU_5490	COG0561R	hypothetical protein	DEG10140208	MYPU_5490		Mycoplasma pulmonis UAB CTIP
nrdI	MYPU_5400	COG1780F	ribonucleotide reductase stimulatory protein	DEG10140204	MYPU_5400		Mycoplasma pulmonis UAB CTIP
-	MYPU_5190	COG0466O	heat shock ATP-dependent protease	DEG10140200	MYPU_5190		Mycoplasma pulmonis UAB CTIP
-	MYPU_5170	COG3887T	hypothetical protein	DEG10140198	MYPU_5170		Mycoplasma pulmonis UAB CTIP
-	MYPU_5140	COG1253R	hemolysin C	DEG10140195	MYPU_5140		Mycoplasma pulmonis UAB CTIP
-	MYPU_5060	COG0229O	methionine sulfoxide reductase B	DEG10140192	MYPU_5060		Mycoplasma pulmonis UAB CTIP
-	MYPU_4930	COG0275M	methyltransferase	DEG10140188	MYPU_4930		Mycoplasma pulmonis UAB CTIP
-	MYPU_4920	-	hypothetical protein	DEG10140187	MYPU_4920		Mycoplasma pulmonis UAB CTIP
-	MYPU_4880	COG0006E	XAA-Pro aminopeptidase	DEG10140184	MYPU_4880		Mycoplasma pulmonis UAB CTIP
-	MYPU_4840	COG0392S	hypothetical protein	DEG10140181	MYPU_4840		Mycoplasma pulmonis UAB CTIP
-	MYPU_4770	-	hypothetical protein	DEG10140179	MYPU_4770		Mycoplasma pulmonis UAB CTIP
-	MYPU_4760	-	hypothetical protein	DEG10140178	MYPU_4760		Mycoplasma pulmonis UAB CTIP
-	MYPU_4480	-	hypothetical protein	DEG10140164	MYPU_4480		Mycoplasma pulmonis UAB CTIP
-	MYPU_4440	COG2194R	hypothetical protein	DEG10140163	MYPU_4440		Mycoplasma pulmonis UAB CTIP
-	MYPU_4210	COG3356S	potassium channel protein	DEG10140155	MYPU_4210		Mycoplasma pulmonis UAB CTIP
-	MYPU_4080	COG2239P	Mg2+ transporter	DEG10140153	MYPU_4080		Mycoplasma pulmonis UAB CTIP
-	MYPU_4070	COG1624S	hypothetical protein	DEG10140152	MYPU_4070		Mycoplasma pulmonis UAB CTIP
-	MYPU_4060	COG2268S	hypothetical protein	DEG10140151	MYPU_4060		Mycoplasma pulmonis UAB CTIP
-	MYPU_3950	COG3421S	type III restriction-modification system: methylase	DEG10050383| DEG10050384	MYPU_3950		Mycoplasma pulmonis UAB CTIP
-	MYPU_3590	COG1307S	hypothetical protein	DEG10140138	MYPU_3590		Mycoplasma pulmonis UAB CTIP
smpB	MYPU_3520	COG0691O	SsrA-binding protein	DEG10140135	MYPU_3520		Mycoplasma pulmonis UAB CTIP
-	MYPU_3130	COG2755E	hypothetical protein	DEG10140119	MYPU_3130		Mycoplasma pulmonis UAB CTIP
acpD	MYPU_3120	COG1182I	azoreductase	DEG10060272| DEG10140118	MYPU_3120		Mycoplasma pulmonis UAB CTIP
-	MYPU_3050	COG3599D	hypothetical protein	DEG10140115	MYPU_3050		Mycoplasma pulmonis UAB CTIP
-	MYPU_3030	COG0219J	tRNA/rRNA methyltransferase	DEG10140114	MYPU_3030		Mycoplasma pulmonis UAB CTIP
-	MYPU_3010	COG0561R	hypothetical protein	DEG10140113	MYPU_3010		Mycoplasma pulmonis UAB CTIP
-	MYPU_2980	COG0564J	pseudouridylate synthase	DEG10140111	MYPU_2980		Mycoplasma pulmonis UAB CTIP
-	MYPU_2930	COG0534V	hypothetical protein	DEG10140109	MYPU_2930		Mycoplasma pulmonis UAB CTIP
-	MYPU_2560	COG4608E	hypothetical protein	DEG10140089	MYPU_2560		Mycoplasma pulmonis UAB CTIP
-	MYPU_2530	COG0445D	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	DEG10140088	MYPU_2530		Mycoplasma pulmonis UAB CTIP
-	MYPU_2510	-	hypothetical protein	DEG10140087	MYPU_2510		Mycoplasma pulmonis UAB CTIP
-	MYPU_2440	COG0561R	hypothetical protein	DEG10140085	MYPU_2440		Mycoplasma pulmonis UAB CTIP
-	MYPU_2330	COG2176L	hypothetical protein	DEG10140078	MYPU_2330		Mycoplasma pulmonis UAB CTIP
-	MYPU_2310	-	hypothetical protein	DEG10140077	MYPU_2310		Mycoplasma pulmonis UAB CTIP
frr	MYPU_2190	COG0233J	ribosome recycling factor	DEG10140072	MYPU_2190		Mycoplasma pulmonis UAB CTIP
-	MYPU_1990	COG0721J	hypothetical protein	DEG10140067	MYPU_1990		Mycoplasma pulmonis UAB CTIP
-	MYPU_1760	-	hypothetical protein	DEG10140061	MYPU_1760		Mycoplasma pulmonis UAB CTIP
-	MYPU_1740	COG0822C	nitrogen fixation protein NIFU	DEG10140060	MYPU_1740		Mycoplasma pulmonis UAB CTIP
-	MYPU_1730	COG0520E	nitrogen fixation protein NifS	DEG10140059	MYPU_1730		Mycoplasma pulmonis UAB CTIP
-	MYPU_1610	COG1461R	hypothetical protein	DEG10140055	MYPU_1610		Mycoplasma pulmonis UAB CTIP
-	MYPU_1550	COG0474P	cation-transporting P-type ATPase	DEG10140053	MYPU_1550		Mycoplasma pulmonis UAB CTIP
-	MYPU_1490	-	hypothetical protein	DEG10140049	MYPU_1490		Mycoplasma pulmonis UAB CTIP
-	MYPU_1460	COG3763S	hypothetical protein	DEG10140047	MYPU_1460		Mycoplasma pulmonis UAB CTIP
-	MYPU_1440	COG0168P	potassium uptake protein KTRB	DEG10140046	MYPU_1440		Mycoplasma pulmonis UAB CTIP
hrcA	MYPU_1420	COG1420K	heat-inducible transcription repressor	DEG10140044	MYPU_1420		Mycoplasma pulmonis UAB CTIP
-	MYPU_1370	COG0569P	potassium uptake protein KTRA	DEG10140042	MYPU_1370		Mycoplasma pulmonis UAB CTIP
-	MYPU_1330	-	hypothetical protein	DEG10140041	MYPU_1330		Mycoplasma pulmonis UAB CTIP
-	MYPU_1200	COG0802R	hypothetical protein	DEG10140037	MYPU_1200		Mycoplasma pulmonis UAB CTIP
-	MYPU_1190	COG1214O	hypothetical protein	DEG10140036	MYPU_1190		Mycoplasma pulmonis UAB CTIP
-	MYPU_1180	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10140035	MYPU_1180		Mycoplasma pulmonis UAB CTIP
-	MYPU_1060	COG2890J	protoporphirogen oxidase HEMK	DEG10140029	MYPU_1060		Mycoplasma pulmonis UAB CTIP
-	MYPU_0110	-	hypothetical protein	DEG10140008	MYPU_0110		Mycoplasma pulmonis UAB CTIP
-	MYPU_0060	-	hypothetical protein	DEG10140003	MYPU_0060		Mycoplasma pulmonis UAB CTIP

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
dnaA	SAOUHSC_00001	COG0593L	chromosomal replication initiation protein	DEG10020001	SAOUHSC_00001	SAOUHSC_00001	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00002	COG0592L	DNA polymerase III subunit beta	DEG10170002	SAOUHSC_00002	SAOUHSC_00002	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00005	COG0187L	DNA gyrase subunit B	DEG10170004	SAOUHSC_00005	SAOUHSC_00005	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00006	COG0188L	DNA gyrase subunit A	DEG10170005	SAOUHSC_00006	SAOUHSC_00006	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00009	COG0172J	seryl-tRNA synthetase	DEG10170006	SAOUHSC_00009	SAOUHSC_00009	Staphylococcus aureus NCTC 8325
rplI	SAOUHSC_00017	COG0359J	50S ribosomal protein L9			SAOUHSC_00017	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00018	COG0305L	replicative DNA helicase	DEG10170008	SAOUHSC_00018	SAOUHSC_00018	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00020	COG0745TK	two-component response regulator	DEG10170009	SAOUHSC_00020	SAOUHSC_00020	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00021	COG5002T	sensory box histidine kinase VicK	DEG10170010	SAOUHSC_00021	SAOUHSC_00021	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00221	COG1063ER	alcohol dehydrogenase			SAOUHSC_00221	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00223	COG1887M	teichoic acid biosynthesis protein F	DEG10170011	SAOUHSC_00223	SAOUHSC_00223	Staphylococcus aureus NCTC 8325
ispD	SAOUHSC_00225	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	DEG10170012	SAOUHSC_00225	SAOUHSC_00225	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00226	COG1063ER	hypothetical protein	DEG10170013	SAOUHSC_00226	SAOUHSC_00226	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00336	COG0183I	acetyl-CoA acetyltransferase	DEG10170015	SAOUHSC_00336	SAOUHSC_00336	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00346	COG0012J	GTP-dependent nucleic acid-binding protein EngD	DEG10020018	SAOUHSC_00346	SAOUHSC_00346	Staphylococcus aureus NCTC 8325
rpsF	SAOUHSC_00348	COG0360J	30S ribosomal protein S6	DEG10020019	SAOUHSC_00348	SAOUHSC_00348	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00349	COG0629L	bacteriophage L54a single-stranded DNA binding protein	DEG10020020	SAOUHSC_00349	SAOUHSC_00349	Staphylococcus aureus NCTC 8325
rpsR	SAOUHSC_00350	COG0238J	30S ribosomal protein S18	DEG10020021	SAOUHSC_00350	SAOUHSC_00350	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00359	COG0406G	phosphoglycerate mutase family protein			SAOUHSC_00359	Staphylococcus aureus NCTC 8325
guaA	SAOUHSC_00375	COG0519F	GMP synthase	DEG10170020	SAOUHSC_00375	SAOUHSC_00375	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00442	COG2812L	DNA polymerase III subunits gamma and tau	DEG10170021	SAOUHSC_00442	SAOUHSC_00442	Staphylococcus aureus NCTC 8325
tmk	SAOUHSC_00451	COG0125F	thymidylate kinase	DEG10020028	SAOUHSC_00451	SAOUHSC_00451	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00454	COG0470L	DNA polymerase III subunit delta'	DEG10170024	SAOUHSC_00454	SAOUHSC_00454	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00461	COG0143J	methionyl-tRNA synthetase	DEG10170025	SAOUHSC_00461	SAOUHSC_00461	Staphylococcus aureus NCTC 8325
glmU	SAOUHSC_00471	COG1207M	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	DEG10170026	SAOUHSC_00471	SAOUHSC_00471	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00472	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10020034	SAOUHSC_00472	SAOUHSC_00472	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00474	COG1825J	50S ribosomal protein L25/general stress protein Ctc	DEG10170028	SAOUHSC_00474	SAOUHSC_00474	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00475	COG0193J	peptidyl-tRNA hydrolase	DEG10020035	SAOUHSC_00475	SAOUHSC_00475	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00488	COG0031E	hypothetical protein			SAOUHSC_00488	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00489	COG0294H	dihydropteroate synthase	DEG10170032	SAOUHSC_00489	SAOUHSC_00489	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00490	COG1539H	dihydroneopterin aldolase	DEG10170033	SAOUHSC_00490	SAOUHSC_00490	Staphylococcus aureus NCTC 8325
lysS	SAOUHSC_00493	COG1190J	lysyl-tRNA synthetase	DEG10020039	SAOUHSC_00493	SAOUHSC_00493	Staphylococcus aureus NCTC 8325
gltX	SAOUHSC_00509	COG0008J	glutamyl-tRNA synthetase	DEG10020041	SAOUHSC_00509	SAOUHSC_00509	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00510	COG1045E	serine acetyltransferase	DEG10170037	SAOUHSC_00510	SAOUHSC_00510	Staphylococcus aureus NCTC 8325
cysS	SAOUHSC_00511	COG0215J	cysteinyl-tRNA synthetase	DEG10170038	SAOUHSC_00511	SAOUHSC_00511	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
secE	SAOUHSC_00516	COG0690U	preprotein translocase subunit SecE	DEG10170039	SAOUHSC_00516	SAOUHSC_00516	Staphylococcus aureus NCTC 8325
rplK	SAOUHSC_00518	COG0080J	50S ribosomal protein L11	DEG10020043	SAOUHSC_00518	SAOUHSC_00518	Staphylococcus aureus NCTC 8325
rplA	SAOUHSC_00519	COG0081J	50S ribosomal protein L1	DEG10170041	SAOUHSC_00519	SAOUHSC_00519	Staphylococcus aureus NCTC 8325
rplJ	SAOUHSC_00520	COG0244J	50S ribosomal protein L10	DEG10020045	SAOUHSC_00520	SAOUHSC_00520	Staphylococcus aureus NCTC 8325
rplL	SAOUHSC_00521	COG0222J	50S ribosomal protein L7/L12	DEG10020046	SAOUHSC_00521	SAOUHSC_00521	Staphylococcus aureus NCTC 8325
rpoB	SAOUHSC_00524	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10020047	SAOUHSC_00524	SAOUHSC_00524	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00525	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10170045	SAOUHSC_00525	SAOUHSC_00525	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00526	COG1358J	50S ribosomal protein L7Ae-like protein			SAOUHSC_00526	Staphylococcus aureus NCTC 8325
rpsL	SAOUHSC_00527	COG0048J	30S ribosomal protein S12	DEG10020049	SAOUHSC_00527	SAOUHSC_00527	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00528	COG0049J	30S ribosomal protein S7	DEG10020050	SAOUHSC_00528	SAOUHSC_00528	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00529	COG0480J	elongation factor G	DEG10020051	SAOUHSC_00529	SAOUHSC_00529	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00530	COG0050J	elongation factor Tu	DEG10020052	SAOUHSC_00530	SAOUHSC_00530	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00549	COG1469S	GTP cyclohydrolase	DEG10170050	SAOUHSC_00549	SAOUHSC_00549	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00558	COG0183I	acetyl-CoA acetyltransferase			SAOUHSC_00558	Staphylococcus aureus NCTC 8325
eutD	SAOUHSC_00574	COG0280C	phosphotransacetylase	DEG10020053	SAOUHSC_00574	SAOUHSC_00574	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00577	COG1577I	mevalonate kinase	DEG10170053	SAOUHSC_00577	SAOUHSC_00577	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00578	COG3407I	mevalonate diphosphate decarboxylase	DEG10170054	SAOUHSC_00578	SAOUHSC_00578	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00579	COG1577I	phosphomevalonate kinase	DEG10170055	SAOUHSC_00579	SAOUHSC_00579	Staphylococcus aureus NCTC 8325
argS	SAOUHSC_00611	COG0018J	arginyl-tRNA synthetase	DEG10170056	SAOUHSC_00611	SAOUHSC_00611	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00640	COG1922M	teichoic acid biosynthesis protein	DEG10170058	SAOUHSC_00640	SAOUHSC_00640	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00641	COG1134GM	teichoic acids export protein ATP-binding subunit	DEG10170059	SAOUHSC_00641	SAOUHSC_00641	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00642	COG1682GM	teichoic acid biosynthesis protein	DEG10170060	SAOUHSC_00642	SAOUHSC_00642	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00645	COG0615MI	glycerol-3-phosphate cytidylyltransferase	DEG10170062	SAOUHSC_00645	SAOUHSC_00645	Staphylococcus aureus NCTC 8325
nrdI	SAOUHSC_00741	COG1780F	ribonucleotide reductase stimulatory protein	DEG10170064	SAOUHSC_00741	SAOUHSC_00741	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00742	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10170065	SAOUHSC_00742	SAOUHSC_00742	Staphylococcus aureus NCTC 8325
nrdF	SAOUHSC_00743	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10170066	SAOUHSC_00743	SAOUHSC_00743	Staphylococcus aureus NCTC 8325
murB	SAOUHSC_00752	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10170067	SAOUHSC_00752	SAOUHSC_00752	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00756	COG1929G	hypothetical protein			SAOUHSC_00756	Staphylococcus aureus NCTC 8325
secA	SAOUHSC_00769	COG0653U	preprotein translocase subunit SecA	DEG10020064	SAOUHSC_00769	SAOUHSC_00769	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00771	COG1186J	peptide chain release factor 2			SAOUHSC_00771	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00785	COG0492O	thioredoxin reductase	DEG10170073	SAOUHSC_00785	SAOUHSC_00785	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00795	COG0057G	glyceraldehyde-3-phosphate dehydrogenase	DEG10020070	SAOUHSC_00795	SAOUHSC_00795	Staphylococcus aureus NCTC 8325
pgk	SAOUHSC_00796	COG0126G	phosphoglycerate kinase	DEG10020071	SAOUHSC_00796	SAOUHSC_00796	Staphylococcus aureus NCTC 8325
tpiA	SAOUHSC_00797	COG0149G	triosephosphate isomerase	DEG10170079	SAOUHSC_00797	SAOUHSC_00797	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00798	COG0696G	phosphoglyceromutase	DEG10170080	SAOUHSC_00798	SAOUHSC_00798	Staphylococcus aureus NCTC 8325
eno	SAOUHSC_00799	COG0148G	phosphopyruvate hydratase	DEG10020073	SAOUHSC_00799	SAOUHSC_00799	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00803	COG0557K	ribonuclease R	DEG10170082	SAOUHSC_00803	SAOUHSC_00803	Staphylococcus aureus NCTC 8325
smpB	SAOUHSC_00804	COG0691O	SsrA-binding protein	DEG10170083	SAOUHSC_00804	SAOUHSC_00804	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00827	COG0406G	hypothetical protein			SAOUHSC_00827	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00849	COG0520E	aminotransferase	DEG10170086	SAOUHSC_00849	SAOUHSC_00849	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_00869	COG1020Q	D-alanine--poly(phosphoribitol) ligase subunit 1	DEG10170090	SAOUHSC_00869	SAOUHSC_00869	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00871	COG0236IQ	D-alanine--poly(phosphoribitol) ligase subunit 2	DEG10170092	SAOUHSC_00871	SAOUHSC_00871	Staphylococcus aureus NCTC 8325
pgi	SAOUHSC_00900	COG0166G	glucose-6-phosphate isomerase	DEG10170096	SAOUHSC_00900	SAOUHSC_00900	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00903	COG0681U	signal peptidase IB			SAOUHSC_00903	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00920	COG0332I	3-oxoacyl-(acyl carrier protein) synthase III	DEG10170098	SAOUHSC_00920	SAOUHSC_00920	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00921	COG0304IQ	3-oxoacyl- synthase	DEG10170099	SAOUHSC_00921	SAOUHSC_00921	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00933	COG0180J	tryptophanyl-tRNA synthetase	DEG10020084	SAOUHSC_00933	SAOUHSC_00933	Staphylococcus aureus NCTC 8325
spxA	SAOUHSC_00934	COG1393P	transcriptional regulator Spx	DEG10170102	SAOUHSC_00934	SAOUHSC_00934	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00942	COG2357S	GTP pyrophosphokinase			SAOUHSC_00942	Staphylococcus aureus NCTC 8325
ppnK	SAOUHSC_00943	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10170103	SAOUHSC_00943	SAOUHSC_00943	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00947	COG0623I	enoyl-(acyl carrier protein) reductase	DEG10170104	SAOUHSC_00947	SAOUHSC_00947	Staphylococcus aureus NCTC 8325
-	SAOUHSC_00954	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase	DEG10170105	SAOUHSC_00954	SAOUHSC_00954	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01035	COG0595R	hypothetical protein	DEG10020093	SAOUHSC_01035	SAOUHSC_01035	Staphylococcus aureus NCTC 8325
def	SAOUHSC_01038	COG0242J	peptide deformylase	DEG10170112	SAOUHSC_01038	SAOUHSC_01038	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01040	COG1071C	pyruvate dehydrogenase complex, E1 component subunit alpha	DEG10170113	SAOUHSC_01040	SAOUHSC_01040	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01041	COG0022C	pyruvate dehydrogenase complex, E1 component subunit beta	DEG10020094	SAOUHSC_01041	SAOUHSC_01041	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01063	COG0772D	hypothetical protein	DEG10170115	SAOUHSC_01063	SAOUHSC_01063	Staphylococcus aureus NCTC 8325
coaD	SAOUHSC_01075	COG0669H	phosphopantetheine adenylyltransferase	DEG10170116	SAOUHSC_01075	SAOUHSC_01075	Staphylococcus aureus NCTC 8325
pheS	SAOUHSC_01092	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10170120	SAOUHSC_01092	SAOUHSC_01092	Staphylococcus aureus NCTC 8325
pheT	SAOUHSC_01093	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10170121	SAOUHSC_01093	SAOUHSC_01093	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01100	COG3118O	thioredoxin	DEG10170122	SAOUHSC_01100	SAOUHSC_01100	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01106	COG0796M	glutamate racemase	DEG10020105	SAOUHSC_01106	SAOUHSC_01106	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01145	COG0768M	penicillin-binding protein 1	DEG10170126	SAOUHSC_01145	SAOUHSC_01145	Staphylococcus aureus NCTC 8325
mraY	SAOUHSC_01146	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10020107	SAOUHSC_01146	SAOUHSC_01146	Staphylococcus aureus NCTC 8325
murD	SAOUHSC_01147	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	DEG10020108	SAOUHSC_01147	SAOUHSC_01147	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01150	COG0206D	cell division protein FtsZ	DEG10020110	SAOUHSC_01150	SAOUHSC_01150	Staphylococcus aureus NCTC 8325
ileS	SAOUHSC_01159	COG0060J	isoleucyl-tRNA synthetase	DEG10020112	SAOUHSC_01159	SAOUHSC_01159	Staphylococcus aureus NCTC 8325
gmk	SAOUHSC_01176	COG0194F	guanylate kinase	DEG10170134	SAOUHSC_01176	SAOUHSC_01176	Staphylococcus aureus NCTC 8325
rpoZ	SAOUHSC_01177	COG1758K	DNA-directed RNA polymerase subunit omega			SAOUHSC_01177	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01178	COG0452H	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	DEG10020114	SAOUHSC_01178	SAOUHSC_01178	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01179	COG1198L	primosomal protein N	DEG10170136	SAOUHSC_01179	SAOUHSC_01179	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01183	COG0223J	methionyl-tRNA formyltransferase	DEG10170137	SAOUHSC_01183	SAOUHSC_01183	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01189	COG0036G	ribulose-phosphate 3-epimerase	DEG10170139	SAOUHSC_01189	SAOUHSC_01189	Staphylococcus aureus NCTC 8325
rpmB	SAOUHSC_01191	COG0227J	50S ribosomal protein L28	DEG10020117	SAOUHSC_01191	SAOUHSC_01191	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01194	COG1200LK	ATP-dependent DNA helicase RecG			SAOUHSC_01194	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01197	COG0416I	glycerol-3-phosphate acyltransferase PlsX	DEG10170142	SAOUHSC_01197	SAOUHSC_01197	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01198	COG0331I	malonyl CoA-acyl carrier protein transacylase	DEG10170143	SAOUHSC_01198	SAOUHSC_01198	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01199	COG1028IQR	3-oxoacyl-(acyl-carrier-protein) reductase			SAOUHSC_01199	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_01205	COG0552U	signal recognition particle-docking protein FtsY	DEG10170146	SAOUHSC_01205	SAOUHSC_01205	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01207	COG0541U	signal recognition particle protein	DEG10170147	SAOUHSC_01207	SAOUHSC_01207	Staphylococcus aureus NCTC 8325
rpsP	SAOUHSC_01208	COG0228J	30S ribosomal protein S16	DEG10020125	SAOUHSC_01208	SAOUHSC_01208	Staphylococcus aureus NCTC 8325
trmD	SAOUHSC_01210	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10170150	SAOUHSC_01210	SAOUHSC_01210	Staphylococcus aureus NCTC 8325
rplS	SAOUHSC_01211	COG0335J	50S ribosomal protein L19	DEG10170151	SAOUHSC_01211	SAOUHSC_01211	Staphylococcus aureus NCTC 8325
rbgA	SAOUHSC_01214	COG1161R	ribosomal biogenesis GTPase	DEG10170152	SAOUHSC_01214	SAOUHSC_01214	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01222	COG0550L	DNA topoisomerase I	DEG10170154	SAOUHSC_01222	SAOUHSC_01222	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01223	COG1206J	tRNA (uracil-5-)-methyltransferase Gid	DEG10020130	SAOUHSC_01223	SAOUHSC_01223	Staphylococcus aureus NCTC 8325
tsf	SAOUHSC_01234	COG0264J	elongation factor Ts	DEG10170156	SAOUHSC_01234	SAOUHSC_01234	Staphylococcus aureus NCTC 8325
pyrH	SAOUHSC_01235	COG0528F	uridylate kinase	DEG10170157	SAOUHSC_01235	SAOUHSC_01235	Staphylococcus aureus NCTC 8325
frr	SAOUHSC_01236	COG0233J	ribosome recycling factor	DEG10170158	SAOUHSC_01236	SAOUHSC_01236	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01237	COG0020I	undecaprenyl pyrophosphate synthase	DEG10170159	SAOUHSC_01237	SAOUHSC_01237	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01238	COG0575I	phosphatidate cytidylyltransferase	DEG10020133	SAOUHSC_01238	SAOUHSC_01238	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01240	COG0442J	prolyl-tRNA synthetase	DEG10170161	SAOUHSC_01240	SAOUHSC_01240	Staphylococcus aureus NCTC 8325
polC	SAOUHSC_01241	COG2176L	DNA polymerase III PolC			SAOUHSC_01241	Staphylococcus aureus NCTC 8325
nusA	SAOUHSC_01243	COG0195K	transcription elongation factor NusA	DEG10020136	SAOUHSC_01243	SAOUHSC_01243	Staphylococcus aureus NCTC 8325
infB	SAOUHSC_01246	COG0532J	translation initiation factor IF-2	DEG10170166	SAOUHSC_01246	SAOUHSC_01246	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01249	COG0196H	riboflavin biosynthesis protein RibF	DEG10170167	SAOUHSC_01249	SAOUHSC_01249	Staphylococcus aureus NCTC 8325
rpsO	SAOUHSC_01250	COG0184J	30S ribosomal protein S15	DEG10170168	SAOUHSC_01250	SAOUHSC_01250	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01252	COG0595R	hypothetical protein	DEG10170169	SAOUHSC_01252	SAOUHSC_01252	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01257	COG1028IQR	hypothetical protein			SAOUHSC_01257	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01260	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	DEG10020141	SAOUHSC_01260	SAOUHSC_01260	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01287	COG0174E	glutamine synthetase	DEG10170172	SAOUHSC_01287	SAOUHSC_01287	Staphylococcus aureus NCTC 8325
rpmG	SAOUHSC_01328	COG0267J	50S ribosomal protein L33			SAOUHSC_01328	Staphylococcus aureus NCTC 8325
rpsN	SAOUHSC_01329	COG0199J	30S ribosomal protein S14			SAOUHSC_01329	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01333	COG1974KT	LexA repressor	DEG10170173	SAOUHSC_01333	SAOUHSC_01333	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01337	COG0021G	transketolase	DEG10170174	SAOUHSC_01337	SAOUHSC_01337	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01350	COG0344S	hypothetical protein	DEG10170175	SAOUHSC_01350	SAOUHSC_01350	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01351	COG0187L	DNA topoisomerase IV subunit B	DEG10170176	SAOUHSC_01351	SAOUHSC_01351	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01352	COG0188L	DNA topoisomerase IV subunit A	DEG10170177	SAOUHSC_01352	SAOUHSC_01352	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01361	COG1316K	transcriptional regulator	DEG10170179	SAOUHSC_01361	SAOUHSC_01361	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01373	COG2348V	methicillin resistance factor FemA	DEG10170181	SAOUHSC_01373	SAOUHSC_01373	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01374	COG2348V	methicillin resistance factor	DEG10170182	SAOUHSC_01374	SAOUHSC_01374	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01400	COG0787M	alanine racemase			SAOUHSC_01400	Staphylococcus aureus NCTC 8325
murG	SAOUHSC_01424	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	DEG10170183	SAOUHSC_01424	SAOUHSC_01424	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01434	COG0262H	dihydrofolate reductase	DEG10020156	SAOUHSC_01434	SAOUHSC_01434	Staphylococcus aureus NCTC 8325
thyA	SAOUHSC_01435	COG0207F	thymidylate synthase	DEG10170185	SAOUHSC_01435	SAOUHSC_01435	Staphylococcus aureus NCTC 8325
recU	SAOUHSC_01466	COG3331R	Holliday junction-specific endonuclease	DEG10170187	SAOUHSC_01466	SAOUHSC_01466	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01467	COG0744M	penicillin-binding protein 2	DEG10170188	SAOUHSC_01467	SAOUHSC_01467	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_01473	COG0340H	bifunctional biotin operon repressor/biotin--[acetyl-CoA-carboxylase] synthetase BirA	DEG10170190	SAOUHSC_01473	SAOUHSC_01473	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01474	COG0617J	tRNA CCA-pyrophosphorylase	DEG10170191	SAOUHSC_01474	SAOUHSC_01474	Staphylococcus aureus NCTC 8325
ndk	SAOUHSC_01485	COG0105F	nucleoside diphosphate kinase			SAOUHSC_01485	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01490	COG0776L	DNA-binding protein HU	DEG10170193	SAOUHSC_01490	SAOUHSC_01490	Staphylococcus aureus NCTC 8325
engA	SAOUHSC_01492	COG1160R	GTP-binding protein EngA	DEG10020161	SAOUHSC_01492	SAOUHSC_01492	Staphylococcus aureus NCTC 8325
rpsA	SAOUHSC_01493	COG0539J	30S ribosomal protein S1			SAOUHSC_01493	Staphylococcus aureus NCTC 8325
cmk	SAOUHSC_01496	COG0283F	cytidylate kinase	DEG10020162	SAOUHSC_01496	SAOUHSC_01496	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01592	COG0735P	transcriptional regulator Fur	DEG10170198	SAOUHSC_01592	SAOUHSC_01592	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01599	COG0364G	glucose-6-phosphate 1-dehydrogenase	DEG10170200	SAOUHSC_01599	SAOUHSC_01599	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01605	COG0362G	6-phosphogluconate dehydrogenase	DEG10170201	SAOUHSC_01605	SAOUHSC_01605	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01623	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	DEG10170202	SAOUHSC_01623	SAOUHSC_01623	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01624	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein	DEG10170203	SAOUHSC_01624	SAOUHSC_01624	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01625	COG0231J	elongation factor P	DEG10020167	SAOUHSC_01625	SAOUHSC_01625	Staphylococcus aureus NCTC 8325
rpmG	SAOUHSC_01651	COG0267J	50S ribosomal protein L33	DEG10020168	SAOUHSC_01651	SAOUHSC_01651	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01662	COG0568K	RNA polymerase sigma factor RpoD	DEG10020169	SAOUHSC_01662	SAOUHSC_01662	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01663	COG0358L	DNA primase	DEG10170208	SAOUHSC_01663	SAOUHSC_01663	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01666	COG0423J	glycyl-tRNA synthetase	DEG10170209	SAOUHSC_01666	SAOUHSC_01666	Staphylococcus aureus NCTC 8325
rpsU	SAOUHSC_01678	COG0828J	30S ribosomal protein S21	DEG10020171	SAOUHSC_01678	SAOUHSC_01678	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01682	COG0484O	chaperone protein DnaJ	DEG10020172	SAOUHSC_01682	SAOUHSC_01682	Staphylococcus aureus NCTC 8325
dnaK	SAOUHSC_01683	COG0443O	molecular chaperone DnaK	DEG10020173	SAOUHSC_01683	SAOUHSC_01683	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01684	COG0576O	heat shock protein GrpE	DEG10170215	SAOUHSC_01684	SAOUHSC_01684	Staphylococcus aureus NCTC 8325
rpsT	SAOUHSC_01689	COG0268J	30S ribosomal protein S20	DEG10020175	SAOUHSC_01689	SAOUHSC_01689	Staphylococcus aureus NCTC 8325
holA	SAOUHSC_01690	COG1466L	DNA polymerase III subunit delta	DEG10170216	SAOUHSC_01690	SAOUHSC_01690	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01697	COG1057H	nicotinate (nicotinamide) nucleotide adenylyltransferase	DEG10170217	SAOUHSC_01697	SAOUHSC_01697	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01709	COG0439I	acetyl-CoA carboxylase biotin carboxylase			SAOUHSC_01709	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01710	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein			SAOUHSC_01710	Staphylococcus aureus NCTC 8325
greA	SAOUHSC_01714	COG0782K	transcription elongation factor GreA	DEG10020176	SAOUHSC_01714	SAOUHSC_01714	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01720	COG0816L	Holliday junction resolvase-like protein	DEG10170221	SAOUHSC_01720	SAOUHSC_01720	Staphylococcus aureus NCTC 8325
alaS	SAOUHSC_01722	COG0013J	alanyl-tRNA synthetase	DEG10020178	SAOUHSC_01722	SAOUHSC_01722	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01727	COG1104E	hypothetical protein	DEG10170226	SAOUHSC_01727	SAOUHSC_01727	Staphylococcus aureus NCTC 8325
aspS	SAOUHSC_01737	COG0173J	aspartyl-tRNA synthetase	DEG10170227	SAOUHSC_01737	SAOUHSC_01737	Staphylococcus aureus NCTC 8325
hisS	SAOUHSC_01738	COG0124J	histidyl-tRNA synthetase	DEG10020182	SAOUHSC_01738	SAOUHSC_01738	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01741	COG1490J	D-tyrosyl-tRNA(Tyr) deacylase	DEG10170230	SAOUHSC_01741	SAOUHSC_01741	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01742	COG0317TK	GTP pyrophosphokinase	DEG10170231	SAOUHSC_01742	SAOUHSC_01742	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01746	COG0341U	bifunctional preprotein translocase subunit SecD/SecF	DEG10170232	SAOUHSC_01746	SAOUHSC_01746	Staphylococcus aureus NCTC 8325
ruvB	SAOUHSC_01750	COG2255L	Holliday junction DNA helicase RuvB	DEG10170233	SAOUHSC_01750	SAOUHSC_01750	Staphylococcus aureus NCTC 8325
ruvA	SAOUHSC_01751	COG0632L	Holliday junction DNA helicase RuvA	DEG10170234	SAOUHSC_01751	SAOUHSC_01751	Staphylococcus aureus NCTC 8325
obgE	SAOUHSC_01753	COG0536R	GTPase ObgE	DEG10020183	SAOUHSC_01753	SAOUHSC_01753	Staphylococcus aureus NCTC 8325
rpmA	SAOUHSC_01755	COG0211J	50S ribosomal protein L27	DEG10020184	SAOUHSC_01755	SAOUHSC_01755	Staphylococcus aureus NCTC 8325
rplU	SAOUHSC_01757	COG0261J	50S ribosomal protein L21	DEG10020185	SAOUHSC_01757	SAOUHSC_01757	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01766	COG0285H	folylpolyglutamate synthase/dihydrofolate synthase	DEG10170239	SAOUHSC_01766	SAOUHSC_01766	Staphylococcus aureus NCTC 8325
valS	SAOUHSC_01767	COG0525J	valyl-tRNA synthetase	DEG10020186	SAOUHSC_01767	SAOUHSC_01767	Staphylococcus aureus NCTC 8325
engB	SAOUHSC_01777	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10170242	SAOUHSC_01777	SAOUHSC_01777	Staphylococcus aureus NCTC 8325
rplT	SAOUHSC_01784	COG0292J	50S ribosomal protein L20	DEG10020189	SAOUHSC_01784	SAOUHSC_01784	Staphylococcus aureus NCTC 8325
rpmI	SAOUHSC_01785	COG0291J	50S ribosomal protein L35	DEG10020190	SAOUHSC_01785	SAOUHSC_01785	Staphylococcus aureus NCTC 8325
infC	SAOUHSC_01786	COG0290J	translation initiation factor IF-3	DEG10170246	SAOUHSC_01786	SAOUHSC_01786	Staphylococcus aureus NCTC 8325
thrS	SAOUHSC_01788	COG0441J	threonyl-tRNA synthetase	DEG10170248	SAOUHSC_01788	SAOUHSC_01788	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01791	COG1484L	primosomal protein DnaI	DEG10170249	SAOUHSC_01791	SAOUHSC_01791	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_01794	COG0057G	glyceraldehyde 3-phosphate dehydrogenase 2	DEG10020194	SAOUHSC_01794	SAOUHSC_01794	Staphylococcus aureus NCTC 8325
coaE	SAOUHSC_01795	COG0237H	dephospho-CoA kinase	DEG10170251	SAOUHSC_01795	SAOUHSC_01795	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01797	COG0749L	DNA polymerase I			SAOUHSC_01797	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01801	COG0538C	isocitrate dehydrogenase			SAOUHSC_01801	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01806	COG0469G	pyruvate kinase	DEG10020196	SAOUHSC_01806	SAOUHSC_01806	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01807	COG0205G	6-phosphofructokinase	DEG10020197	SAOUHSC_01807	SAOUHSC_01807	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01808	COG0825I	acetyl-CoA carboxylase carboxyltransferase subunit alpha	DEG10170254	SAOUHSC_01808	SAOUHSC_01808	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01809	COG0777I	acetyl-CoA carboxylase subunit beta	DEG10020199	SAOUHSC_01809	SAOUHSC_01809	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01811	COG0587L	DNA polymerase III subunit alpha superfamily protein	DEG10170256	SAOUHSC_01811	SAOUHSC_01811	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01825	COG1104E	hypothetical protein			SAOUHSC_01825	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01827	COG4477D	septation ring formation regulator EzrA	DEG10170257	SAOUHSC_01827	SAOUHSC_01827	Staphylococcus aureus NCTC 8325
rpsD	SAOUHSC_01829	COG0522J	30S ribosomal protein S4	DEG10020203	SAOUHSC_01829	SAOUHSC_01829	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01833	COG0111HE	D-3-phosphoglycerate dehydrogenase			SAOUHSC_01833	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01837	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein	DEG10170259	SAOUHSC_01837	SAOUHSC_01837	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01839	COG0162J	tyrosyl-tRNA synthetase	DEG10020205	SAOUHSC_01839	SAOUHSC_01839	Staphylococcus aureus NCTC 8325
murC	SAOUHSC_01856	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10020208	SAOUHSC_01856	SAOUHSC_01856	Staphylococcus aureus NCTC 8325
leuS	SAOUHSC_01875	COG0495J	leucyl-tRNA synthetase	DEG10170264	SAOUHSC_01875	SAOUHSC_01875	Staphylococcus aureus NCTC 8325
-	SAOUHSC_01909	COG0192H	S-adenosylmethionine synthetase	DEG10170266	SAOUHSC_01909	SAOUHSC_01909	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02008	-	hypothetical protein			SAOUHSC_02008	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02009	COG1134GM	hypothetical protein			SAOUHSC_02009	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02067	COG0305L	bacteriophage L54a DnaB-like helicase family protein			SAOUHSC_02067	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02102	COG0024J	methionine aminopeptidase	DEG10020214	SAOUHSC_02102	SAOUHSC_02102	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02110	COG0847L	hypothetical protein			SAOUHSC_02110	Staphylococcus aureus NCTC 8325
gatB	SAOUHSC_02116	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10020216	SAOUHSC_02116	SAOUHSC_02116	Staphylococcus aureus NCTC 8325
gatA	SAOUHSC_02117	COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A	DEG10170275	SAOUHSC_02117	SAOUHSC_02117	Staphylococcus aureus NCTC 8325
gatC	SAOUHSC_02118	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10170276	SAOUHSC_02118	SAOUHSC_02118	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02122	COG0272L	NAD-dependent DNA ligase	DEG10170277	SAOUHSC_02122	SAOUHSC_02122	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02123	COG0210L	ATP-dependent DNA helicase PcrA	DEG10170278	SAOUHSC_02123	SAOUHSC_02123	Staphylococcus aureus NCTC 8325
nadE	SAOUHSC_02132	COG0171H	NAD synthetase	DEG10170279	SAOUHSC_02132	SAOUHSC_02132	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02133	COG1488H	nicotinate phosphoribosyltransferase	DEG10170280	SAOUHSC_02133	SAOUHSC_02133	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02140	COG1227C	manganese-dependent inorganic pyrophosphatase	DEG10170281	SAOUHSC_02140	SAOUHSC_02140	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02141	-	hypothetical protein			SAOUHSC_02141	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02143	COG2706G	hypothetical protein			SAOUHSC_02143	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02145	-	hypothetical protein			SAOUHSC_02145	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02146	COG4927R	hypothetical protein			SAOUHSC_02146	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02147	-	hypothetical protein			SAOUHSC_02147	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02149	-	hypothetical protein			SAOUHSC_02149	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02150	-	hypothetical protein			SAOUHSC_02150	Staphylococcus aureus NCTC 8325
groEL	SAOUHSC_02254	COG0459O	chaperonin GroEL	DEG10170284	SAOUHSC_02254	SAOUHSC_02254	Staphylococcus aureus NCTC 8325
groES	SAOUHSC_02255	COG0234O	co-chaperonin GroES	DEG10020224	SAOUHSC_02255	SAOUHSC_02255	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02298	COG1191K	RNA polymerase sigma factor SigB			SAOUHSC_02298	Staphylococcus aureus NCTC 8325
acpS	SAOUHSC_02306	COG0736I	4'-phosphopantetheinyl transferase	DEG10170290	SAOUHSC_02306	SAOUHSC_02306	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02317	COG0770M	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	DEG10170291	SAOUHSC_02317	SAOUHSC_02317	Staphylococcus aureus NCTC 8325
ddl	SAOUHSC_02318	COG1181M	D-alanyl-alanine synthetase A	DEG10020230	SAOUHSC_02318	SAOUHSC_02318	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02327	COG0706U	hypothetical protein	DEG10170293	SAOUHSC_02327	SAOUHSC_02327	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_02334	COG0629L	bacteriophage L54a single-stranded DNA binding protein			SAOUHSC_02334	Staphylococcus aureus NCTC 8325
fabZ	SAOUHSC_02336	COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	DEG10170294	SAOUHSC_02336	SAOUHSC_02336	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02337	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	DEG10170295	SAOUHSC_02337	SAOUHSC_02337	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02347	COG0711C	F0F1 ATP synthase subunit B	DEG10020232	SAOUHSC_02347	SAOUHSC_02347	Staphylococcus aureus NCTC 8325
prfA	SAOUHSC_02359	COG0216J	peptide chain release factor 1	DEG10020235	SAOUHSC_02359	SAOUHSC_02359	Staphylococcus aureus NCTC 8325
rpmE2	SAOUHSC_02361	COG0254J	50S ribosomal protein L31 type B	DEG10020237	SAOUHSC_02361	SAOUHSC_02361	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02366	COG0191G	fructose-bisphosphate aldolase	DEG10020239	SAOUHSC_02366	SAOUHSC_02366	Staphylococcus aureus NCTC 8325
pyrG	SAOUHSC_02368	COG0504F	CTP synthetase	DEG10170300	SAOUHSC_02368	SAOUHSC_02368	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02371	COG5146H	pantothenate kinase	DEG10170301	SAOUHSC_02371	SAOUHSC_02371	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02399	COG0449M	glucosamine--fructose-6-phosphate aminotransferase	DEG10170302	SAOUHSC_02399	SAOUHSC_02399	Staphylococcus aureus NCTC 8325
glmM	SAOUHSC_02405	COG1109G	phosphoglucosamine mutase	DEG10170303	SAOUHSC_02405	SAOUHSC_02405	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02453	COG1105G	tagatose-6-phosphate kinase			SAOUHSC_02453	Staphylococcus aureus NCTC 8325
rpsI	SAOUHSC_02477	COG0103J	30S ribosomal protein S9	DEG10170305	SAOUHSC_02477	SAOUHSC_02477	Staphylococcus aureus NCTC 8325
rplM	SAOUHSC_02478	COG0102J	50S ribosomal protein L13	DEG10020248	SAOUHSC_02478	SAOUHSC_02478	Staphylococcus aureus NCTC 8325
rplQ	SAOUHSC_02484	COG0203J	50S ribosomal protein L17	DEG10020251	SAOUHSC_02484	SAOUHSC_02484	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02485	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10020252	SAOUHSC_02485	SAOUHSC_02485	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02486	COG0100J	30S ribosomal protein S11	DEG10020253	SAOUHSC_02486	SAOUHSC_02486	Staphylococcus aureus NCTC 8325
rpsM	SAOUHSC_02487	COG0099J	30S ribosomal protein S13	DEG10020254	SAOUHSC_02487	SAOUHSC_02487	Staphylococcus aureus NCTC 8325
rpmJ	SAOUHSC_02488	COG0257J	50S ribosomal protein L36	DEG10020255	SAOUHSC_02488	SAOUHSC_02488	Staphylococcus aureus NCTC 8325
infA	SAOUHSC_02489	COG0361J	translation initiation factor IF-1	DEG10020256	SAOUHSC_02489	SAOUHSC_02489	Staphylococcus aureus NCTC 8325
adk	SAOUHSC_02490	COG0563F	adenylate kinase	DEG10020257	SAOUHSC_02490	SAOUHSC_02490	Staphylococcus aureus NCTC 8325
secY	SAOUHSC_02491	COG0201U	preprotein translocase subunit SecY	DEG10020258	SAOUHSC_02491	SAOUHSC_02491	Staphylococcus aureus NCTC 8325
rplO	SAOUHSC_02492	COG0200J	50S ribosomal protein L15	DEG10020259	SAOUHSC_02492	SAOUHSC_02492	Staphylococcus aureus NCTC 8325
rpmD	SAOUHSC_02493	COG1841J	50S ribosomal protein L30	DEG10020260	SAOUHSC_02493	SAOUHSC_02493	Staphylococcus aureus NCTC 8325
rpsE	SAOUHSC_02494	COG0098J	30S ribosomal protein S5	DEG10020261	SAOUHSC_02494	SAOUHSC_02494	Staphylococcus aureus NCTC 8325
rplR	SAOUHSC_02495	COG0256J	50S ribosomal protein L18	DEG10020262	SAOUHSC_02495	SAOUHSC_02495	Staphylococcus aureus NCTC 8325
rplF	SAOUHSC_02496	COG0097J	50S ribosomal protein L6	DEG10020263	SAOUHSC_02496	SAOUHSC_02496	Staphylococcus aureus NCTC 8325
rpsH	SAOUHSC_02498	COG0096J	30S ribosomal protein S8	DEG10020264	SAOUHSC_02498	SAOUHSC_02498	Staphylococcus aureus NCTC 8325
rpsN	SAOUHSC_02499	COG0199J	30S ribosomal protein S14	DEG10020265	SAOUHSC_02499	SAOUHSC_02499	Staphylococcus aureus NCTC 8325
rplE	SAOUHSC_02500	COG0094J	50S ribosomal protein L5	DEG10020266	SAOUHSC_02500	SAOUHSC_02500	Staphylococcus aureus NCTC 8325
rplX	SAOUHSC_02501	COG0198J	50S ribosomal protein L24	DEG10020267	SAOUHSC_02501	SAOUHSC_02501	Staphylococcus aureus NCTC 8325
rplN	SAOUHSC_02502	COG0093J	50S ribosomal protein L14	DEG10020268	SAOUHSC_02502	SAOUHSC_02502	Staphylococcus aureus NCTC 8325
rpsQ	SAOUHSC_02503	COG0186J	30S ribosomal protein S17	DEG10170325	SAOUHSC_02503	SAOUHSC_02503	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02504	COG0255J	50S ribosomal protein L29	DEG10020270	SAOUHSC_02504	SAOUHSC_02504	Staphylococcus aureus NCTC 8325
rplP	SAOUHSC_02505	COG0197J	50S ribosomal protein L16	DEG10020271	SAOUHSC_02505	SAOUHSC_02505	Staphylococcus aureus NCTC 8325
rpsC	SAOUHSC_02506	COG0092J	30S ribosomal protein S3	DEG10020272	SAOUHSC_02506	SAOUHSC_02506	Staphylococcus aureus NCTC 8325
rplV	SAOUHSC_02507	COG0091J	50S ribosomal protein L22	DEG10020273	SAOUHSC_02507	SAOUHSC_02507	Staphylococcus aureus NCTC 8325
rpsS	SAOUHSC_02508	COG0185J	30S ribosomal protein S19	DEG10020274	SAOUHSC_02508	SAOUHSC_02508	Staphylococcus aureus NCTC 8325
rplB	SAOUHSC_02509	COG0090J	50S ribosomal protein L2	DEG10020275	SAOUHSC_02509	SAOUHSC_02509	Staphylococcus aureus NCTC 8325
rplW	SAOUHSC_02510	COG0089J	50S ribosomal protein L23	DEG10020276	SAOUHSC_02510	SAOUHSC_02510	Staphylococcus aureus NCTC 8325
rplD	SAOUHSC_02511	COG0088J	50S ribosomal protein L4	DEG10020277	SAOUHSC_02511	SAOUHSC_02511	Staphylococcus aureus NCTC 8325
rplC	SAOUHSC_02512	COG0087J	50S ribosomal protein L3	DEG10020278	SAOUHSC_02512	SAOUHSC_02512	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02512a	-	30S ribosomal protein S10	DEG10020279	SAOUHSC_02512a	SAOUHSC_02512a	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02517	COG0550L	DNA topoisomerase III			SAOUHSC_02517	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02527	COG2348V	peptidoglycan pentaglycine interpeptide biosynthesis protein FmhB	DEG10170335	SAOUHSC_02527	SAOUHSC_02527	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02612	COG0120G	ribose-5-phosphate isomerase A	DEG10170339	SAOUHSC_02612	SAOUHSC_02612	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02623	COG1304C	isopentenyl pyrophosphate isomerase	DEG10170340	SAOUHSC_02623	SAOUHSC_02623	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02654	COG0492O	hypothetical protein			SAOUHSC_02654	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02723	COG1929G	glycerate kinase			SAOUHSC_02723	Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_02859	COG1257I	hydroxymethylglutaryl-CoA reductase	DEG10170345	SAOUHSC_02859	SAOUHSC_02859	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02860	COG3425I	HMG-CoA synthase	DEG10170346	SAOUHSC_02860	SAOUHSC_02860	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02926	COG3588G	fructose-1,6-bisphosphate aldolase			SAOUHSC_02926	Staphylococcus aureus NCTC 8325
-	SAOUHSC_02985	COG0653U	preprotein translocase subunit SecA			SAOUHSC_02985	Staphylococcus aureus NCTC 8325
secY	SAOUHSC_02989	COG0201U	preprotein translocase subunit SecY			SAOUHSC_02989	Staphylococcus aureus NCTC 8325
-	SAOUHSC_03052	COG0445D	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	DEG10170348	SAOUHSC_03052	SAOUHSC_03052	Staphylococcus aureus NCTC 8325
rpmH	SAOUHSC_03055	-	50S ribosomal protein L34	DEG10020302	SAOUHSC_03055	SAOUHSC_03055	Staphylococcus aureus NCTC 8325
recF	SAOUHSC_00004	COG1195L	recombination protein F	DEG10020002	SAOUHSC_00004		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00101	COG1015G	phosphopentomutase	DEG10020010	SAOUHSC_00101		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00202	COG3189S	hypothetical protein	DEG10020015	SAOUHSC_00202		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00374	COG0516F	inosine-5'-monophosphate dehydrogenase	DEG10020023	SAOUHSC_00374		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00444	COG0718S	hypothetical protein	DEG10020027	SAOUHSC_00444		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00458	COG2827L	hypothetical protein	DEG10020029	SAOUHSC_00458		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00459	COG0313R	hypothetical protein	DEG10020030	SAOUHSC_00459		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00462	COG0084L	hypothetical protein	DEG10020032	SAOUHSC_00462		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00481	COG1188J	hypothetical protein	DEG10020036	SAOUHSC_00481		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00486	COG0465O	hypothetical protein	DEG10020038	SAOUHSC_00486		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00505	COG0542O	endopeptidase	DEG10020040	SAOUHSC_00505		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00667	COG1136V	ABC transporter ATP-binding protein	DEG10020057	SAOUHSC_00667		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00781	COG1493T	HPr kinase/phosphorylase	DEG10020068	SAOUHSC_00781		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00789	COG1481S	hypothetical protein	DEG10020069	SAOUHSC_00789		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00800	-	hypothetical protein	DEG10020074	SAOUHSC_00800		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00845	-	hypothetical protein	DEG10020077	SAOUHSC_00845		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00847	COG0396O	ABC transporter ATP-binding protein	DEG10020078	SAOUHSC_00847		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00861	COG0320H	lipoyl synthase	DEG10020080	SAOUHSC_00861		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00925	COG0444EP	hypothetical protein	DEG10020083	SAOUHSC_00925		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01001	COG0843C	quinol oxidase subunit I	DEG10020088	SAOUHSC_01001		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01010	COG0152F	phosphoribosylaminoimidazole-succinocarboxamide synthase	DEG10020089	SAOUHSC_01010		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01028	COG1925G	phosphocarrier protein HPr	DEG10020091	SAOUHSC_01028		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01046	COG3842E	ABC transporter	DEG10020097	SAOUHSC_01046		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01053	COG1914P	manganese transport protein MntH	DEG10020098	SAOUHSC_01053		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01058	COG1217T	GTP-binding protein TypA	DEG10020099	SAOUHSC_01058		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01149	COG0849D	cell division protein	DEG10020109	SAOUHSC_01149		Staphylococcus aureus NCTC 8325
pyrC	SAOUHSC_01168	COG0044F	dihydroorotase	DEG10020113	SAOUHSC_01168		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01187	COG2815S	hypothetical protein	DEG10020116	SAOUHSC_01187		Staphylococcus aureus NCTC 8325
rnc	SAOUHSC_01203	COG0571K	ribonuclease III	DEG10020121	SAOUHSC_01203		Staphylococcus aureus NCTC 8325
rbfA	SAOUHSC_01247	COG0858J	ribosome-binding factor A	DEG10020138	SAOUHSC_01247		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01251	COG1185J	polynucleotide phosphorylase/polyadenylase	DEG10020139	SAOUHSC_01251		Staphylococcus aureus NCTC 8325
recA	SAOUHSC_01262	COG0468L	recombinase A	DEG10020142	SAOUHSC_01262		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01283	COG2262R	hypothetical protein	DEG10020145	SAOUHSC_01283		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01336	COG4224S	hypothetical protein	DEG10020146	SAOUHSC_01336		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01356	COG3711K	transcription antiterminator	DEG10020151	SAOUHSC_01356		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01425	COG1670J	hypothetical protein	DEG10020155	SAOUHSC_01425		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01721	COG4472S	hypothetical protein	DEG10020177	SAOUHSC_01721		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01772	COG0113H	delta-aminolevulinic acid dehydratase	DEG10020187	SAOUHSC_01772		Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
nrdR	SAOUHSC_01793	COG1327K	transcriptional regulator NrdR	DEG10020193	SAOUHSC_01793		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01820	COG0282C	acetate kinase	DEG10020202	SAOUHSC_01820		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01850	COG1609K	catabolite control protein A	DEG10020207	SAOUHSC_01850		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01858	COG0073R	hypothetical protein	DEG10020209	SAOUHSC_01858		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02099	COG4585T	histidine kinase	DEG10020213	SAOUHSC_02099		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02126	COG0015F	adenylosuccinate lyase	DEG10020220	SAOUHSC_02126		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02316	COG0513LKJ	DEAD-box ATP dependent DNA helicase	DEG10020228	SAOUHSC_02316		Staphylococcus aureus NCTC 8325
upp	SAOUHSC_02353	COG0035F	uracil phosphoribosyltransferase	DEG10020233	SAOUHSC_02353		Staphylococcus aureus NCTC 8325
glyA	SAOUHSC_02354	COG0112E	serine hydroxymethyltransferase	DEG10020234	SAOUHSC_02354		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02402	COG4668G	PTS system mannitol-specific transporter subunit IIA	DEG10020243	SAOUHSC_02402		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02406	COG4856S	hypothetical protein	DEG10020245	SAOUHSC_02406		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02455	COG0698G	galactose-6-phosphate isomerase subunit LacA	DEG10020246	SAOUHSC_02455		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02481	COG0619P	cobalt transport protein	DEG10020249	SAOUHSC_02481		Staphylococcus aureus NCTC 8325
cbiO	SAOUHSC_02482	COG1122P	cobalt transporter ATP-binding subunit	DEG10020250	SAOUHSC_02482		Staphylococcus aureus NCTC 8325
ureA	SAOUHSC_02558	COG0831E	urease subunit gamma	DEG10020280	SAOUHSC_02558		Staphylococcus aureus NCTC 8325
ureC	SAOUHSC_02561	COG0804E	urease subunit alpha	DEG10020282	SAOUHSC_02561		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02976	COG1482G	mannose-6-phosphate isomerase	DEG10020296	SAOUHSC_02976		Staphylococcus aureus NCTC 8325
-	SAOUHSC_03036	COG1136V	ABC transporter ATP-binding protein	DEG10020298	SAOUHSC_03036		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01420	COG0745TK	DNA-binding response regulator	DEG10030698	SAOUHSC_01420		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00911	COG1835I	hypothetical protein	DEG10050134	SAOUHSC_00911		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01095	COG1039L	ribonuclease HIII	DEG10060167	SAOUHSC_01095		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00003	COG2501S	hypothetical protein	DEG10170003	SAOUHSC_00003		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00015	COG3887T	hypothetical protein	DEG10170007	SAOUHSC_00015		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00227	COG1887M	hypothetical protein	DEG10170014	SAOUHSC_00227		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00345	COG4481S	hypothetical protein	DEG10170016	SAOUHSC_00345		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00482	COG2919D	hypothetical protein	DEG10170030	SAOUHSC_00482		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00484	COG0037D	hypothetical protein	DEG10170031	SAOUHSC_00484		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00491	COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	DEG10170034	SAOUHSC_00491		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00575	COG0095H	hypothetical protein	DEG10170052	SAOUHSC_00575		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00620	-	accessory regulator A	DEG10170057	SAOUHSC_00620		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00643	COG1887M	teichoic acid biosynthesis protein TagB	DEG10170061	SAOUHSC_00643		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00728	COG1368M	hypothetical protein	DEG10170063	SAOUHSC_00728		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00760	COG2199T	hypothetical protein	DEG10170068	SAOUHSC_00760		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00762	COG0472M	hypothetical protein	DEG10170069	SAOUHSC_00762		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00788	COG0391S	hypothetical protein	DEG10170074	SAOUHSC_00788		Staphylococcus aureus NCTC 8325
clpP	SAOUHSC_00790	COG0740OU	ATP-dependent Clp protease proteolytic subunit	DEG10170075	SAOUHSC_00790		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00793	-	hypothetical protein	DEG10170076	SAOUHSC_00793		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00848	COG0719O	hypothetical protein	DEG10170085	SAOUHSC_00848		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00850	COG0822C	hypothetical protein	DEG10170087	SAOUHSC_00850		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00851	COG0719O	hypothetical protein	DEG10170088	SAOUHSC_00851		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00868	-	hypothetical protein	DEG10170089	SAOUHSC_00868		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00870	COG1696M	D-alanine transfer protein DltB	DEG10170091	SAOUHSC_00870		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00872	COG3966M	extramembranal protein	DEG10170093	SAOUHSC_00872		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00881	COG2050Q	hypothetical protein	DEG10170094	SAOUHSC_00881		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00892	COG1098J	hypothetical protein	DEG10170095	SAOUHSC_00892		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00922	-	hypothetical protein	DEG10170100	SAOUHSC_00922		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00957	COG0861P	hypothetical protein	DEG10170106	SAOUHSC_00957		Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_00980	COG1575H	1,4-dihydroxy-2-naphthoate octaprenyltransferase	DEG10170107	SAOUHSC_00980		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00998	COG1680V	methicillin resistance protein FmtA	DEG10170108	SAOUHSC_00998		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01036	COG5503S	hypothetical protein	DEG10170111	SAOUHSC_01036		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01050	-	hypothetical protein	DEG10170114	SAOUHSC_01050		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01077	COG1399R	hypothetical protein	DEG10170117	SAOUHSC_01077		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01119	-	hypothetical protein	DEG10170124	SAOUHSC_01119		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01144	COG4839D	cell division protein	DEG10170125	SAOUHSC_01144		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01148	COG1589M	cell division protein	DEG10170129	SAOUHSC_01148		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01154	COG1799S	hypothetical protein	DEG10170132	SAOUHSC_01154		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01188	COG1162R	hypothetical protein	DEG10170138	SAOUHSC_01188		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01190	COG1564H	hypothetical protein	DEG10170140	SAOUHSC_01190		Staphylococcus aureus NCTC 8325
acpP	SAOUHSC_01201	COG0236IQ	acyl carrier protein	DEG10170145	SAOUHSC_01201		Staphylococcus aureus NCTC 8325
rimM	SAOUHSC_01209	COG0806J	16S rRNA-processing protein RimM	DEG10170149	SAOUHSC_01209		Staphylococcus aureus NCTC 8325
sucC	SAOUHSC_01216	COG0045C	succinyl-CoA synthetase subunit beta	DEG10170153	SAOUHSC_01216		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01244	COG2740K	hypothetical protein	DEG10170164	SAOUHSC_01244		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01245	COG1358J	hypothetical protein	DEG10170165	SAOUHSC_01245		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01285	COG0789K	glutamine synthetase repressor	DEG10170171	SAOUHSC_01285		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01359	COG2898S	hypothetical protein	DEG10170178	SAOUHSC_01359		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01462	COG3599D	hypothetical protein	DEG10170186	SAOUHSC_01462		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01470	COG3935L	hypothetical protein	DEG10170189	SAOUHSC_01470		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01477	COG2738R	hypothetical protein	DEG10170192	SAOUHSC_01477		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01501	COG5271R	elastin binding protein	DEG10170196	SAOUHSC_01501		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01598	COG1234R	AtsA/ElaC family protein	DEG10170199	SAOUHSC_01598		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01627	-	hypothetical protein	DEG10170205	SAOUHSC_01627		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01661	COG2384R	hypothetical protein	DEG10170206	SAOUHSC_01661		Staphylococcus aureus NCTC 8325
era	SAOUHSC_01668	COG1159R	GTP-binding protein Era	DEG10170210	SAOUHSC_01668		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01672	COG0319R	hypothetical protein	DEG10170211	SAOUHSC_01672		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01700	COG1161R	GTP-binding protein YqeH	DEG10170218	SAOUHSC_01700		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01701	COG2179R	hypothetical protein	DEG10170219	SAOUHSC_01701		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01739	COG0860M	hypothetical protein	DEG10170229	SAOUHSC_01739		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01756	COG2868J	hypothetical protein	DEG10170237	SAOUHSC_01756		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01770	-	hypothetical protein	DEG10170241	SAOUHSC_01770		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01782	COG4112R	hypothetical protein	DEG10170243	SAOUHSC_01782		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01787	COG0833E	hypothetical protein	DEG10170247	SAOUHSC_01787		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01792	COG3611L	hypothetical protein	DEG10170250	SAOUHSC_01792		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01871	COG2244R	polysaccharide biosynthesis protein	DEG10170263	SAOUHSC_01871		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01908	-	hypothetical protein	DEG10170265	SAOUHSC_01908		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01928	-	transposase family protein	DEG10170267	SAOUHSC_01928		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01930	-	hypothetical protein	DEG10170268	SAOUHSC_01930		Staphylococcus aureus NCTC 8325
-	SAOUHSC_01979	COG1476K	hypothetical protein	DEG10170269	SAOUHSC_01979		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02106	COG3442R	hypothetical protein	DEG10170271	SAOUHSC_02106		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02107	COG0769M	UDP-N-acetylmuramyl tripeptide synthetase	DEG10170272	SAOUHSC_02107		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02114	COG1597IR	lipid kinase	DEG10170273	SAOUHSC_02114		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02151	-	hypothetical protein	DEG10170282	SAOUHSC_02151		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02152	COG1131V	ABC transporter ATP-binding protein	DEG10170283	SAOUHSC_02152		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02260	-	delta-hemolysin	DEG10170286	SAOUHSC_02260		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02277	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10170287	SAOUHSC_02277		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02279	COG1214O	hypothetical protein	DEG10170288	SAOUHSC_02279		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02280	COG0802R	hypothetical protein	DEG10170289	SAOUHSC_02280		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02357	COG0009J	hypothetical protein	DEG10170296	SAOUHSC_02357		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02407	COG1624S	hypothetical protein	DEG10170304	SAOUHSC_02407		Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SAOUHSC_02571	COG3942R	secretory antigen	DEG10170336	SAOUHSC_02571		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02572	-	hypothetical protein	DEG10170337	SAOUHSC_02572		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02575	COG3296S	hypothetical protein	DEG10170338	SAOUHSC_02575		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02720	-	hypothetical protein	DEG10170341	SAOUHSC_02720		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02757	COG2161D	hypothetical protein	DEG10170342	SAOUHSC_02757		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02791	COG0494LR	pyrophosphohydrolase	DEG10170343	SAOUHSC_02791		Staphylococcus aureus NCTC 8325
-	SAOUHSC_02805	-	hypothetical protein	DEG10170344	SAOUHSC_02805		Staphylococcus aureus NCTC 8325
-	SAOUHSC_03049	COG1475K	hypothetical protein	DEG10170347	SAOUHSC_03049		Staphylococcus aureus NCTC 8325
trmE	SAOUHSC_03053	COG0486R	tRNA modification GTPase TrmE	DEG10170349	SAOUHSC_03053		Staphylococcus aureus NCTC 8325
rnpA	SAOUHSC_03054	COG0594J	ribonuclease P	DEG10170350	SAOUHSC_03054		Staphylococcus aureus NCTC 8325
-	SAOUHSC_00778	COG3039L	hypothetical protein	DEG10180236	SAOUHSC_00778		Staphylococcus aureus NCTC 8325

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SP_1777	COG0780R	7-cyano-7-deazaguanine reductase	DEG10070215	SP_1777	SP_1777	Streptococcus pneumoniae R6
secY	SP_1763	COG0201U	preprotein translocase subunit SecY			sp_1763	Streptococcus pneumoniae R6
nadD	SP_1747	COG1057H	nicotinic acid mononucleotide adenylyltransferase	DEG10070097	SP_1747	SP_1747	Streptococcus pneumoniae R6
gmk	SP_1738	COG0194F	guanylate kinase			sp_1738	Streptococcus pneumoniae R6
-	SP_1737	COG1758K	DNA-directed RNA polymerase subunit omega	DEG10070096	SP_1737	SP_1737	Streptococcus pneumoniae R6
fmt	SP_1735	COG0223J	methionyl-tRNA formyltransferase	DEG10070214	SP_1735	SP_1735	Streptococcus pneumoniae R6
-	SP_1732	COG2815S	serine/threonine protein kinase	DEG10070094	SP_1732	SP_1732	Streptococcus pneumoniae R6
-	SP_1727	COG3425I	hydroxymethylglutaryl-CoA synthase	DEG10070213	SP_1727	SP_1727	Streptococcus pneumoniae R6
-	SP_1726	COG1257I	3-hydroxy-3-methylglutaryl-CoA reductase	DEG10070093	SP_1726	SP_1726	Streptococcus pneumoniae R6
-	SP_1724	COG1621G	sucrose-6-phosphate hydrolase			SP_1724	Streptococcus pneumoniae R6
-	SP_1711	COG1484L	primosomal protein DnaI	DEG10070212	SP_1711	SP_1711	Streptococcus pneumoniae R6
engA	SP_1709	COG1160R	GTP-binding protein EngA	DEG10070211	SP_1709	SP_1709	Streptococcus pneumoniae R6
secA	SP_1702	COG0653U	preprotein translocase subunit SecA			SP_1702	Streptococcus pneumoniae R6
acpS	SP_1699	COG0736I	4'-phosphopantetheinyl transferase	DEG10070210	SP_1699	SP_1699	Streptococcus pneumoniae R6
alr	SP_1698	COG0787M	alanine racemase	DEG10070209	SP_1698	SP_1698	Streptococcus pneumoniae R6
-	SP_1673	COG0768M	penicillin-binding protein 2B			SP_1673	Streptococcus pneumoniae R6
ddl	SP_1671	COG1181M	D-alanyl-alanine synthetase A	DEG10070207	SP_1671	SP_1671	Streptococcus pneumoniae R6
-	SP_1670	COG0770M	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	DEG10070206	SP_1670	SP_1670	Streptococcus pneumoniae R6
-	SP_1667	COG0849D	cell division protein FtsA	DEG10070205	SP_1667	SP_1667	Streptococcus pneumoniae R6
-	SP_1666	COG0206D	cell division protein FtsZ	DEG10070204	SP_1666	SP_1666	Streptococcus pneumoniae R6
-	SP_1665	COG0325R	hypothetical protein	DEG10070092	SP_1665	SP_1665	Streptococcus pneumoniae R6
-	SP_1661	COG3599D	cell division protein DivIVA	DEG10070091	SP_1661	SP_1661	Streptococcus pneumoniae R6
ileS	SP_1659	COG0060J	isoleucyl-tRNA synthetase	DEG10070203	SP_1659	SP_1659	Streptococcus pneumoniae R6
gpmA	SP_1655	COG0588G	phosphoglyceromutase			SP_1655	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SP_1650	COG0803P	manganese ABC transporter manganese-binding adhesion liprotein			sp_1650	Streptococcus pneumoniae R6
-	SP_1649	COG1108P	manganese ABC transporter permease			sp_1649	Streptococcus pneumoniae R6
-	SP_1648	COG1121P	manganese ABC transporter ATP-binding protein	DEG10070090	SP_1648	SP_1648	Streptococcus pneumoniae R6
-	SP_1645	COG0317TK	GTP pyrophosphokinase	DEG10070089	SP_1645	SP_1645	Streptococcus pneumoniae R6
thrS	SP_1631	COG0441J	threonyl-tRNA synthetase	DEG10070202	SP_1631	SP_1631	Streptococcus pneumoniae R6
rpsO	SP_1626	COG0184J	30S ribosomal protein S15			SP_1626	Streptococcus pneumoniae R6
-	SP_1624	COG0204I	acyltransferase	DEG10070088	SP_1624	SP_1624	Streptococcus pneumoniae R6
-	SP_1616	COG0036G	allulose-6-phosphate 3-epimerase	DEG10070087	SP_1616	SP_1616	Streptococcus pneumoniae R6
-	SP_1607	COG1087M	UDP-glucose 4-epimerase	DEG10070200	SP_1607	SP_1607	Streptococcus pneumoniae R6
-	SP_1605	COG1141C	ferredoxin	DEG10070199	SP_1605	SP_1605	Streptococcus pneumoniae R6
-	SP_1598	COG0351H	phosphomethylpyrimidine kinase	DEG10070085	SP_1598	SP_1598	Streptococcus pneumoniae R6
-	SP_1589	COG0769M	hypothetical protein	DEG10070083	SP_1589	SP_1589	Streptococcus pneumoniae R6
-	SP_1586	COG0513LKJ	ATP-dependent RNA helicase			SP_1586	Streptococcus pneumoniae R6
-	SP_1584	COG4465K	transcriptional repressor CodY	DEG10070198	SP_1584	SP_1584	Streptococcus pneumoniae R6
-	SP_1576	COG1897E	homoserine O-succinyltransferase	DEG10070197	SP_1576	SP_1576	Streptococcus pneumoniae R6
tpiA	SP_1574	COG0149G	triosephosphate isomerase	DEG10070195	SP_1574	SP_1574	Streptococcus pneumoniae R6
-	SP_1571	COG0262H	dihydrofolate reductase	DEG10070193	SP_1571	SP_1571	Streptococcus pneumoniae R6
engB	SP_1568	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10070082	SP_1568	SP_1568	Streptococcus pneumoniae R6
-	SP_1563	COG0492O	pyridine nucleotide-disulfide oxidoreductase family protein			SP_1563	Streptococcus pneumoniae R6
glmM	SP_1559	COG1109G	phosphoglucosamine mutase	DEG10070081	SP_1559	SP_1559	Streptococcus pneumoniae R6
-	SP_1555	COG0289E	dihydrodipicolinate reductase	DEG10070080	SP_1555	SP_1555	Streptococcus pneumoniae R6
-	SP_1554	COG0617J	tRNA CCA-pyrophosphorylase	DEG10070190	SP_1554	SP_1554	Streptococcus pneumoniae R6
-	SP_1549	COG0242J	peptide deformylase			SP_1549	Streptococcus pneumoniae R6
asnC	SP_1542	COG0017J	asparaginyl-tRNA synthetase	DEG10070078	SP_1542	SP_1542	Streptococcus pneumoniae R6
rpsF	SP_1541	COG0360J	30S ribosomal protein S6			SP_1541	Streptococcus pneumoniae R6
-	SP_1540	COG0629L	single-stranded DNA-binding protein	DEG10070077	SP_1540	SP_1540	Streptococcus pneumoniae R6
rpsR	SP_1539	COG0238J	30S ribosomal protein S18	DEG10210051	SP_1539	SP_1539	Streptococcus pneumoniae R6
-	SP_1534	COG1227C	manganese-dependent inorganic pyrophosphatase	DEG10070076	SP_1534	SP_1534	Streptococcus pneumoniae R6
murE	SP_1530	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase	DEG10070075	SP_1530	SP_1530	Streptococcus pneumoniae R6
-	SP_1529	COG2244R	polysaccharide biosynthesis protein	DEG10070074	SP_1529	SP_1529	Streptococcus pneumoniae R6
-	SP_1527	COG4166E	oligopeptide ABC transporter oligopeptide-binding protein AliB			sp_1527	Streptococcus pneumoniae R6
murC	SP_1521	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10070186	SP_1521	SP_1521	Streptococcus pneumoniae R6
greA	SP_1517	COG0782K	transcription elongation factor GreA	DEG10070073	SP_1517	SP_1517	Streptococcus pneumoniae R6
-	SP_1513	COG0356C	ATP synthase F0F1 subunit A			SP_1513	Streptococcus pneumoniae R6
-	SP_1512	COG0711C	ATP synthase F0F1 subunit B	DEG10070185	SP_1512	SP_1512	Streptococcus pneumoniae R6
-	SP_1510	COG0056C	ATP synthase F0F1 subunit alpha	DEG10070184	SP_1510	SP_1510	Streptococcus pneumoniae R6
-	SP_1509	COG0224C	ATP synthase F0F1 subunit gamma	DEG10070183	SP_1509	SP_1509	Streptococcus pneumoniae R6
-	SP_1508	COG0055C	ATP synthase F0F1 subunit beta	DEG10070182	SP_1508	SP_1508	Streptococcus pneumoniae R6
atpC	SP_1507	COG0355C	ATP synthase F0F1 subunit epsilon	DEG10070181	SP_1507	SP_1507	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
tuf	SP_1489	COG0050J	elongation factor Tu			SP_1489	Streptococcus pneumoniae R6
glyQ	SP_1475	COG0752J	glycyl-tRNA synthetase subunit alpha	DEG10070180	SP_1475	SP_1475	Streptococcus pneumoniae R6
glyS	SP_1474	COG0751J	glycyl-tRNA synthetase subunit beta			SP_1474	Streptococcus pneumoniae R6
-	SP_1458	COG0492O	thioredoxin reductase	DEG10070179	SP_1458	SP_1458	Streptococcus pneumoniae R6
def	SP_1456	COG0242J	peptide deformylase	DEG10070178	SP_1456	SP_1456	Streptococcus pneumoniae R6
-	SP_1438	COG1122P	ABC transporter ATP-binding protein			sp_1438	Streptococcus pneumoniae R6
-	SP_1437	COG0619P	hypothetical protein			sp_1437	Streptococcus pneumoniae R6
-	SP_1423	COG1476K	transcriptional repressor			SP_1423	Streptococcus pneumoniae R6
-	SP_1421	COG1488H	nicotinate phosphoribosyltransferase	DEG10070072	SP_1421	SP_1421	Streptococcus pneumoniae R6
nadE	SP_1420	COG0171H	NAD synthetase			SP_1420	Streptococcus pneumoniae R6
rpsU	SP_1414	-	30S ribosomal protein S21			SP_1414	Streptococcus pneumoniae R6
murB	SP_1390	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10070176	SP_1390	SP_1390	Streptococcus pneumoniae R6
alaS	SP_1383	COG0013J	alanyl-tRNA synthetase			SP_1383	Streptococcus pneumoniae R6
rpmE2	SP_1299	COG0254J	50S ribosomal protein L31			SP_1299	Streptococcus pneumoniae R6
rplS	SP_1293	COG0335J	50S ribosomal protein L19			SP_1293	Streptococcus pneumoniae R6
-	SP_1287	COG0541U	signal recognition particle protein	DEG10070070	SP_1287	SP_1287	Streptococcus pneumoniae R6
-	SP_1270	COG1063ER	zinc-containing alcohol dehydrogenase	DEG10070068	SP_1270	SP_1270	Streptococcus pneumoniae R6
-	SP_1267	COG4750M	licC protein			SP_1267	Streptococcus pneumoniae R6
-	SP_1263	COG0550L	DNA topoisomerase I	DEG10070067	SP_1263	SP_1263	Streptococcus pneumoniae R6
-	SP_1244	COG0552U	signal recognition particle-docking protein FtsY	DEG10070065	SP_1244	SP_1244	Streptococcus pneumoniae R6
-	SP_1231	COG0452H	phosphopantothenoylcysteine decarboxylase	DEG10070173	SP_1231	SP_1231	Streptococcus pneumoniae R6
-	SP_1230	COG0452H	phosphopantothenate--cysteine ligase			SP_1230	Streptococcus pneumoniae R6
-	SP_1227	COG0745TK	DNA-binding response regulator	DEG10070064	SP_1227	SP_1227	Streptococcus pneumoniae R6
-	SP_1226	COG5002T	sensory box sensor histidine kinase			sp_1226	Streptococcus pneumoniae R6
-	SP_1219	COG0188L	DNA gyrase subunit A			SP_1219	Streptococcus pneumoniae R6
-	SP_1203	COG1438K	transcriptional repressor			SP_1203	Streptococcus pneumoniae R6
-	SP_1202	COG0497L	DNA repair protein RecN			SP_1202	Streptococcus pneumoniae R6
-	SP_1197	COG3414G	hypothetical protein			SP_1197	Streptococcus pneumoniae R6
nrdF	SP_1180	COG0208F	ribonucleotide-diphosphate reductase subunit beta			SP_1180	Streptococcus pneumoniae R6
-	SP_1179	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10070171	SP_1179	SP_1179	Streptococcus pneumoniae R6
rbgA	SP_1155	COG1161R	ribosomal biogenesis GTPase	DEG10070063	SP_1155	SP_1155	Streptococcus pneumoniae R6
eno	SP_1128	COG0148G	phosphopyruvate hydratase	DEG10070168	SP_1128	SP_1128	Streptococcus pneumoniae R6
ligA	SP_1117	COG0272L	NAD-dependent DNA ligase LigA	DEG10070167	SP_1117	SP_1117	Streptococcus pneumoniae R6
-	SP_1113	COG0776L	DNA-binding protein HU	DEG10070062	SP_1113	SP_1113	Streptococcus pneumoniae R6
rpmA	SP_1107	COG0211J	50S ribosomal protein L27			SP_1107	Streptococcus pneumoniae R6
rplU	SP_1105	COG0261J	50S ribosomal protein L21			SP_1105	Streptococcus pneumoniae R6
ppnK	SP_1098	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10070061	SP_1098	SP_1098	Streptococcus pneumoniae R6
-	SP_1097	COG2357S	hypothetical protein	DEG10070060	SP_1097	SP_1097	Streptococcus pneumoniae R6
-	SP_1095	COG0462FE	ribose-phosphate pyrophosphokinase			sp_1095	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SP_1094	COG1104E	class-V aminotransferase	DEG10070166	SP_1094	SP_1094	Streptococcus pneumoniae R6
radC	SP_1088	COG2003L	DNA repair protein RadC	DEG10070165	SP_1088	SP_1088	Streptococcus pneumoniae R6
-	SP_1084	COG0024J	methionine aminopeptidase	DEG10070164	SP_1084	SP_1084	Streptococcus pneumoniae R6
-	SP_1081	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	DEG10070059	SP_1081	SP_1081	Streptococcus pneumoniae R6
obgE	SP_1079	COG0536R	GTPase ObgE	DEG10070058	SP_1079	SP_1079	Streptococcus pneumoniae R6
-	SP_1076	COG0438M	group 1 glycosyl transferase	DEG10070163	SP_1076	SP_1076	Streptococcus pneumoniae R6
-	SP_1073	COG0568K	RNA polymerase sigma factor RpoD	DEG10070162	SP_1073	SP_1073	Streptococcus pneumoniae R6
dnaG	SP_1072	COG0358L	DNA primase	DEG10070161	SP_1072	SP_1072	Streptococcus pneumoniae R6
-	SP_1067	COG0772D	cell division protein FtsW	DEG10070057	SP_1067	SP_1067	Streptococcus pneumoniae R6
prfA	SP_1020	COG0216J	peptide chain release factor 1	DEG10070056	SP_1020	SP_1020	Streptococcus pneumoniae R6
-	SP_1002	COG0803P	adhesion lipoprotein	DEG10070158	SP_1002	SP_1002	Streptococcus pneumoniae R6
-	SP_0993	COG0847L	DNA polymerase III subunit epsilon			sp_0993	Streptococcus pneumoniae R6
glmU	SP_0988	COG1207M	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	DEG10070055	SP_0988	SP_0988	Streptococcus pneumoniae R6
-	SP_0984	COG0406G	phosphoglycerate mutase			SP_0984	Streptococcus pneumoniae R6
-	SP_0978	COG4469R	competence protein CoiA	DEG10070156	SP_0978	SP_0978	Streptococcus pneumoniae R6
secG	SP_0974	COG1314U	preprotein translocase subunit SecG	DEG10070054	SP_0974	SP_0974	Streptococcus pneumoniae R6
rpmG	SP_0973	COG0267J	50S ribosomal protein L33			SP_0973	Streptococcus pneumoniae R6
coaE	SP_0971	COG0237H	dephospho-CoA kinase	DEG10070053	SP_0971	SP_0971	Streptococcus pneumoniae R6
-	SP_0968	COG0818M	diacylglycerol kinase			SP_0968	Streptococcus pneumoniae R6
rplT	SP_0961	COG0292J	50S ribosomal protein L20			SP_0961	Streptococcus pneumoniae R6
rpmI	SP_0960	COG0291J	50S ribosomal protein L35			SP_0960	Streptococcus pneumoniae R6
infC	SP_0959	COG0290J	translation initiation factor IF-3	DEG10070155	SP_0959	SP_0959	Streptococcus pneumoniae R6
-	SP_0955	COG2333R	competence protein CelB			SP_0955	Streptococcus pneumoniae R6
-	SP_0954	COG1555L	competence protein CelA	DEG10070154	SP_0954	SP_0954	Streptococcus pneumoniae R6
frr	SP_0945	COG0233J	ribosome recycling factor	DEG10070051	SP_0945	SP_0945	Streptococcus pneumoniae R6
pyrH	SP_0944	COG0528F	uridylate kinase	DEG10070153	SP_0944	SP_0944	Streptococcus pneumoniae R6
-	SP_0936	COG0470L	DNA polymerase III subunit delta'	DEG10070050	SP_0936	SP_0936	Streptococcus pneumoniae R6
tmk	SP_0935	COG0125F	thymidylate kinase			sp_0935	Streptococcus pneumoniae R6
-	SP_0928	COG0597MU	lipoprotein signal peptidase			sp_0928	Streptococcus pneumoniae R6
-	SP_0897	COG0469G	pyruvate kinase	DEG10070152	SP_0897	SP_0897	Streptococcus pneumoniae R6
pfkA	SP_0896	COG0205G	6-phosphofructokinase	DEG10070151	SP_0896	SP_0896	Streptococcus pneumoniae R6
dnaE	SP_0895	COG0587L	DNA polymerase III DnaE	DEG10070048	SP_0895	SP_0895	Streptococcus pneumoniae R6
-	SP_0893	COG1438K	transcriptional repressor			SP_0893	Streptococcus pneumoniae R6
-	SP_0880	COG1104E	class-V aminotransferase			SP_0880	Streptococcus pneumoniae R6
-	SP_0872	COG1686M	D-alanyl-D-alanine carboxypeptidase			SP_0872	Streptococcus pneumoniae R6
-	SP_0865	COG2812L	DNA polymerase III subunits gamma and tau	DEG10070046	SP_0865	SP_0865	Streptococcus pneumoniae R6
rpsA	SP_0862	COG0539J	30S ribosomal protein S1			SP_0862	Streptococcus pneumoniae R6
-	SP_0855	COG0188L	DNA topoisomerase IV subunit A			SP_0855	Streptococcus pneumoniae R6
-	SP_0852	COG0187L	DNA topoisomerase IV subunit B	DEG10070149	SP_0852	SP_0852	Streptococcus pneumoniae R6
-	SP_0851	COG0344S	glycerol-3-phosphate acyltransferase PlsY	DEG10070148	SP_0851	SP_0851	Streptococcus pneumoniae R6
-	SP_0839	COG1072H	pantothenate kinase	DEG10070044	SP_0839	SP_0839	Streptococcus pneumoniae R6
rpsT	SP_0838	COG0268J	30S ribosomal protein S20			SP_0838	Streptococcus pneumoniae R6
-	SP_0825	COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	DEG10070147	SP_0825	SP_0825	Streptococcus pneumoniae R6
-	SP_0807	COG4477D	septation ring formation regulator EzrA	DEG10070043	SP_0807	SP_0807	Streptococcus pneumoniae R6
gyrB	SP_0806	COG0187L	DNA gyrase subunit B	DEG10070042	SP_0806	SP_0806	Streptococcus pneumoniae R6
-	SP_0803	COG0772D	rod shape-determining protein RodA	DEG10070041	SP_0803	SP_0803	Streptococcus pneumoniae R6
fabG	SP_0793	COG1028IQR	3-ketoacyl-ACP reductase			sp_0793	Streptococcus pneumoniae R6
metG	SP_0788	COG0143J	methionyl-tRNA synthetase			SP_0788	Streptococcus pneumoniae R6
-	SP_0783	COG1268R	hypothetical protein			sp_0783	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
trmD	SP_0779	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10070040	SP_0779	SP_0779	Streptococcus pneumoniae R6
rimM	SP_0778	COG0806J	16S rRNA-processing protein RimM	DEG10070039	SP_0778	SP_0778	Streptococcus pneumoniae R6
rpsP	SP_0775	COG0228J	30S ribosomal protein S16			SP_0775	Streptococcus pneumoniae R6
holA	SP_0765	COG1466L	DNA polymerase III subunit delta			sp_0765	Streptococcus pneumoniae R6
-	SP_0762	COG0192H	S-adenosylmethionine synthetase	DEG10070146	SP_0762	SP_0762	Streptococcus pneumoniae R6
-	SP_0757	COG2177D	cell division ABC transporter permease FtsX			SP_0757	Streptococcus pneumoniae R6
-	SP_0756	COG2884D	cell division ABC transporter ATP-binding protein FtsE	DEG10070144	SP_0756	SP_0756	Streptococcus pneumoniae R6
prfB	SP_0755	COG1186J	peptide chain release factor 2	DEG10070038	SP_0755	SP_0755	Streptococcus pneumoniae R6
-	SP_0727	COG3682K	transcriptional repressor			SP_0727	Streptococcus pneumoniae R6
-	SP_0721	-	hypothetical protein			sp_0721	Streptococcus pneumoniae R6
-	SP_0720	COG1122P	ABC transporter ATP-binding protein			sp_0720	Streptococcus pneumoniae R6
lysS	SP_0713	COG1190J	lysyl-tRNA synthetase	DEG10070142	SP_0713	SP_0713	Streptococcus pneumoniae R6
murG	SP_0689	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	DEG10070141	SP_0689	SP_0689	Streptococcus pneumoniae R6
murD	SP_0688	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	DEG10070140	SP_0688	SP_0688	Streptococcus pneumoniae R6
miaA	SP_0671	COG0324J	tRNA delta(2)-isopentenylpyrophosphate transferase			SP_0671	Streptococcus pneumoniae R6
thyA	SP_0669	COG0207F	thymidylate synthase	DEG10070139	SP_0669	SP_0669	Streptococcus pneumoniae R6
-	SP_0647	COG3775G	PTS system transporter subunit IIC			SP_0647	Streptococcus pneumoniae R6
-	SP_0646	COG3414G	PTS system transporter subunit IIB			SP_0646	Streptococcus pneumoniae R6
-	SP_0645	COG1762GT	PTS system transporter subunit IIA			SP_0645	Streptococcus pneumoniae R6
rplA	SP_0631	COG0081J	50S ribosomal protein L1			SP_0631	Streptococcus pneumoniae R6
rplK	SP_0630	COG0080J	50S ribosomal protein L11			SP_0630	Streptococcus pneumoniae R6
-	SP_0613	COG0595R	metallo-beta-lactamase superfamily protein	DEG10070034	SP_0613	SP_0613	Streptococcus pneumoniae R6
-	SP_0605	COG0191G	fructose-bisphosphate aldolase	DEG10070138	SP_0605	SP_0605	Streptococcus pneumoniae R6
cysS	SP_0591	COG0215J	cysteinyl-tRNA synthetase			SP_0591	Streptococcus pneumoniae R6
-	SP_0585	COG0620E	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase			SP_0585	Streptococcus pneumoniae R6
pheT	SP_0581	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10070033	SP_0581	SP_0581	Streptococcus pneumoniae R6
-	SP_0580	COG0456R	acetyltransferase	DEG10070032	SP_0580	SP_0580	Streptococcus pneumoniae R6
pheS	SP_0579	COG0016J	phenylalanyl-tRNA synthetase subunit alpha			sp_0579	Streptococcus pneumoniae R6
valS	SP_0568	COG0525J	valyl-tRNA synthetase			SP_0568	Streptococcus pneumoniae R6
nusA	SP_0553	COG0195K	transcription elongation factor NusA	DEG10070137	SP_0553	SP_0553	Streptococcus pneumoniae R6
dnaK	SP_0517	COG0443O	molecular chaperone DnaK			sp_0517	Streptococcus pneumoniae R6
pgk	SP_0499	COG0126G	phosphoglycerate kinase	DEG10070030	SP_0499	SP_0499	Streptococcus pneumoniae R6
-	SP_0493	COG3343K	DNA-directed RNA polymerase subunit delta			sp_0493	Streptococcus pneumoniae R6
-	SP_0484	COG0619P	hypothetical protein			sp_0484	Streptococcus pneumoniae R6
-	SP_0483	COG1123R	ABC transporter ATP-binding protein			sp_0483	Streptococcus pneumoniae R6
-	SP_0458	COG0389L	DNA polymerase IV			SP_0458	Streptococcus pneumoniae R6
uppP	SP_0457	COG1968V	UDP pyrophosphate phosphatase	DEG10070029	SP_0457	SP_0457	Streptococcus pneumoniae R6
rpmB	SP_0441	COG0227J	50S ribosomal protein L28			SP_0441	Streptococcus pneumoniae R6
gatC	SP_0438	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10070136	SP_0438	SP_0438	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
gatA	SP_0437	COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A			SP_0437	Streptococcus pneumoniae R6
gatB	SP_0436	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10070135	SP_0436	SP_0436	Streptococcus pneumoniae R6
-	SP_0435	COG0231J	elongation factor P	DEG10070028	SP_0435	SP_0435	Streptococcus pneumoniae R6
nusB	SP_0433	COG0781K	transcription antitermination protein NusB	DEG10070027	SP_0433	SP_0433	Streptococcus pneumoniae R6
-	SP_0427	COG0825I	acetyl-CoA carboxylase subunit alpha	DEG10070026	SP_0427	SP_0427	Streptococcus pneumoniae R6
-	SP_0426	COG0777I	acetyl-CoA carboxylase subunit beta	DEG10070025	SP_0426	SP_0426	Streptococcus pneumoniae R6
-	SP_0425	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	DEG10070024	SP_0425	SP_0425	Streptococcus pneumoniae R6
fabZ	SP_0424	COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	DEG10070023	SP_0424	SP_0424	Streptococcus pneumoniae R6
-	SP_0423	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	DEG10070022	SP_0423	SP_0423	Streptococcus pneumoniae R6
-	SP_0422	COG0304IQ	3-oxoacyl-ACP synthase	DEG10070021	SP_0422	SP_0422	Streptococcus pneumoniae R6
fabG	SP_0421	COG1028IQR	3-ketoacyl-ACP reductase	DEG10070020	SP_0421	SP_0421	Streptococcus pneumoniae R6
-	SP_0420	COG0331I	ACP S-malonyltransferase	DEG10070019	SP_0420	SP_0420	Streptococcus pneumoniae R6
-	SP_0419	COG2070R	enoyl-ACP reductase	DEG10070018	SP_0419	SP_0419	Streptococcus pneumoniae R6
-	SP_0411	COG0172J	seryl-tRNA synthetase	DEG10070134	SP_0411	SP_0411	Streptococcus pneumoniae R6
-	SP_0402	COG0681U	signal peptidase I	DEG10070017	SP_0402	SP_0402	Streptococcus pneumoniae R6
-	SP_0397	COG0246G	mannitol-1-phosphate 5-dehydrogenase	DEG10070133	SP_0397	SP_0397	Streptococcus pneumoniae R6
-	SP_0396	COG4668G	PTS system mannitol-specific transporter subunit IIA			SP_0396	Streptococcus pneumoniae R6
-	SP_0394	COG2213G	PTS system mannitol-specific transporter subunit IIBC	DEG10070132	SP_0394	SP_0394	Streptococcus pneumoniae R6
-	SP_0384	COG1304C	isopentenyl pyrophosphate isomerase			SP_0384	Streptococcus pneumoniae R6
-	SP_0381	COG1577I	mevalonate kinase	DEG10070131	SP_0381	SP_0381	Streptococcus pneumoniae R6
recU	SP_0370	COG3331R	Holliday junction-specific endonuclease	DEG10070016	SP_0370	SP_0370	Streptococcus pneumoniae R6
-	SP_0369	COG0744M	penicillin-binding protein 1A			SP_0369	Streptococcus pneumoniae R6
-	SP_0358	COG1086MG	capsular polysaccharide biosynthesis protein Cps4J			SP_0358	Streptococcus pneumoniae R6
-	SP_0347	COG4464GM	capsular polysaccharide biosynthesis protein Cps4B	DEG10070015	SP_0347	SP_0347	Streptococcus pneumoniae R6
-	SP_0338	COG0542O	ATP-dependent Clp protease ATP-binding subunit			SP_0338	Streptococcus pneumoniae R6
mraY	SP_0337	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10070014	SP_0337	SP_0337	Streptococcus pneumoniae R6
-	SP_0336	COG0768M	penicillin-binding protein 2X	DEG10070129	SP_0336	SP_0336	Streptococcus pneumoniae R6
-	SP_0326	COG1862U	preprotein translocase subunit YajC			sp_0326	Streptococcus pneumoniae R6
rpsI	SP_0295	COG0103J	30S ribosomal protein S9			SP_0295	Streptococcus pneumoniae R6
rplM	SP_0294	COG0102J	50S ribosomal protein L13			SP_0294	Streptococcus pneumoniae R6
-	SP_0292	COG0801H	bifunctional folate synthesis protein	DEG10070128	SP_0292	SP_0292	Streptococcus pneumoniae R6
folE	SP_0291	COG0302H	GTP cyclohydrolase I	DEG10070127	SP_0291	SP_0291	Streptococcus pneumoniae R6
-	SP_0290	COG0285H	dihydrofolate synthetase	DEG10070126	SP_0290	SP_0290	Streptococcus pneumoniae R6
-	SP_0289	COG0294H	dihydropteroate synthase	DEG10070125	SP_0289	SP_0289	Streptococcus pneumoniae R6
polC	SP_0274	COG2176L	DNA polymerase III PolC			sp_0274	Streptococcus pneumoniae R6
-	SP_0273	COG0480J	elongation factor G	DEG10070012	SP_0273	SP_0273	Streptococcus pneumoniae R6
-	SP_0272	COG0049J	30S ribosomal protein S7			SP_0272	Streptococcus pneumoniae R6
rpsL	SP_0271	COG0048J	30S ribosomal protein S12			SP_0271	Streptococcus pneumoniae R6
-	SP_0266	COG0449M	glucosamine--fructose-6-phosphate aminotransferase	DEG10070011	SP_0266	SP_0266	Streptococcus pneumoniae R6
-	SP_0264	COG0442J	prolyl-tRNA synthetase	DEG10070124	SP_0264	SP_0264	Streptococcus pneumoniae R6
-	SP_0262	COG0575I	phosphatidate cytidylyltransferase			SP_0262	Streptococcus pneumoniae R6
ruvB	SP_0259	COG2255L	Holliday junction DNA helicase RuvB	DEG10070009	SP_0259	SP_0259	Streptococcus pneumoniae R6
leuS	SP_0254	COG0495J	leucyl-tRNA synthetase			SP_0254	Streptococcus pneumoniae R6
-	SP_0240	COG0406G	phosphoglycerate mutase			SP_0240	Streptococcus pneumoniae R6
rplQ	SP_0237	COG0203J	50S ribosomal protein L17			SP_0237	Streptococcus pneumoniae R6
-	SP_0236	COG0202K	DNA-directed RNA polymerase subunit alpha			sp_0236	Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SP_0235	COG0100J	30S ribosomal protein S11	DEG10210028	SP_0235	SP_0235	Streptococcus pneumoniae R6
rpsM	SP_0234	COG0099J	30S ribosomal protein S13			SP_0234	Streptococcus pneumoniae R6
rpmJ	SP_0233	COG0257J	50S ribosomal protein L36			SP_0233	Streptococcus pneumoniae R6
infA	SP_0232	COG0361J	translation initiation factor IF-1	DEG10210027	SP_0232	SP_0232	Streptococcus pneumoniae R6
adk	SP_0231	COG0563F	adenylate kinase	DEG10070123	SP_0231	SP_0231	Streptococcus pneumoniae R6
secY	SP_0230	COG0201U	preprotein translocase subunit SecY			sp_0230	Streptococcus pneumoniae R6
rplO	SP_0229	COG0200J	50S ribosomal protein L15			SP_0229	Streptococcus pneumoniae R6
rpmD	SP_0228	COG1841J	50S ribosomal protein L30			SP_0228	Streptococcus pneumoniae R6
rpsE	SP_0227	COG0098J	30S ribosomal protein S5			SP_0227	Streptococcus pneumoniae R6
rplR	SP_0226	COG0256J	50S ribosomal protein L18			SP_0226	Streptococcus pneumoniae R6
rplF	SP_0225	COG0097J	50S ribosomal protein L6			SP_0225	Streptococcus pneumoniae R6
rpsH	SP_0224	COG0096J	30S ribosomal protein S8			SP_0224	Streptococcus pneumoniae R6
rpsN	SP_0222	COG0199J	30S ribosomal protein S14			SP_0222	Streptococcus pneumoniae R6
rplE	SP_0221	COG0094J	50S ribosomal protein L5			SP_0221	Streptococcus pneumoniae R6
rplX	SP_0220	COG0198J	50S ribosomal protein L24			SP_0220	Streptococcus pneumoniae R6
rplN	SP_0219	COG0093J	50S ribosomal protein L14			SP_0219	Streptococcus pneumoniae R6
rpsQ	SP_0218	COG0186J	30S ribosomal protein S17	DEG10210018	SP_0218	SP_0218	Streptococcus pneumoniae R6
rpmC	SP_0217	COG0255J	50S ribosomal protein L29			SP_0217	Streptococcus pneumoniae R6
rplP	SP_0216	COG0197J	50S ribosomal protein L16			SP_0216	Streptococcus pneumoniae R6
rpsC	SP_0215	COG0092J	30S ribosomal protein S3			SP_0215	Streptococcus pneumoniae R6
rplV	SP_0214	COG0091J	50S ribosomal protein L22			SP_0214	Streptococcus pneumoniae R6
rpsS	SP_0213	COG0185J	30S ribosomal protein S19	DEG10210014	SP_0213	SP_0213	Streptococcus pneumoniae R6
rplB	SP_0212	COG0090J	50S ribosomal protein L2			SP_0212	Streptococcus pneumoniae R6
rplW	SP_0211	COG0089J	50S ribosomal protein L23			SP_0211	Streptococcus pneumoniae R6
rplD	SP_0210	COG0088J	50S ribosomal protein L4			SP_0210	Streptococcus pneumoniae R6
rplC	SP_0209	COG0087J	50S ribosomal protein L3			SP_0209	Streptococcus pneumoniae R6
rpsJ	SP_0208	COG0051J	30S ribosomal protein S10			SP_0208	Streptococcus pneumoniae R6
-	SP_0197	COG0285H	dihydrofolate synthetase			SP_0197	Streptococcus pneumoniae R6
ruvA	SP_0179	COG0632L	Holliday junction DNA helicase RuvA	DEG10070007	SP_0179	SP_0179	Streptococcus pneumoniae R6
-	SP_0121	COG0595R	metallo-beta-lactamase superfamily protein	DEG10070004	SP_0121	SP_0121	Streptococcus pneumoniae R6
-	SP_0092	COG1653G	ABC transporter substrate-binding protein			SP_0092	Streptococcus pneumoniae R6
-	SP_0091	COG0395G	ABC transporter permease			SP_0091	Streptococcus pneumoniae R6
-	SP_0090	COG4209G	ABC transporter permease	DEG10070115	SP_0090	SP_0090	Streptococcus pneumoniae R6
rpsD	SP_0085	COG0522J	30S ribosomal protein S4			SP_0085	Streptococcus pneumoniae R6
-	SP_0051	COG0151F	phosphoribosylamine--glycine ligase			sp_0051	Streptococcus pneumoniae R6
purN	SP_0048	COG0299F	phosphoribosylglycinamide formyltransferase	DEG10070114	SP_0048	SP_0048	Streptococcus pneumoniae R6
-	SP_0046	COG0034F	amidophosphoribosyltransferase	DEG10070113	SP_0046	SP_0046	Streptococcus pneumoniae R6
-	SP_0037	COG0416I	glycerol-3-phosphate acyltransferase PlsX			SP_0037	Streptococcus pneumoniae R6
recO	SP_0036	COG1381L	DNA repair protein RecO			SP_0036	Streptococcus pneumoniae R6
-	SP_0032	COG0749L	DNA polymerase I			sp_0032	Streptococcus pneumoniae R6
-	SP_0027	COG0462FE	ribose-phosphate pyrophosphokinase			sp_0027	Streptococcus pneumoniae R6
-	SP_0012	COG0634F	hypoxanthine-guanine phosphoribosyltransferase	DEG10070003	SP_0012	SP_0012	Streptococcus pneumoniae R6
-	SP_0005	COG0193J	peptidyl-tRNA hydrolase	DEG10070002	SP_0005	SP_0005	Streptococcus pneumoniae R6
-	SP_0004	COG0012J	GTP-dependent nucleic acid-binding protein EngD	DEG10070001	SP_0004	SP_0004	Streptococcus pneumoniae R6
-	SP_0002	COG0592L	DNA polymerase III subunit beta			sp_0002	Streptococcus pneumoniae R6
dnaA	SP_0001	COG0593L	chromosome replication initiator DnaA			SP_0001	Streptococcus pneumoniae R6
-	SP_2183	-	hypothetical protein	DEG10070240	SP_2183		Streptococcus pneumoniae R6
-	SP_2165	COG4154G	fucose operon FucU protein	DEG10070238	SP_2165		Streptococcus pneumoniae R6
-	SP_2157	COG1454C	iron-containing alcohol dehydrogenase	DEG10070237	SP_2157		Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SP_2142	COG1940KG	ROK family protein	DEG10070236	SP_2142		Streptococcus pneumoniae R6
-	SP_2104	-	hypothetical protein	DEG10070235	SP_2104		Streptococcus pneumoniae R6
rnpA	SP_2042	COG0594J	ribonuclease P	DEG10070230	SP_2042		Streptococcus pneumoniae R6
-	SP_2040	COG1847R	jag protein	DEG10070107	SP_2040		Streptococcus pneumoniae R6
-	SP_1990	COG1658L	primase-like protein	DEG10070228	SP_1990		Streptococcus pneumoniae R6
-	SP_1882	COG3763S	hypothetical protein	DEG10070224	SP_1882		Streptococcus pneumoniae R6
-	SP_1859	COG3201H	transporter	DEG10070222	SP_1859		Streptococcus pneumoniae R6
-	SP_1856	COG0789K	MerR family transcriptional regulator	DEG10070221	SP_1856		Streptococcus pneumoniae R6
-	SP_1851	COG2050Q	hypothetical protein	DEG10070220	SP_1851		Streptococcus pneumoniae R6
-	SP_1838	COG2148M	glycosyl transferase family protein	DEG10070102	SP_1838		Streptococcus pneumoniae R6
-	SP_1750	COG2179R	hypothetical protein	DEG10070100	SP_1750		Streptococcus pneumoniae R6
-	SP_1749	COG1161R	GTP-binding protein YqeH	DEG10070099	SP_1749		Streptococcus pneumoniae R6
-	SP_1748	COG1534J	hypothetical protein	DEG10070098	SP_1748		Streptococcus pneumoniae R6
-	SP_1733	COG0631T	phosphatase	DEG10070095	SP_1733		Streptococcus pneumoniae R6
-	SP_1691	COG2731G	hypothetical protein	DEG10070208	SP_1691		Streptococcus pneumoniae R6
-	SP_1627	COG2910R	hypothetical protein	DEG10070201	SP_1627		Streptococcus pneumoniae R6
-	SP_1610	COG2384R	hypothetical protein	DEG10070086	SP_1610		Streptococcus pneumoniae R6
-	SP_1590	COG3442R	hypothetical protein	DEG10070084	SP_1590		Streptococcus pneumoniae R6
-	SP_1575	COG3935L	hypothetical protein	DEG10070196	SP_1575		Streptococcus pneumoniae R6
-	SP_1572	COG0783P	non-heme iron-containing ferritin	DEG10070194	SP_1572		Streptococcus pneumoniae R6
clpX	SP_1569	COG1219O	ATP-dependent protease ATP-binding subunit ClpX	DEG10070192	SP_1569		Streptococcus pneumoniae R6
-	SP_1561	COG1624S	hypothetical protein	DEG10070191	SP_1561		Streptococcus pneumoniae R6
-	SP_1552	COG0053P	cation efflux family protein	DEG10070189	SP_1552		Streptococcus pneumoniae R6
-	SP_1551	COG0474P	cation transporter E1-E2 family ATPase	DEG10070188	SP_1551		Streptococcus pneumoniae R6
-	SP_1550	COG0625O	glutathione S-transferase	DEG10070187	SP_1550		Streptococcus pneumoniae R6
-	SP_1545	COG5353S	hypothetical protein	DEG10070079	SP_1545		Streptococcus pneumoniae R6
-	SP_1429	COG0826O	U32 family peptidase	DEG10070177	SP_1429		Streptococcus pneumoniae R6
-	SP_1427	COG0826O	U32 family peptidase	DEG10070177	SP_1427		Streptococcus pneumoniae R6
rplJ	SP_1355	COG0244J	50S ribosomal protein L10		SP_1355		Streptococcus pneumoniae R6
rplL	SP_1354	COG0222J	50S ribosomal protein L7/L12		SP_1354		Streptococcus pneumoniae R6
-	SP_1288	COG2739S	DNA-binding protein	DEG10070071	SP_1288		Streptococcus pneumoniae R6
-	SP_1280	COG1399R	hypothetical protein	DEG10070175	SP_1280		Streptococcus pneumoniae R6
-	SP_1272	COG2244R	polysaccharide biosynthesis protein	DEG10070174	SP_1272		Streptococcus pneumoniae R6
ispD	SP_1271	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	DEG10070069	SP_1271		Streptococcus pneumoniae R6
-	SP_1247	COG1196D	hypothetical protein	DEG10070066	SP_1247		Streptococcus pneumoniae R6
-	SP_1198	COG1762GT	hypothetical protein	DEG10070172	SP_1198		Streptococcus pneumoniae R6
-	SP_1178	COG0695O	NrdH-redoxin	DEG10070170	SP_1178		Streptococcus pneumoniae R6
-	SP_1177	COG1925G	phosphocarrier protein HPr	DEG10070169	SP_1177		Streptococcus pneumoniae R6
-	SP_0979	COG1164E	oligoendopeptidase F	DEG10070157	SP_0979		Streptococcus pneumoniae R6
-	SP_0967	COG0319R	metalloprotease	DEG10070052	SP_0967		Streptococcus pneumoniae R6
-	SP_0913	COG3127Q	ABC transporter permease	DEG10070049	SP_0913		Streptococcus pneumoniae R6
-	SP_0884	COG4947S	hypothetical protein	DEG10070150	SP_0884		Streptococcus pneumoniae R6
-	SP_0873	COG0628R	hypothetical protein	DEG10070047	SP_0873		Streptococcus pneumoniae R6
-	SP_0864	COG1956T	hypothetical protein	DEG10070045	SP_0864		Streptococcus pneumoniae R6
-	SP_0761	COG0513LKJ	DEAD/DEAH box helicase	DEG10070145	SP_0761		Streptococcus pneumoniae R6
-	SP_0741	COG2081R	hypothetical protein	DEG10070037	SP_0741		Streptococcus pneumoniae R6
-	SP_0674	COG1234R	ribonuclease Z	DEG10070036	SP_0674		Streptococcus pneumoniae R6
-	SP_0672	COG2262R	GTP-binding protein HflX	DEG10070035	SP_0672		Streptococcus pneumoniae R6
-	SP_0554	COG2740K	hypothetical protein	DEG10070031	SP_0554		Streptococcus pneumoniae R6
-	SP_0368	COG0366G	cell wall surface anchor family protein	DEG10070130	SP_0368		Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
mraW	SP_0334	COG0275M	S-adenosyl-methyltransferase MraW	DEG10070013	SP_0334		Streptococcus pneumoniae R6
-	SP_0263	COG0750M	eep protein	DEG10070010	SP_0263		Streptococcus pneumoniae R6
-	SP_0192	COG4472S	hypothetical protein	DEG10070008	SP_0192		Streptococcus pneumoniae R6
spxA	SP_0189	COG1393P	transcriptional regulator Spx	DEG10070122	SP_0189		Streptococcus pneumoniae R6
-	SP_0158	COG1780F	flavoprotein NrdI	DEG10070121	SP_0158		Streptococcus pneumoniae R6
-	SP_0146	COG1296E	hypothetical protein	DEG10070120	SP_0146		Streptococcus pneumoniae R6
-	SP_0129	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10070006	SP_0129		Streptococcus pneumoniae R6
-	SP_0127	COG1214O	hypothetical protein	DEG10070117	SP_0127		Streptococcus pneumoniae R6
-	SP_0122	COG5503S	hypothetical protein	DEG10070005	SP_0122		Streptococcus pneumoniae R6
-	SP_0102	COG1215M	glycosyl transferase family protein	DEG10070116	SP_0102		Streptococcus pneumoniae R6
-	SP_0003	COG4481S	hypothetical protein	DEG10070112	SP_0003		Streptococcus pneumoniae R6

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
dnaA	PA14_00010	COG0593L	chromosomal replication initiation protein	DEG10150001	PA14_00010	PA14_00010	Pseudomonas aeruginosa UCBPP-PA14
dnaN	PA14_00020	COG0592L	DNA polymerase III subunit beta			PA14_00020	Pseudomonas aeruginosa UCBPP-PA14
recF	PA14_00030	COG1195L	recombination protein F				Pseudomonas aeruginosa UCBPP-PA14
gyrB	PA14_00050	COG0187L	DNA gyrase subunit B			PA14_00050	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00060	COG0204I	acyltransferase			PA14_00060	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00070	COG0241E	D,D-heptose 1,7-bisphosphate phosphatase			PA14_00070	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00080	-	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
glyS	PA14_00090	COG0751J	glycyl-tRNA synthetase subunit beta	DEG10150002	PA14_00090	PA14_00090	Pseudomonas aeruginosa UCBPP-PA14
glyQ	PA14_00100	COG0752J	glycyl-tRNA synthetase subunit alpha	DEG10150003	PA14_00100	PA14_00100	Pseudomonas aeruginosa UCBPP-PA14
tag	PA14_00110	COG2818L	DNA-3-methyladenine glycosidase I				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00120	COG1560M	lipid A biosynthesis lauroyl acyltransferase	DEG10300001	PA14_00120	PA14_00120	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00130	-	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00140	COG1738S	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00150	-	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00160	COG4783R	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
trkA	PA14_00170	COG0569P	potassium transporter peripheral membrane protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00180	COG0144J	tRNA and rRNA cytosine-C5-methylases				Pseudomonas aeruginosa UCBPP-PA14
fmt	PA14_00190	COG0223J	methionyl-tRNA formyltransferase	DEG10150004	PA14_00190	PA14_00190	Pseudomonas aeruginosa UCBPP-PA14
def	PA14_00200	COG0242J	peptide deformylase	DEG10150005	PA14_00200	PA14_00200	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00210	COG1652S	lysin domain-containing protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00230	COG0758LU	Rossmann fold nucleotide-binding protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00240	COG0009J	hypothetical protein	DEG10150006	PA14_00240		Pseudomonas aeruginosa UCBPP-PA14
qor	PA14_00250	COG0604CR	quinone oxidoreductase				Pseudomonas aeruginosa UCBPP-PA14
hemF	PA14_00280	COG0408H	coproporphyrinogen III oxidase	DEG10150007	PA14_00280	PA14_00280	Pseudomonas aeruginosa UCBPP-PA14
aroE	PA14_00290	COG0169E	shikimate 5-dehydrogenase				Pseudomonas aeruginosa UCBPP-PA14
plcB	PA14_00300	-	phospholipase C, PlcB				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00310	COG0760O	peptidyl-prolyl isomerase				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00320	-	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00340	COG0659P	sulfate transporter				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00360	COG2113E	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14
betC	PA14_00380	COG3119P	choline sulfatase				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00400	COG0583K	LysR family transcriptional regulator				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00410	COG3805Q	dioxygenase				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00420	COG2198T	histidine phosphotransfer domain-containing protein				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00430	COG2197TK	two-component response regulator				Pseudomonas aeruginosa UCBPP-PA14
trpA	PA14_00440	COG0159E	tryptophan synthase subunit alpha				Pseudomonas aeruginosa UCBPP-PA14
trpB	PA14_00450	COG0133E	tryptophan synthase subunit beta				Pseudomonas aeruginosa UCBPP-PA14
trpI	PA14_00460	COG0583K	transcriptional regulator TrpI				Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00470	COG3360S	hypothetical protein				Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
atpB	PA14_73310	COG0356C	F0F1 ATP synthase subunit A			PA14_73310	Pseudomonas aeruginosa UCBPP-PA14
atpE	PA14_73300	COG0636C	F0F1 ATP synthase subunit C	DEG10150335	PA14_73300	PA14_73300	Pseudomonas aeruginosa UCBPP-PA14
atpF	PA14_73290	COG0711C	F0F1 ATP synthase subunit B			PA14_73290	Pseudomonas aeruginosa UCBPP-PA14
atpH	PA14_73280	COG0712C	F0F1 ATP synthase subunit delta			PA14_73280	Pseudomonas aeruginosa UCBPP-PA14
atpA	PA14_73260	COG0056C	F0F1 ATP synthase subunit alpha	DEG10150334	PA14_73260	PA14_73260	Pseudomonas aeruginosa UCBPP-PA14
atpG	PA14_73250	COG0224C	F0F1 ATP synthase subunit gamma			PA14_73250	Pseudomonas aeruginosa UCBPP-PA14
atpD	PA14_73240	COG0055C	F0F1 ATP synthase subunit beta			PA14_73240	Pseudomonas aeruginosa UCBPP-PA14
atpC	PA14_73230	COG0355C	F0F1 ATP synthase subunit epsilon			PA14_73230	Pseudomonas aeruginosa UCBPP-PA14
glmU	PA14_73220	COG1207M	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase			PA14_73220	Pseudomonas aeruginosa UCBPP-PA14
glmS	PA14_73170	COG0449M	glucosamine--fructose-6-phosphate aminotransferase	DEG10150333	PA14_73170	PA14_73170	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_72880	COG1028IQR	short-chain dehydrogenase			PA14_72880	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_72870	COG0001H	aminotransferase			PA14_72870	Pseudomonas aeruginosa UCBPP-PA14
pdxY	PA14_72780	COG2240H	pyridoxamine kinase			PA14_72780	Pseudomonas aeruginosa UCBPP-PA14
polA	PA14_72490	COG0749L	DNA polymerase I			PA14_72490	Pseudomonas aeruginosa UCBPP-PA14
engB	PA14_72480	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10150332	PA14_72480	PA14_72480	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_71890	COG0427C	coenzyme A transferase			PA14_71890	Pseudomonas aeruginosa UCBPP-PA14
ubiA	PA14_70730	COG0382H	4-hydroxybenzoate octaprenyltransferase			PA14_70730	Pseudomonas aeruginosa UCBPP-PA14
ubiC	PA14_70720	COG3161H	hypothetical protein			PA14_70720	Pseudomonas aeruginosa UCBPP-PA14
rpoZ	PA14_70450	COG1758K	DNA-directed RNA polymerase subunit omega			PA14_70450	Pseudomonas aeruginosa UCBPP-PA14
gmk	PA14_70440	COG0194F	guanylate kinase			PA14_70440	Pseudomonas aeruginosa UCBPP-PA14
algC	PA14_70270	COG1109G	phosphomannomutase			PA14_70270	Pseudomonas aeruginosa UCBPP-PA14
dut	PA14_70260	COG0756F	deoxyuridine 5'-triphosphate nucleotidohydrolase	DEG10150327	PA14_70260	PA14_70260	Pseudomonas aeruginosa UCBPP-PA14
coaC	PA14_70240	COG0452H	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase	DEG10150326	PA14_70240	PA14_70240	Pseudomonas aeruginosa UCBPP-PA14
rpmB	PA14_70190	COG0227J	50S ribosomal protein L28	DEG10150325	PA14_70190	PA14_70190	Pseudomonas aeruginosa UCBPP-PA14
rpmG	PA14_70180	COG0267J	50S ribosomal protein L33			PA14_70180	Pseudomonas aeruginosa UCBPP-PA14
xpt	PA14_69940	COG0503F	xanthine phosphoribosyltransferase			PA14_69940	Pseudomonas aeruginosa UCBPP-PA14
rep	PA14_69910	COG0210L	ATP-dependent DNA helicase Rep			PA14_69910	Pseudomonas aeruginosa UCBPP-PA14
dapF	PA14_69690	COG0253E	diaminopimelate epimerase			PA14_69690	Pseudomonas aeruginosa UCBPP-PA14
hemC	PA14_69450	COG0181H	porphobilinogen deaminase	DEG10150323	PA14_69450	PA14_69450	Pseudomonas aeruginosa UCBPP-PA14
hemD	PA14_69440	COG1587H	uroporphyrinogen-III synthase	DEG10150322	PA14_69440	PA14_69440	Pseudomonas aeruginosa UCBPP-PA14
algQ	PA14_69390	COG3160K	anti-RNA polymerase sigma 70 factor			PA14_69390	Pseudomonas aeruginosa UCBPP-PA14
hemB	PA14_69240	COG0113H	delta-aminolevulinic acid dehydratase			PA14_69240	Pseudomonas aeruginosa UCBPP-PA14
ppk	PA14_69230	COG0855P	polyphosphate kinase			PA14_69230	Pseudomonas aeruginosa UCBPP-PA14
trxA	PA14_69200	COG3118O	thioredoxin	DEG10150321	PA14_69200	PA14_69200	Pseudomonas aeruginosa UCBPP-PA14
ubiH	PA14_68980	COG0654HC	2-octaprenyl-6-methoxyphenyl hydroxylase			PA14_68980	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_68955	COG0654HC	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase			PA14_68955	Pseudomonas aeruginosa UCBPP-PA14
rmlC	PA14_68210	COG1898M	dTDP-4-dehydrorhamnose 3,5-epimerase			PA14_68210	Pseudomonas aeruginosa UCBPP-PA14
rmlA	PA14_68200	COG1209M	glucose-1-phosphate thymidylyltransferase	DEG10150320	PA14_68200	PA14_68200	Pseudomonas aeruginosa UCBPP-PA14
rmlD	PA14_68190	COG1091M	dTDP-4-dehydrorhamnose reductase			PA14_68190	Pseudomonas aeruginosa UCBPP-PA14
rmlB	PA14_68170	COG1088M	dTDP-D-glucose 4,6-dehydratase			PA14_68170	Pseudomonas aeruginosa UCBPP-PA14
secB	PA14_67720	COG1952U	preprotein translocase subunit SecB			PA14_67720	Pseudomonas aeruginosa UCBPP-PA14
glnA	PA14_67600	COG0174E	glutamine synthetase	DEG10150318	PA14_67600	PA14_67600	Pseudomonas aeruginosa UCBPP-PA14
fbp	PA14_67490	COG0158G	fructose-1,6-bisphosphatase	DEG10150317	PA14_67490	PA14_67490	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
-	PA14_66990	COG1385S	16S ribosomal RNA methyltransferase RsmE	DEG10150316|D	PA14_66990	PA14_66990	Pseudomonas aeruginosa UCBPP-PA14
tatC	PA14_66980	COG0805U	sec-independent protein translocase TatC			PA14_66980	Pseudomonas aeruginosa UCBPP-PA14
tatB	PA14_66970	COG1826U	sec-independent translocase	DEG10150315	PA14_66970	PA14_66970	Pseudomonas aeruginosa UCBPP-PA14
tatA	PA14_66960	COG1826U	twin arginine translocase A	DEG10150314	PA14_66960	PA14_66960	Pseudomonas aeruginosa UCBPP-PA14
ubiE	PA14_66900	COG2226H	ubiquinone/menaquinone biosynthesis methyltransferase	DEG10150312	PA14_66900	PA14_66900	Pseudomonas aeruginosa UCBPP-PA14
argS	PA14_66750	COG0018J	arginyl-tRNA synthetase			PA14_66750	Pseudomonas aeruginosa UCBPP-PA14
priA	PA14_66720	COG1198L	primosome assembly protein PriA	DEG10150311	PA14_66720	PA14_66720	Pseudomonas aeruginosa UCBPP-PA14
rpmE	PA14_66710	COG0254J	50S ribosomal protein L31			PA14_66710	Pseudomonas aeruginosa UCBPP-PA14
ponA	PA14_66670	COG5009M	penicillin-binding protein 1A			PA14_66670	Pseudomonas aeruginosa UCBPP-PA14
hemE	PA14_66550	COG0407H	uroporphyrinogen decarboxylase	DEG10150309	PA14_66550	PA14_66550	Pseudomonas aeruginosa UCBPP-PA14
waaF	PA14_66250	COG0859M	heptosyltransferase II			PA14_66250	Pseudomonas aeruginosa UCBPP-PA14
waaC	PA14_66240	COG0859M	lipopolysaccharide heptosyltransferase I			PA14_66240	Pseudomonas aeruginosa UCBPP-PA14
waaG	PA14_66230	COG0438M	UDP-glucose:(heptosyl) LPS alpha 1,3-glucosyltransferase WaaG	DEG10150308	PA14_66230	PA14_66230	Pseudomonas aeruginosa UCBPP-PA14
waaP	PA14_66220	-	lipopolysaccharide kinase WaaP			PA14_66220	Pseudomonas aeruginosa UCBPP-PA14
rfaE	PA14_66060	COG2870M	bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase	DEG10150304	PA14_66060	PA14_66060	Pseudomonas aeruginosa UCBPP-PA14
waaA	PA14_65960	COG1519M	3-deoxy-D-manno-octulosonic-acid transferase	DEG10150301	PA14_65960	PA14_65960	Pseudomonas aeruginosa UCBPP-PA14
parE	PA14_65660	COG0187L	DNA topoisomerase IV subunit B	DEG10150299	PA14_65660	PA14_65660	Pseudomonas aeruginosa UCBPP-PA14
parC	PA14_65605	COG0188L	DNA topoisomerase IV subunit A	DEG10150298	PA14_65605	PA14_65605	Pseudomonas aeruginosa UCBPP-PA14
psd	PA14_65500	COG0688I	phosphatidylserine decarboxylase	DEG10150297	PA14_65500	PA14_65500	Pseudomonas aeruginosa UCBPP-PA14
hfq	PA14_65310	COG1923R	RNA-binding protein Hfq	DEG10150296	PA14_65310	PA14_65310	Pseudomonas aeruginosa UCBPP-PA14
purA	PA14_65230	COG0104F	adenylosuccinate synthetase			PA14_65230	Pseudomonas aeruginosa UCBPP-PA14
rnr	PA14_65200	COG0557K	exoribonuclease RNase R			PA14_65200	Pseudomonas aeruginosa UCBPP-PA14
rpsF	PA14_65180	COG0360J	30S ribosomal protein S6			PA14_65180	Pseudomonas aeruginosa UCBPP-PA14
rpsR	PA14_65170	COG0238J	30S ribosomal protein S18			PA14_65170	Pseudomonas aeruginosa UCBPP-PA14
rplI	PA14_65150	COG0359J	50S ribosomal protein L9			PA14_65150	Pseudomonas aeruginosa UCBPP-PA14
dnaB	PA14_65130	COG0305L	replicative DNA helicase			PA14_65130	Pseudomonas aeruginosa UCBPP-PA14
purH	PA14_64200	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase			PA14_64200	Pseudomonas aeruginosa UCBPP-PA14
accC	PA14_64110	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	DEG10150294	PA14_64110	PA14_64110	Pseudomonas aeruginosa UCBPP-PA14
accB	PA14_64100	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	DEG10150293	PA14_64100	PA14_64100	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_64000	COG0023J	translation initiation factor Sui1			PA14_64000	Pseudomonas aeruginosa UCBPP-PA14
fabG	PA14_63270	COG1028IQR	3-ketoacyl-ACP reductase			PA14_63270	Pseudomonas aeruginosa UCBPP-PA14
grpE	PA14_62990	COG0576O	heat shock protein GrpE	DEG10150290	PA14_62990	PA14_62990	Pseudomonas aeruginosa UCBPP-PA14
dnaK	PA14_62970	COG0443O	molecular chaperone DnaK			PA14_62970	Pseudomonas aeruginosa UCBPP-PA14
dapB	PA14_62940	COG0289E	dihydrodipicolinate reductase	DEG10150289	PA14_62940	PA14_62940	Pseudomonas aeruginosa UCBPP-PA14
ftsH	PA14_62860	COG0465O	cell division protein FtsH			PA14_62860	Pseudomonas aeruginosa UCBPP-PA14
folP	PA14_62850	COG0294H	dihydropteroate synthase	DEG10150288	PA14_62850	PA14_62850	Pseudomonas aeruginosa UCBPP-PA14
glmM	PA14_62840	COG1109G	phosphoglucosamine mutase			PA14_62840	Pseudomonas aeruginosa UCBPP-PA14
secG	PA14_62810	COG1314U	preprotein translocase subunit SecG			PA14_62810	Pseudomonas aeruginosa UCBPP-PA14
infB	PA14_62760	COG0532J	translation initiation factor IF-2	DEG10150286	PA14_62760	PA14_62760	Pseudomonas aeruginosa UCBPP-PA14
rpsO	PA14_62720	COG0184J	30S ribosomal protein S15	DEG10150285	PA14_62720	PA14_62720	Pseudomonas aeruginosa UCBPP-PA14
pnp	PA14_62710	COG1185J	polynucleotide phosphorylase			PA14_62710	Pseudomonas aeruginosa UCBPP-PA14
pgi	PA14_62620	COG0166G	glucose-6-phosphate isomerase			PA14_62620	Pseudomonas aeruginosa UCBPP-PA14
folK	PA14_62570	COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase			PA14_62570	Pseudomonas aeruginosa UCBPP-PA14
pcnB	PA14_62560	COG0617J	poly(A) polymerase			PA14_62560	Pseudomonas aeruginosa UCBPP-PA14
mrcB	PA14_62200	COG0744M	penicillin-binding protein 1B			PA14_62200	Pseudomonas aeruginosa UCBPP-PA14
pssA	PA14_62120	COG1183I	phosphatidylserine synthase			PA14_62120	Pseudomonas aeruginosa UCBPP-PA14
pth	PA14_61790	COG0193J	peptidyl-tRNA hydrolase	DEG10150283	PA14_61790	PA14_61790	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_61780	COG1825J	50S ribosomal protein L25			PA14_61780	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
prs	PA14_61770	COG0462FE	ribose-phosphate pyrophosphokinase			PA14_61770	Pseudomonas aeruginosa UCBPP-PA14
ipk	PA14_61750	COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	DEG10150282	PA14_61750	PA14_61750	Pseudomonas aeruginosa UCBPP-PA14
hemA	PA14_61710	COG0373H	glutamyl-tRNA reductase	DEG10150280	PA14_61710	PA14_61710	Pseudomonas aeruginosa UCBPP-PA14
prfA	PA14_61700	COG0216J	peptide chain release factor 1	DEG10150279	PA14_61700	PA14_61700	Pseudomonas aeruginosa UCBPP-PA14
murI	PA14_61660	COG0796M	glutamate racemase	DEG10150278	PA14_61660	PA14_61660	Pseudomonas aeruginosa UCBPP-PA14
hemH	PA14_61580	COG0276H	ferrochelatase	DEG10150277	PA14_61580	PA14_61580	Pseudomonas aeruginosa UCBPP-PA14
upp	PA14_61470	COG0035F	uracil phosphoribosyltransferase			PA14_61470	Pseudomonas aeruginosa UCBPP-PA14
glyA	PA14_60890	COG0112E	serine hydroxymethyltransferase	DEG10150275	PA14_60890	PA14_60890	Pseudomonas aeruginosa UCBPP-PA14
ispB	PA14_60470	COG0142H	octaprenyl-diphosphate synthase			PA14_60470	Pseudomonas aeruginosa UCBPP-PA14
rplU	PA14_60460	COG0261J	50S ribosomal protein L21			PA14_60460	Pseudomonas aeruginosa UCBPP-PA14
rpmA	PA14_60450	COG0211J	50S ribosomal protein L27	DEG10150274	PA14_60450	PA14_60450	Pseudomonas aeruginosa UCBPP-PA14
rpsT	PA14_60400	COG0268J	30S ribosomal protein S20	DEG10150273	PA14_60400	PA14_60400	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_60390	COG0728R	virulence factor, membrane protein	DEG10150272	PA14_60390	PA14_60390	Pseudomonas aeruginosa UCBPP-PA14
ribF	PA14_60380	COG0196H	bifunctional riboflavin kinase/FMN adenylyltransferase			PA14_60380	Pseudomonas aeruginosa UCBPP-PA14
ileS	PA14_60370	COG0060J	isoleucyl-tRNA synthetase	DEG10150271	PA14_60370	PA14_60370	Pseudomonas aeruginosa UCBPP-PA14
lspA	PA14_60360	COG0597MU	lipoprotein signal peptidase	DEG10150270	PA14_60360	PA14_60360	Pseudomonas aeruginosa UCBPP-PA14
ispH	PA14_60330	COG0761IM	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	DEG10150268	PA14_60330	PA14_60330	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_59150	COG0629L	single-stranded DNA-binding protein			PA14_59150	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_58990	COG0305L	DNA helicase			PA14_58990	Pseudomonas aeruginosa UCBPP-PA14
coaE	PA14_58780	COG0237H	dephospho-CoA kinase	DEG10150266	PA14_58780	PA14_58780	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_58610	COG2194R	hypothetical protein			PA14_58610	Pseudomonas aeruginosa UCBPP-PA14
gatB	PA14_58190	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10150264	PA14_58190	PA14_58190	Pseudomonas aeruginosa UCBPP-PA14
gatC	PA14_58170	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10150263	PA14_58170	PA14_58170	Pseudomonas aeruginosa UCBPP-PA14
mreB	PA14_58150	COG1077D	rod shape-determining protein MreB	DEG10150262	PA14_58150	PA14_58150	Pseudomonas aeruginosa UCBPP-PA14
mreD	PA14_58120	COG2891M	rod shape-determining protein MreD	DEG10150261	PA14_58120	PA14_58120	Pseudomonas aeruginosa UCBPP-PA14
rpoN	PA14_57940	COG1508K	RNA polymerase factor sigma-54			PA14_57940	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57930	COG1137R	ABC transporter ATP-binding protein			PA14_57930	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57900	COG1778R	hypothetical protein			PA14_57900	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57890	COG0794M	hypothetical protein			PA14_57890	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57880	COG1127Q	ABC transporter ATP-binding protein			PA14_57880	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57870	COG0767Q	ABC transporter permease			PA14_57870	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57850	COG1463Q	hypothetical protein			PA14_57850	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57840	COG2854Q	hypothetical protein			PA14_57840	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57830	COG1366T	hypothetical protein	DEG10150259	PA14_57830	PA14_57830	Pseudomonas aeruginosa UCBPP-PA14
murA	PA14_57810	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase			PA14_57810	Pseudomonas aeruginosa UCBPP-PA14
trpS	PA14_57670	COG0180J	tryptophanyl-tRNA synthetase			PA14_57670	Pseudomonas aeruginosa UCBPP-PA14
rplM	PA14_57590	COG0102J	50S ribosomal protein L13	DEG10150258	PA14_57590	PA14_57590	Pseudomonas aeruginosa UCBPP-PA14
rpsI	PA14_57580	COG0103J	30S ribosomal protein S9			PA14_57580	Pseudomonas aeruginosa UCBPP-PA14
gmhA	PA14_57500	COG0279G	phosphoheptose isomerase	DEG10150257	PA14_57500	PA14_57500	Pseudomonas aeruginosa UCBPP-PA14
ftsL	PA14_57440	COG3116D	cell division protein FtsL	DEG10150256	PA14_57440	PA14_57440	Pseudomonas aeruginosa UCBPP-PA14
ftsI	PA14_57425	COG0768M	penicillin-binding protein 3			PA14_57425	Pseudomonas aeruginosa UCBPP-PA14
murE	PA14_57410	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	DEG10150255	PA14_57410	PA14_57410	Pseudomonas aeruginosa UCBPP-PA14
murF	PA14_57390	COG0770M	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate--D-alanyl-D-alanine ligase	DEG10150254	PA14_57390	PA14_57390	Pseudomonas aeruginosa UCBPP-PA14
mraY	PA14_57380	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10150253	PA14_57380	PA14_57380	Pseudomonas aeruginosa UCBPP-PA14
murD	PA14_57370	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase			PA14_57370	Pseudomonas aeruginosa UCBPP-PA14
ftsW	PA14_57360	COG0772D	cell division protein FtsW	DEG10150252	PA14_57360	PA14_57360	Pseudomonas aeruginosa UCBPP-PA14
murG	PA14_57340	COG0707M	UDPdiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	DEG10150251	PA14_57340	PA14_57340	Pseudomonas aeruginosa UCBPP-PA14
murC	PA14_57330	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10150250	PA14_57330	PA14_57330	Pseudomonas aeruginosa UCBPP-PA14
ftsQ	PA14_57300	COG1589M	cell division protein FtsQ			PA14_57300	Pseudomonas aeruginosa UCBPP-PA14
ftsA	PA14_57290	COG0849D	cell division protein FtsA	DEG10150249	PA14_57290	PA14_57290	Pseudomonas aeruginosa UCBPP-PA14
ftsZ	PA14_57275	COG0206D	cell division protein FtsZ			PA14_57275	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
lpxC	PA14_57260	COG0774M	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase			PA14_57260	Pseudomonas aeruginosa UCBPP-PA14
secA	PA14_57220	COG0653U	preprotein translocase subunit SecA	DEG10150247	PA14_57220	PA14_57220	Pseudomonas aeruginosa UCBPP-PA14
fabG	PA14_57050	COG1028IQR	3-ketoacyl-ACP reductase			PA14_57050	Pseudomonas aeruginosa UCBPP-PA14
groES	PA14_57020	COG0234O	co-chaperonin GroES	DEG10150246	PA14_57020	PA14_57020	Pseudomonas aeruginosa UCBPP-PA14
groEL	PA14_57010	COG0459O	chaperonin GroEL			PA14_57010	Pseudomonas aeruginosa UCBPP-PA14
sodB	PA14_56780	COG0605P	superoxide dismutase	DEG10150244	PA14_56780	PA14_56780	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_56570	COG0204I	acyltransferase			PA14_56570	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_55550	COG1595K	ECF subfamily RNA polymerase sigma-70 factor			PA14_55550	Pseudomonas aeruginosa UCBPP-PA14
algU	PA14_54430	COG1595K	RNA polymerase sigma factor AlgU	DEG10300023	PA14_54430	PA14_54430	Pseudomonas aeruginosa UCBPP-PA14
era	PA14_54320	COG1159R	GTP-binding protein Era	DEG10150241	PA14_54320	PA14_54320	Pseudomonas aeruginosa UCBPP-PA14
pdxJ	PA14_54290	COG0854H	pyridoxine 5'-phosphate synthase			PA14_54290	Pseudomonas aeruginosa UCBPP-PA14
argD	PA14_52720	COG4992E	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase			PA14_52720	Pseudomonas aeruginosa UCBPP-PA14
alaS	PA14_52600	COG0013J	alanyl-tRNA synthetase			PA14_52600	Pseudomonas aeruginosa UCBPP-PA14
lysC	PA14_52580	COG0527E	aspartate kinase			PA14_52580	Pseudomonas aeruginosa UCBPP-PA14
mazG	PA14_52160	COG3956R	nucleoside triphosphate pyrophosphohydrolase			PA14_52160	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_52010	COG0593L	DNA replication initiation factor	DEG10150237	PA14_52010	PA14_52010	Pseudomonas aeruginosa UCBPP-PA14
proS	PA14_51900	COG0442J	prolyl-tRNA synthetase	DEG10150236	PA14_51900	PA14_51900	Pseudomonas aeruginosa UCBPP-PA14
aspS	PA14_51820	COG0173J	aspartyl-tRNA synthetase			PA14_51820	Pseudomonas aeruginosa UCBPP-PA14
ruvA	PA14_51790	COG0632L	Holliday junction DNA helicase RuvA	DEG10300026	PA14_51790	PA14_51790	Pseudomonas aeruginosa UCBPP-PA14
ruvB	PA14_51780	COG2255L	Holliday junction DNA helicase RuvB	DEG10300027	PA14_51780	PA14_51780	Pseudomonas aeruginosa UCBPP-PA14
dapA	PA14_51270	COG0329EM	dihydrodipicolinate synthase	DEG10150232	PA14_51270	PA14_51270	Pseudomonas aeruginosa UCBPP-PA14
pdxH	PA14_50800	COG0259H	pyridoxamine 5'-phosphate oxidase	DEG10150231	PA14_50800	PA14_50800	Pseudomonas aeruginosa UCBPP-PA14
nrdB	PA14_49470	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10150229	PA14_49470	PA14_49470	Pseudomonas aeruginosa UCBPP-PA14
nrdA	PA14_49460	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10150228	PA14_49460	PA14_49460	Pseudomonas aeruginosa UCBPP-PA14
dapE	PA14_49380	COG0624E	succinyl-diaminopimelate desuccinylase			PA14_49380	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_47400	COG1595K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_47400	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_46810	COG4941K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_46810	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_46660	COG1595K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_46660	Pseudomonas aeruginosa UCBPP-PA14
fabF2	PA14_46490	COG0304IQ	3-oxoacyl-ACP synthase			PA14_46490	Pseudomonas aeruginosa UCBPP-PA14
ccmA	PA14_45380	COG4133O	cytochrome c biogenesis protein CcmA	DEG10150218	PA14_45380	PA14_45380	Pseudomonas aeruginosa UCBPP-PA14
ccmB	PA14_45370	COG2386O	heme exporter protein CcmB			PA14_45370	Pseudomonas aeruginosa UCBPP-PA14
ccmC	PA14_45350	COG0755O	heme exporter protein CcmC	DEG10150217	PA14_45350	PA14_45350	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_45340	COG3114U	heme exporter protein	DEG10150216	PA14_45340	PA14_45340	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_44770	COG0402FR	guanine deaminase			PA14_44770	Pseudomonas aeruginosa UCBPP-PA14
zipA	PA14_44670	COG3115D	cell division protein ZipA			PA14_44670	Pseudomonas aeruginosa UCBPP-PA14
ligA	PA14_44660	COG0272L	NAD-dependent DNA ligase LigA	DEG10150213	PA14_44660	PA14_44660	Pseudomonas aeruginosa UCBPP-PA14
dnaX	PA14_44630	COG2812L	DNA polymerase III subunits gamma and tau			PA14_44630	Pseudomonas aeruginosa UCBPP-PA14
hemN	PA14_44470	COG0635H	coproporphyrinogen III oxidase			PA14_44470	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_44270	COG0425O	sulfur transfer protein SirA	DEG10150212	PA14_44270	PA14_44270	Pseudomonas aeruginosa UCBPP-PA14
sdhC	PA14_44060	COG2009C	succinate dehydrogenase, cytochrome b556 subunit	DEG10150209	PA14_44060	PA14_44060	Pseudomonas aeruginosa UCBPP-PA14
sdhD	PA14_44050	COG2142C	succinate dehydrogenase (D subunit)	DEG10150208	PA14_44050	PA14_44050	Pseudomonas aeruginosa UCBPP-PA14
sdhA	PA14_44030	COG1053C	succinate dehydrogenase flavoprotein subunit	DEG10150207	PA14_44030	PA14_44030	Pseudomonas aeruginosa UCBPP-PA14
sdhB	PA14_44020	COG0479C	succinate dehydrogenase iron-sulfur subunit	DEG10150206	PA14_44020	PA14_44020	Pseudomonas aeruginosa UCBPP-PA14
sucC	PA14_43950	COG0045C	succinyl-CoA synthetase subunit beta			PA14_43950	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
sucD	PA14_43940	COG0074C	succinyl-CoA synthetase subunit alpha			PA14_43940	Pseudomonas aeruginosa UCBPP-PA14
htpG	PA14_43850	COG0326O	heat shock protein 90			PA14_43850	Pseudomonas aeruginosa UCBPP-PA14
fabB	PA14_43690	COG0304IQ	3-oxoacyl-ACP synthase			PA14_43690	Pseudomonas aeruginosa UCBPP-PA14
fabA	PA14_43680	COG0764I	3-hydroxydecanoyl-ACP dehydratase	DEG10150203	PA14_43680	PA14_43680	Pseudomonas aeruginosa UCBPP-PA14
pscU	PA14_42660	COG4792U	translocation protein in type III secretion			PA14_42660	Pseudomonas aeruginosa UCBPP-PA14
pscT	PA14_42640	COG4791U	translocation protein in type III secretion			PA14_42640	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_42630	COG4794U	translocation protein in type III secretion			PA14_42630	Pseudomonas aeruginosa UCBPP-PA14
pscR	PA14_42620	COG4790U	type III secretion system protein			PA14_42620	Pseudomonas aeruginosa UCBPP-PA14
pscQ	PA14_42610	COG1886NU	type III secretion system protein			PA14_42610	Pseudomonas aeruginosa UCBPP-PA14
pscO	PA14_42580	-	translocation protein in type III secretion	DEG10150198	PA14_42580	PA14_42580	Pseudomonas aeruginosa UCBPP-PA14
pscN	PA14_42570	COG1157NU	type III secretion system ATPase			PA14_42570	Pseudomonas aeruginosa UCBPP-PA14
popN	PA14_42550	-	Type III secretion outer membrane protein PopN precursor			PA14_42550	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_42540	-	protein in type III secretion	DEG10150197	PA14_42540	PA14_42540	Pseudomonas aeruginosa UCBPP-PA14
pcrD	PA14_42500	COG4789U	type III secretory apparatus protein PcrD			PA14_42500	Pseudomonas aeruginosa UCBPP-PA14
pscC	PA14_42350	COG1450NU	Type III secretion outer membrane protein PscC precursor			PA14_42350	Pseudomonas aeruginosa UCBPP-PA14
pscG	PA14_42300	-	type III export protein PscG	DEG10150196	PA14_42300	PA14_42300	Pseudomonas aeruginosa UCBPP-PA14
pscH	PA14_42290	-	type III export protein PscH	DEG10150195	PA14_42290	PA14_42290	Pseudomonas aeruginosa UCBPP-PA14
pscJ	PA14_42270	COG4669U	pscJ type III export protein			PA14_42270	Pseudomonas aeruginosa UCBPP-PA14
pscL	PA14_42250	COG1317NU	type III secretion system protein			PA14_42250	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_41400	COG2908S	UDP-2,3-diacylglucosamine hydrolase	DEG10150192	PA14_41400	PA14_41400	Pseudomonas aeruginosa UCBPP-PA14
glnS	PA14_41380	COG0008J	glutaminyl-tRNA synthetase	DEG10150191	PA14_41380	PA14_41380	Pseudomonas aeruginosa UCBPP-PA14
cysS	PA14_41360	COG0215J	cysteinyl-tRNA synthetase	DEG10150190	PA14_41360	PA14_41360	Pseudomonas aeruginosa UCBPP-PA14
folD	PA14_41350	COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	DEG10150189	PA14_41350	PA14_41350	Pseudomonas aeruginosa UCBPP-PA14
fabI	PA14_41170	COG0623I	NADH-dependent enoyl-ACP reductase			PA14_41170	Pseudomonas aeruginosa UCBPP-PA14
rnhA	PA14_41060	COG0328L	ribonuclease H	DEG10150188	PA14_41060	PA14_41060	Pseudomonas aeruginosa UCBPP-PA14
dnaQ	PA14_41050	COG0847L	DNA polymerase III subunit epsilon	DEG10150187	PA14_41050	PA14_41050	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_40900	COG1028IQR	short-chain dehydrogenase			PA14_40900	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_39800	COG1595K	ECF subfamily RNA polymerase sigma-70 factor			PA14_39800	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_39690	COG1328F	anaerobic ribonucleoside triphosphate reductase			PA14_39690	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_39540	COG2080C	ferredoxin	DEG10150183	PA14_39540	PA14_39540	Pseudomonas aeruginosa UCBPP-PA14
galU	PA14_38350	COG1210M	UTP-glucose-1-phosphate uridylyltransferase			PA14_38350	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_37830	COG1104E	pyridoxal-phosphate dependent protein			PA14_37830	Pseudomonas aeruginosa UCBPP-PA14
pbpC	PA14_35190	COG0768M	penicillin-binding protein 3A			PA14_35190	Pseudomonas aeruginosa UCBPP-PA14
msuE	PA14_34180	COG0431R	NADH-dependent FMN reductase MsuE			PA14_34180	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_33800	COG1595K	RNA polymerase sigma factor	DEG10150160	PA14_33800	PA14_33800	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_32710	COG1595K	ECF subfamily RNA polymerase sigma-70 factor	DEG10150159	PA14_32710	PA14_32710	Pseudomonas aeruginosa UCBPP-PA14
pgsA	PA14_30670	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	DEG10150154	PA14_30670	PA14_30670	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30400	COG1553P	sulfur transfer complex subunit TusD	DEG10150153	PA14_30400	PA14_30400	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30390	COG2923P	sulfur relay protein TusC	DEG10150152	PA14_30390	PA14_30390	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30380	COG2168P	hypothetical protein	DEG10150151	PA14_30380	PA14_30380	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30370	COG2920P	hypothetical protein	DEG10150150	PA14_30370	PA14_30370	Pseudomonas aeruginosa UCBPP-PA14
serS	PA14_30330	COG0172J	seryl-tRNA synthetase	DEG10150149	PA14_30330	PA14_30330	Pseudomonas aeruginosa UCBPP-PA14
ftsK	PA14_30290	COG1674D	cell division protein FtsK			PA14_30290	Pseudomonas aeruginosa UCBPP-PA14
trxB1	PA14_30280	COG0492O	thioredoxin reductase 1			PA14_30280	Pseudomonas aeruginosa UCBPP-PA14
infA	PA14_30240	COG0361J	translation initiation factor IF-1	DEG10150146	PA14_30240	PA14_30240	Pseudomonas aeruginosa UCBPP-PA14
mnmA	PA14_30150	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10150145	PA14_30150	PA14_30150	Pseudomonas aeruginosa UCBPP-PA14
purB	PA14_30110	COG0015F	adenylosuccinate lyase	DEG10150144	PA14_30110	PA14_30110	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_29600	COG0720H	6-pyruvoyl-tetrahydropterin synthase	DEG10150142|D	PA14_29600	PA14_29600	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
pheS	PA14_28690	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10150140	PA14_28690	PA14_28690	Pseudomonas aeruginosa UCBPP-PA14
rplT	PA14_28680	COG0292J	50S ribosomal protein L20	DEG10150139	PA14_28680	PA14_28680	Pseudomonas aeruginosa UCBPP-PA14
rpmI	PA14_28670	COG0291J	50S ribosomal protein L35	DEG10030596|D	PA14_28670	PA14_28670	Pseudomonas aeruginosa UCBPP-PA14
thrS	PA14_28650	COG0441J	threonyl-tRNA synthetase			PA14_28650	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25900	COG3007S	trans-2-enoyl-CoA reductase	DEG10030340|D	PA14_25900	PA14_25900	Pseudomonas aeruginosa UCBPP-PA14
holB	PA14_25760	COG0470L	DNA polymerase III subunit delta'			PA14_25760	Pseudomonas aeruginosa UCBPP-PA14
tmk	PA14_25740	COG0125F	thymidylate kinase	DEG10150132	PA14_25740	PA14_25740	Pseudomonas aeruginosa UCBPP-PA14
fabF1	PA14_25690	COG0304IQ	3-oxoacyl-ACP synthase			PA14_25690	Pseudomonas aeruginosa UCBPP-PA14
fabG	PA14_25660	COG1028IQR	3-ketoacyl-ACP reductase	DEG10150130	PA14_25660	PA14_25660	Pseudomonas aeruginosa UCBPP-PA14
fabD	PA14_25650	COG0331I	malonyl-CoA-ACP transacylase			PA14_25650	Pseudomonas aeruginosa UCBPP-PA14
plsX	PA14_25640	COG0416I	glycerol-3-phosphate acyltransferase PlsX			PA14_25640	Pseudomonas aeruginosa UCBPP-PA14
rne	PA14_25560	COG1530J	ribonuclease E			PA14_25560	Pseudomonas aeruginosa UCBPP-PA14
murB	PA14_25550	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10150129	PA14_25550	PA14_25550	Pseudomonas aeruginosa UCBPP-PA14
kdsB	PA14_25530	COG1212M	3-deoxy-manno-octulosonate cytidylyltransferase	DEG10150127	PA14_25530	PA14_25530	Pseudomonas aeruginosa UCBPP-PA14
lpxK	PA14_25510	COG1663M	tetraacyldisaccharide 4'-kinase	DEG10150125	PA14_25510	PA14_25510	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25450	COG4591M	hypothetical protein	DEG10150124	PA14_25450	PA14_25450	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25440	COG1136V	lipoprotein releasing system, ATP-binding protein	DEG10150123	PA14_25440	PA14_25440	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25430	COG4591M	hypothetical protein	DEG10150122	PA14_25430	PA14_25430	Pseudomonas aeruginosa UCBPP-PA14
fadB	PA14_25080	COG1250I	multifunctional fatty acid oxidation complex subunit alpha	DEG10300050	PA14_25080	PA14_25080	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_24690	COG2027M	D-alanyl-D-alanine carboxypeptidase			PA14_24690	Pseudomonas aeruginosa UCBPP-PA14
folC	PA14_23880	COG0285H	folylpolyglutamate synthetase			PA14_23880	Pseudomonas aeruginosa UCBPP-PA14
accD	PA14_23860	COG0777I	acetyl-CoA carboxylase subunit beta	DEG10150121	PA14_23860	PA14_23860	Pseudomonas aeruginosa UCBPP-PA14
asd	PA14_23800	COG0136E	aspartate-semialdehyde dehydrogenase	DEG10150120	PA14_23800	PA14_23800	Pseudomonas aeruginosa UCBPP-PA14
gltX	PA14_23560	COG0008J	glutamyl-tRNA synthetase	DEG10150119	PA14_23560	PA14_23560	Pseudomonas aeruginosa UCBPP-PA14
rpsA	PA14_23330	COG0539J	30S ribosomal protein S1			PA14_23330	Pseudomonas aeruginosa UCBPP-PA14
cmk	PA14_23320	COG0283F	cytidylate kinase	DEG10150118	PA14_23320	PA14_23320	Pseudomonas aeruginosa UCBPP-PA14
gyrA	PA14_23260	COG0188L	DNA gyrase subunit A	DEG10150117	PA14_23260	PA14_23260	Pseudomonas aeruginosa UCBPP-PA14
ubiG	PA14_23220	COG2227H	3-demethylubiquinone-9 3-methyltransferase	DEG10150116	PA14_23220	PA14_23220	Pseudomonas aeruginosa UCBPP-PA14
htrB	PA14_22050	COG1560M	lipid A biosynthesis lauroyl acyltransferase			PA14_22050	Pseudomonas aeruginosa UCBPP-PA14
minE	PA14_22010	COG0851D	cell division topological specificity factor MinE	DEG10150115	PA14_22010	PA14_22010	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_21550	COG1595K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_21550	Pseudomonas aeruginosa UCBPP-PA14
phoA	PA14_21410	COG1785P	alkaline phosphatase			PA14_21410	Pseudomonas aeruginosa UCBPP-PA14
rfaD	PA14_20890	COG0451MG	ADP-L-glycero-D-manno-heptose-6-epimerase			PA14_20890	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_19990	COG1595K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_19990	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_19530	COG0431R	NAD(P)H-dependent FMN reductase			PA14_19530	Pseudomonas aeruginosa UCBPP-PA14
dcd	PA14_19090	COG0717F	deoxycytidine triphosphate deaminase			PA14_19090	Pseudomonas aeruginosa UCBPP-PA14
metG	PA14_19050	COG0143J	methionyl-tRNA synthetase			PA14_19050	Pseudomonas aeruginosa UCBPP-PA14
rnt	PA14_18700	COG0847L	ribonuclease T	DEG10150110	PA14_18700	PA14_18700	Pseudomonas aeruginosa UCBPP-PA14
rpmE2	PA14_17700	COG0254J	50S ribosomal protein L31			PA14_17700	Pseudomonas aeruginosa UCBPP-PA14
rpoS	PA14_17480	COG0568K	RNA polymerase sigma factor RpoS			PA14_17480	Pseudomonas aeruginosa UCBPP-PA14
surE	PA14_17450	COG0496R	stationary phase survival protein SurE			PA14_17450	Pseudomonas aeruginosa UCBPP-PA14
ispF	PA14_17420	COG0245I	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase			PA14_17420	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
ispD	PA14_17340	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase			PA14_17340	Pseudomonas aeruginosa UCBPP-PA14
kdsA	PA14_17310	COG2877M	2-dehydro-3-deoxyphosphooctonate aldolase			PA14_17310	Pseudomonas aeruginosa UCBPP-PA14
pyrG	PA14_17290	COG0504F	CTP synthetase	DEG10150107	PA14_17290	PA14_17290	Pseudomonas aeruginosa UCBPP-PA14
accA	PA14_17270	COG0825I	acetyl-CoA carboxylase carboxyltransferase subunit alpha	DEG10150105	PA14_17270	PA14_17270	Pseudomonas aeruginosa UCBPP-PA14
dnaE	PA14_17260	COG0587L	DNA polymerase III subunit alpha	DEG10150104	PA14_17260	PA14_17260	Pseudomonas aeruginosa UCBPP-PA14
rnhB	PA14_17230	COG0164L	ribonuclease HII			PA14_17230	Pseudomonas aeruginosa UCBPP-PA14
lpxB	PA14_17220	COG0763M	lipid-A-disaccharide synthase	DEG10150103	PA14_17220	PA14_17220	Pseudomonas aeruginosa UCBPP-PA14
lpxA	PA14_17210	COG1043M	UDP-N-acetylglucosamine acyltransferase	DEG10150102	PA14_17210	PA14_17210	Pseudomonas aeruginosa UCBPP-PA14
fabZ	PA14_17190	COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	DEG10150101	PA14_17190	PA14_17190	Pseudomonas aeruginosa UCBPP-PA14
lpxD	PA14_17180	COG1044M	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase			PA14_17180	Pseudomonas aeruginosa UCBPP-PA14
dxr	PA14_17130	COG0743I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	DEG10150099	PA14_17130	PA14_17130	Pseudomonas aeruginosa UCBPP-PA14
cdsA	PA14_17120	COG0575I	phosphatidate cytidylyltransferase	DEG10150098	PA14_17120	PA14_17120	Pseudomonas aeruginosa UCBPP-PA14
uppS	PA14_17110	COG0020I	UDP pyrophosphate synthetase	DEG10150097	PA14_17110	PA14_17110	Pseudomonas aeruginosa UCBPP-PA14
frr	PA14_17100	COG0233J	ribosome recycling factor	DEG10150096	PA14_17100	PA14_17100	Pseudomonas aeruginosa UCBPP-PA14
pyrH	PA14_17080	COG0528F	uridylate kinase	DEG10150095	PA14_17080	PA14_17080	Pseudomonas aeruginosa UCBPP-PA14
rpsB	PA14_17060	COG0052J	30S ribosomal protein S2	DEG10150094	PA14_17060	PA14_17060	Pseudomonas aeruginosa UCBPP-PA14
map	PA14_17050	COG0024J	methionine aminopeptidase	DEG10300061	PA14_17050	PA14_17050	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_17030	COG0436E	succinyldiaminopimelate transaminase			PA14_17030	Pseudomonas aeruginosa UCBPP-PA14
dapD	PA14_16950	COG2171E	tetrahydrodipicolinate succinylase	DEG10150093	PA14_16950	PA14_16950	Pseudomonas aeruginosa UCBPP-PA14
plsB	PA14_16860	COG2937I	glycerol-3-phosphate acyltransferase			PA14_16860	Pseudomonas aeruginosa UCBPP-PA14
adk	PA14_16700	COG0563F	adenylate kinase			PA14_16700	Pseudomonas aeruginosa UCBPP-PA14
lysS	PA14_16530	COG1190J	lysyl-tRNA synthetase	DEG10150090	PA14_16530	PA14_16530	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_16510	COG1186J	peptide chain release factor 2			PA14_16510	Pseudomonas aeruginosa UCBPP-PA14
rplS	PA14_16000	COG0335J	50S ribosomal protein L19			PA14_16000	Pseudomonas aeruginosa UCBPP-PA14
rimM	PA14_15980	COG0806J	16S rRNA-processing protein RimM	DEG10150089	PA14_15980	PA14_15980	Pseudomonas aeruginosa UCBPP-PA14
rpsP	PA14_15970	COG0228J	30S ribosomal protein S16	DEG10150088	PA14_15970	PA14_15970	Pseudomonas aeruginosa UCBPP-PA14
ffh	PA14_15960	COG0541U	signal recognition particle protein Ffh			PA14_15960	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_15810	COG2222M	aminotransferase			PA14_15810	Pseudomonas aeruginosa UCBPP-PA14
guaA	PA14_15340	COG0519F	GMP synthase			PA14_15340	Pseudomonas aeruginosa UCBPP-PA14
guaB	PA14_15310	COG0516F	inosine 5'-monophosphate dehydrogenase	DEG10150086	PA14_15310	PA14_15310	Pseudomonas aeruginosa UCBPP-PA14
engA	PA14_14930	COG1160R	GTP-binding protein EngA	DEG10150084	PA14_14930	PA14_14930	Pseudomonas aeruginosa UCBPP-PA14
hisS	PA14_14890	COG0124J	histidyl-tRNA synthetase			PA14_14890	Pseudomonas aeruginosa UCBPP-PA14
ispG	PA14_14880	COG0821I	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	DEG10150083	PA14_14880	PA14_14880	Pseudomonas aeruginosa UCBPP-PA14
ndk	PA14_14820	COG0105F	nucleoside diphosphate kinase	DEG10150082	PA14_14820	PA14_14820	Pseudomonas aeruginosa UCBPP-PA14
fdx2	PA14_14800	COG0633C	ferredoxin 2Fe-2S	DEG10150081	PA14_14800	PA14_14800	Pseudomonas aeruginosa UCBPP-PA14
hscB	PA14_14770	COG1076O	co-chaperone HscB	DEG10150080	PA14_14770	PA14_14770	Pseudomonas aeruginosa UCBPP-PA14
iscS	PA14_14730	COG1104E	cysteine desulfurase			PA14_14730	Pseudomonas aeruginosa UCBPP-PA14
secF	PA14_14650	COG0341U	preprotein translocase subunit SecF	DEG10150077	PA14_14650	PA14_14650	Pseudomonas aeruginosa UCBPP-PA14
yajC	PA14_14610	COG1862U	preprotein translocase subunit YajC			PA14_14610	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14510	COG0795R	hypothetical protein	DEG10150076	PA14_14510	PA14_14510	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14500	COG0795R	hypothetical protein			PA14_14500	Pseudomonas aeruginosa UCBPP-PA14
holC	PA14_14460	COG2927L	DNA polymerase III subunit chi			PA14_14460	Pseudomonas aeruginosa UCBPP-PA14
valS	PA14_14440	COG0525J	valyl-tRNA synthetase	DEG10150075	PA14_14440	PA14_14440	Pseudomonas aeruginosa UCBPP-PA14
prfC	PA14_13410	COG4108J	peptide chain release factor 3	DEG10300067	PA14_13410	PA14_13410	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_13330	COG3540P	hypothetical protein			PA14_13330	Pseudomonas aeruginosa UCBPP-PA14
hemL	PA14_12390	COG0001H	glutamate-1-semialdehyde aminotransferase			PA14_12390	Pseudomonas aeruginosa UCBPP-PA14
leuS	PA14_12230	COG0495J	leucyl-tRNA synthetase			PA14_12230	Pseudomonas aeruginosa UCBPP-PA14
holA	PA14_12200	COG1466L	DNA polymerase III subunit delta	DEG10150067	PA14_12200	PA14_12200	Pseudomonas aeruginosa UCBPP-PA14
lis	PA14_12130	COG0320H	lipoyl synthase	DEG10150066	PA14_12130	PA14_12130	Pseudomonas aeruginosa UCBPP-PA14
lipB	PA14_12120	COG0321H	lipoate-protein ligase B	DEG10150065	PA14_12120	PA14_12120	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
dacC	PA14_12100	COG1686M	D-ala-D-ala-carboxypeptidase			PA14_12100	Pseudomonas aeruginosa UCBPP-PA14
pbpA	PA14_12060	COG0768M	penicillin-binding protein 2			PA14_12060	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11860	COG0163H	aromatic acid decarboxylase	DEG10150063	PA14_11860	PA14_11860	Pseudomonas aeruginosa UCBPP-PA14
ispA	PA14_11560	COG0142H	geranyltranstransferase			PA14_11560	Pseudomonas aeruginosa UCBPP-PA14
dxs	PA14_11550	COG1154HI	1-deoxy-D-xylulose-5-phosphate synthase	DEG10150062	PA14_11550	PA14_11550	Pseudomonas aeruginosa UCBPP-PA14
ribA	PA14_11510	COG0807H	GTP cyclohydrolase II	DEG10150061	PA14_11510	PA14_11510	Pseudomonas aeruginosa UCBPP-PA14
pgpA	PA14_11470	COG1267I	phosphatidylglycerophosphatase A			PA14_11470	Pseudomonas aeruginosa UCBPP-PA14
nusB	PA14_11450	COG0781K	transcription antitermination protein NusB	DEG10150059	PA14_11450	PA14_11450	Pseudomonas aeruginosa UCBPP-PA14
ribH	PA14_11430	COG0054H	6,7-dimethyl-8-ribityllumazine synthase			PA14_11430	Pseudomonas aeruginosa UCBPP-PA14
ribC	PA14_11410	COG0307H	riboflavin synthase subunit alpha	DEG10150058	PA14_11410	PA14_11410	Pseudomonas aeruginosa UCBPP-PA14
ribD	PA14_11400	COG0117H	riboflavin-specific deaminase/reductase	DEG10150057	PA14_11400	PA14_11400	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11340	COG3118O	thioredoxin			PA14_11340	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11260	COG0451MG	epimerase	DEG10150056	PA14_11260	PA14_11260	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11030	COG0001H	aminotransferase			PA14_11030	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11020	COG1028IQR	3-ketoacyl-ACP reductase			PA14_11020	Pseudomonas aeruginosa UCBPP-PA14
tyrS	PA14_10420	COG0162J	tyrosyl-tRNA synthetase			PA14_10420	Pseudomonas aeruginosa UCBPP-PA14
rplQ	PA14_09130	COG0203J	50S ribosomal protein L17	DEG10150053	PA14_09130	PA14_09130	Pseudomonas aeruginosa UCBPP-PA14
rpoA	PA14_09115	COG0202K	DNA-directed RNA polymerase subunit alpha			PA14_09115	Pseudomonas aeruginosa UCBPP-PA14
rpsD	PA14_09100	COG0522J	30S ribosomal protein S4			PA14_09100	Pseudomonas aeruginosa UCBPP-PA14
rpsK	PA14_09090	COG0100J	30S ribosomal protein S11	DEG10150052	PA14_09090	PA14_09090	Pseudomonas aeruginosa UCBPP-PA14
rpsM	PA14_09080	COG0099J	30S ribosomal protein S13	DEG10150051	PA14_09080	PA14_09080	Pseudomonas aeruginosa UCBPP-PA14
rpmJ	PA14_09070	COG0257J	50S ribosomal protein L36	DEG10150050	PA14_09070	PA14_09070	Pseudomonas aeruginosa UCBPP-PA14
secY	PA14_09050	COG0201U	preprotein translocase subunit SecY			PA14_09050	Pseudomonas aeruginosa UCBPP-PA14
rplO	PA14_09040	COG0200J	50S ribosomal protein L15	DEG10150049	PA14_09040	PA14_09040	Pseudomonas aeruginosa UCBPP-PA14
rpmD	PA14_09030	COG1841J	50S ribosomal protein L30	DEG10150048	PA14_09030	PA14_09030	Pseudomonas aeruginosa UCBPP-PA14
rpsE	PA14_09020	COG0098J	30S ribosomal protein S5			PA14_09020	Pseudomonas aeruginosa UCBPP-PA14
rplR	PA14_09010	COG0256J	50S ribosomal protein L18	DEG10150047	PA14_09010	PA14_09010	Pseudomonas aeruginosa UCBPP-PA14
rplF	PA14_09000	COG0097J	50S ribosomal protein L6	DEG10150046	PA14_09000	PA14_09000	Pseudomonas aeruginosa UCBPP-PA14
rpsH	PA14_08990	COG0096J	30S ribosomal protein S8			PA14_08990	Pseudomonas aeruginosa UCBPP-PA14
rpsN	PA14_08980	COG0199J	30S ribosomal protein S14	DEG10150045	PA14_08980	PA14_08980	Pseudomonas aeruginosa UCBPP-PA14
rplE	PA14_08970	COG0094J	50S ribosomal protein L5	DEG10150044	PA14_08970	PA14_08970	Pseudomonas aeruginosa UCBPP-PA14
rplX	PA14_08960	COG0198J	50S ribosomal protein L24	DEG10150043	PA14_08960	PA14_08960	Pseudomonas aeruginosa UCBPP-PA14
rplN	PA14_08950	COG0093J	50S ribosomal protein L14	DEG10150042	PA14_08950	PA14_08950	Pseudomonas aeruginosa UCBPP-PA14
rpsQ	PA14_08940	COG0186J	30S ribosomal protein S17	DEG10150041	PA14_08940	PA14_08940	Pseudomonas aeruginosa UCBPP-PA14
rpmC	PA14_08930	COG0255J	50S ribosomal protein L29	DEG10150040	PA14_08930	PA14_08930	Pseudomonas aeruginosa UCBPP-PA14
rplP	PA14_08920	COG0197J	50S ribosomal protein L16	DEG10150039	PA14_08920	PA14_08920	Pseudomonas aeruginosa UCBPP-PA14
rpsC	PA14_08910	COG0092J	30S ribosomal protein S3	DEG10150038	PA14_08910	PA14_08910	Pseudomonas aeruginosa UCBPP-PA14
rplV	PA14_08900	COG0091J	50S ribosomal protein L22	DEG10150037	PA14_08900	PA14_08900	Pseudomonas aeruginosa UCBPP-PA14
rpsS	PA14_08890	COG0185J	30S ribosomal protein S19	DEG10150036	PA14_08890	PA14_08890	Pseudomonas aeruginosa UCBPP-PA14
rplB	PA14_08880	COG0090J	50S ribosomal protein L2			PA14_08880	Pseudomonas aeruginosa UCBPP-PA14
rplW	PA14_08870	COG0089J	50S ribosomal protein L23			PA14_08870	Pseudomonas aeruginosa UCBPP-PA14
rplD	PA14_08860	COG0088J	50S ribosomal protein L4			PA14_08860	Pseudomonas aeruginosa UCBPP-PA14
rplC	PA14_08850	COG0087J	50S ribosomal protein L3			PA14_08850	Pseudomonas aeruginosa UCBPP-PA14
rpsJ	PA14_08840	COG0051J	30S ribosomal protein S10	DEG10150035	PA14_08840	PA14_08840	Pseudomonas aeruginosa UCBPP-PA14
rpsG	PA14_08810	COG0049J	30S ribosomal protein S7	DEG10150034	PA14_08810	PA14_08810	Pseudomonas aeruginosa UCBPP-PA14
rpsL	PA14_08790	COG0048J	30S ribosomal protein S12			PA14_08790	Pseudomonas aeruginosa UCBPP-PA14
rpoC	PA14_08780	COG0086K	DNA-directed RNA polymerase subunit beta'			PA14_08780	Pseudomonas aeruginosa UCBPP-PA14
rpoB	PA14_08760	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10150033	PA14_08760	PA14_08760	Pseudomonas aeruginosa UCBPP-PA14
rplL	PA14_08750	COG0222J	50S ribosomal protein L7/L12	DEG10150032	PA14_08750	PA14_08750	Pseudomonas aeruginosa UCBPP-PA14
rplJ	PA14_08740	COG0244J	50S ribosomal protein L10			PA14_08740	Pseudomonas aeruginosa UCBPP-PA14
rplA	PA14_08730	COG0081J	50S ribosomal protein L1	DEG10150031	PA14_08730	PA14_08730	Pseudomonas aeruginosa UCBPP-PA14
rplK	PA14_08720	COG0080J	50S ribosomal protein L11	DEG10150030	PA14_08720	PA14_08720	Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
secE	PA14_08695	COG0690U	preprotein translocase subunit SecE			PA14_08695	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08630	COG1521K	pantothenate kinase	DEG10150029	PA14_08630	PA14_08630	Pseudomonas aeruginosa UCBPP-PA14
tyrZ	PA14_08560	COG0162J	tyrosyl-tRNA synthetase			PA14_08560	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08400	COG2941H	hypothetical protein	DEG10150026	PA14_08400	PA14_08400	Pseudomonas aeruginosa UCBPP-PA14
rpe	PA14_07910	COG0036G	ribulose-phosphate 3-epimerase	DEG10150022	PA14_07910	PA14_07910	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_07600	COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase			PA14_07600	Pseudomonas aeruginosa UCBPP-PA14
folB	PA14_07590	COG1539H	dihydroneopterin aldolase	DEG10150021	PA14_07590	PA14_07590	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_07580	COG0344S	glycerol-3-phosphate acyltransferase PlsY			PA14_07580	Pseudomonas aeruginosa UCBPP-PA14
rpsU	PA14_07560	COG0828J	30S ribosomal protein S21			PA14_07560	Pseudomonas aeruginosa UCBPP-PA14
dnaG	PA14_07530	COG0358L	DNA primase			PA14_07530	Pseudomonas aeruginosa UCBPP-PA14
rpoD	PA14_07520	COG0568K	RNA polymerase sigma factor RpoD	DEG10150019	PA14_07520	PA14_07520	Pseudomonas aeruginosa UCBPP-PA14
fda	PA14_07230	COG0191G	fructose-1,6-bisphosphate aldolase	DEG10150018	PA14_07230	PA14_07230	Pseudomonas aeruginosa UCBPP-PA14
tktA	PA14_07130	COG0021G	transketolase			PA14_07130	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_06920	COG4992E	class III pyridoxal phosphate-dependent aminotransferase			PA14_06920	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_06450	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit			PA14_06450	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_05560	COG0513LKJ	ATP-dependent RNA helicase			PA14_05560	Pseudomonas aeruginosa UCBPP-PA14
pyrR	PA14_05270	COG2065F	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase			PA14_05270	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_05040	COG0635H	coproporphyrinogen III oxidase			PA14_05040	Pseudomonas aeruginosa UCBPP-PA14
trmB	PA14_05000	COG0220R	tRNA (guanine-N(7)-)-methyltransferase			PA14_05000	Pseudomonas aeruginosa UCBPP-PA14
mtgA	PA14_04950	COG0744M	monofunctional biosynthetic peptidoglycan transglycosylase			PA14_04950	Pseudomonas aeruginosa UCBPP-PA14
rpoH	PA14_04930	COG0568K	RNA polymerase factor sigma-32			PA14_04930	Pseudomonas aeruginosa UCBPP-PA14
ftsX	PA14_04920	COG2177D	cell division protein FtsX	DEG10300010	PA14_04920	PA14_04920	Pseudomonas aeruginosa UCBPP-PA14
ftsE	PA14_04910	COG2884D	cell division ATP-binding protein FtsE	DEG10300009	PA14_04910	PA14_04910	Pseudomonas aeruginosa UCBPP-PA14
ftsY	PA14_04900	COG0552U	signal recognition particle receptor FtsY			PA14_04900	Pseudomonas aeruginosa UCBPP-PA14
coaD	PA14_04760	COG0669H	phosphopantetheine adenylyltransferase	DEG10150013	PA14_04760	PA14_04760	Pseudomonas aeruginosa UCBPP-PA14
folA	PA14_04580	COG0262H	dihydrofolate reductase	DEG10150012	PA14_04580	PA14_04580	Pseudomonas aeruginosa UCBPP-PA14
thyA	PA14_04480	COG0207F	thymidylate synthase	DEG10150011	PA14_04480	PA14_04480	Pseudomonas aeruginosa UCBPP-PA14
rpiA	PA14_04310	COG0120G	ribose-5-phosphate isomerase A	DEG10150010	PA14_04310	PA14_04310	Pseudomonas aeruginosa UCBPP-PA14
fabG	PA14_02300	COG1028IQR	3-ketoacyl-ACP reductase			PA14_02300	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_01840	COG1595K	RNA polymerase ECF-subfamily sigma-70 factor			PA14_01840	Pseudomonas aeruginosa UCBPP-PA14
nuh	PA14_01760	COG1957F	nonspecific ribonucleoside hydrolase			PA14_01760	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_01660	COG0402FR	guanine deaminase			PA14_01660	Pseudomonas aeruginosa UCBPP-PA14
-	PA14_01190	COG0304IQ	3-oxoacyl-ACP synthase			PA14_01190	Pseudomonas aeruginosa UCBPP-PA14
gltP	PA14_72340	COG1301C	glutamate/aspartate:proton symporter	DEG10300114	PA14_72340		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_72260	COG1247M	hypothetical protein	DEG10300113	PA14_72260		Pseudomonas aeruginosa UCBPP-PA14
aspA	PA14_71650	COG1027E	aspartate ammonia-lyase	DEG10300111	PA14_71650		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_71360	-	hypothetical protein	DEG10300109	PA14_71360		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_70860	COG0226P	hypothetical protein	DEG10300108	PA14_70860		Pseudomonas aeruginosa UCBPP-PA14
pstB	PA14_70810	COG1117P	phosphate transporter ATP-binding protein	DEG10300105	PA14_70810		Pseudomonas aeruginosa UCBPP-PA14
rubA1	PA14_70640	COG1773C	rubredoxin 1	DEG10300104	PA14_70640		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_70560	COG0583K	LysR family transcriptional regulator	DEG10300103	PA14_70560		Pseudomonas aeruginosa UCBPP-PA14
pyrE	PA14_70370	COG0461F	orotate phosphoribosyltransferase	DEG10300102	PA14_70370		Pseudomonas aeruginosa UCBPP-PA14
algR	PA14_69470	COG3279KT	alginate biosynthesis regulatory protein AlgR	DEG10300100	PA14_69470		Pseudomonas aeruginosa UCBPP-PA14
dsbH	PA14_69400	COG1495O	disulfide bond formation protein	DEG10300099	PA14_69400		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_69030	COG3027S	hypothetical protein	DEG10300097	PA14_69030		Pseudomonas aeruginosa UCBPP-PA14
ompR	PA14_68700	COG0745TK	osmolarity response regulator	DEG10300096	PA14_68700		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_67790	COG4942D	membrane-bound metallopeptidase	DEG10300092	PA14_67790		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_67750	COG0607P	rhodanese-like domain-containing protein	DEG10300091	PA14_67750		Pseudomonas aeruginosa UCBPP-PA14
hslU	PA14_66790	COG1220O	ATP-dependent protease ATP-binding subunit HslU	DEG10300089	PA14_66790		Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
hslV	PA14_66770	COG5405O	ATP-dependent protease peptidase subunit	DEG10300088	PA14_66770		Pseudomonas aeruginosa UCBPP-PA14
serB	PA14_65560	COG0560E	phosphoserine phosphatase	DEG10300087	PA14_65560		Pseudomonas aeruginosa UCBPP-PA14
hflK	PA14_65280	COG0330O	protease subunit HflK	DEG10300086	PA14_65280		Pseudomonas aeruginosa UCBPP-PA14
hflC	PA14_65270	COG0330O	protease subunit HflC	DEG10300085	PA14_65270		Pseudomonas aeruginosa UCBPP-PA14
smpB	PA14_63060	COG0691O	SsrA-binding protein	DEG10300083	PA14_63060		Pseudomonas aeruginosa UCBPP-PA14
sspB	PA14_57520	COG2969R	ClpXP protease specificity-enhancing factor	DEG10300081	PA14_57520		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57510	COG2823R	secreted lipoprotein	DEG10300080	PA14_57510		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57240	COG0739M	hypothetical protein	DEG10300077	PA14_57240		Pseudomonas aeruginosa UCBPP-PA14
fxsA	PA14_57030	COG3030R	FxsA protein	DEG10300075	PA14_57030		Pseudomonas aeruginosa UCBPP-PA14
mvaT	PA14_56070	-	transcriptional regulator MvaT, P16 subunit	DEG10300072	PA14_56070		Pseudomonas aeruginosa UCBPP-PA14
tgt	PA14_14600	COG0343J	queuine tRNA-ribosyltransferase	DEG10300064	PA14_14600		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_22320	COG3205S	hypothetical protein	DEG10300058	PA14_22320		Pseudomonas aeruginosa UCBPP-PA14
edd	PA14_22910	COG0129EG	phosphogluconate dehydratase	DEG10300056	PA14_22910		Pseudomonas aeruginosa UCBPP-PA14
mtnA	PA14_23250	COG0182J	methylthioribose-1-phosphate isomerase	DEG10300055	PA14_23250		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25030	-	hypothetical protein	DEG10300052	PA14_25030		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25050	-	hypothetical protein	DEG10300051	PA14_25050		Pseudomonas aeruginosa UCBPP-PA14
sth	PA14_25390	COG1249C	soluble pyridine nucleotide transhydrogenase	DEG10300048	PA14_25390		Pseudomonas aeruginosa UCBPP-PA14
pyrF	PA14_26890	COG0284F	orotidine 5'-phosphate decarboxylase	DEG10300047	PA14_26890		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_27370	COG0513LKJ	ATP-dependent RNA helicase	DEG10300046	PA14_27370		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_27770	COG1131V	ABC transporter ATP-binding protein	DEG10300045	PA14_27770		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_28730	COG0789K	transcriptional regulator	DEG10300042	PA14_28730		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_29720	COG3212S	hypothetical protein	DEG10300040	PA14_29720		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30140	COG2915R	hypothetical protein	DEG10300038	PA14_30140		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30410	COG0670R	hypothetical protein	DEG10300037	PA14_30410		Pseudomonas aeruginosa UCBPP-PA14
ppiC1	PA14_38700	COG0760O	peptidyl-prolyl cis-trans isomerase C1	DEG10300032	PA14_38700		Pseudomonas aeruginosa UCBPP-PA14
tig	PA14_41250	COG0544O	trigger factor	DEG10300030	PA14_41250		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_41590	COG0668M	cytoplasmic membrane protein	DEG10300029	PA14_41590		Pseudomonas aeruginosa UCBPP-PA14
dctA	PA14_49130	COG1301C	C4-dicarboxylate transporter DctA	DEG10300028	PA14_49130		Pseudomonas aeruginosa UCBPP-PA14
relA	PA14_52180	COG0317TK	GTP pyrophosphokinase	DEG10300025	PA14_52180		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08540	COG0739M	hypothetical protein	DEG10300022	PA14_08540		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08500	COG1664M	hypothetical protein	DEG10300021	PA14_08500		Pseudomonas aeruginosa UCBPP-PA14
oprM	PA14_05550	COG1538MU	major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	DEG10300016	PA14_05550		Pseudomonas aeruginosa UCBPP-PA14
pilG	PA14_05320	COG0745TK	twitching motility protein PilG	DEG10300012	PA14_05320		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_05130	COG0762S	hypothetical protein	DEG10300011	PA14_05130		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_04330	COG5528S	hypothetical protein	DEG10300008	PA14_04330		Pseudomonas aeruginosa UCBPP-PA14
spuB	PA14_03880	COG0174E	glutamine synthetase	DEG10300007	PA14_03880		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00590	COG4380S	lipoprotein	DEG10300005	PA14_00590		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_72070	-	hypothetical protein	DEG10150331	PA14_72070		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_71380	-	hypothetical protein	DEG10150330	PA14_71380		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_71370	COG3027S	hypothetical protein	DEG10150329	PA14_71370		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_71300	COG2025C	electron transfer flavoprotein alpha subunit	DEG10150328	PA14_71300		Pseudomonas aeruginosa UCBPP-PA14
lppL	PA14_69660	COG5567N	lipopeptide LppL	DEG10150324	PA14_69660		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_67700	-	hypothetical protein	DEG10150319	PA14_67700		Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
ubiB	PA14_66920	COG0661R	ubiquinone biosynthesis protein UbiB	DEG10150313	PA14_66920		Pseudomonas aeruginosa UCBPP-PA14
aroK	PA14_66610	COG0703E	shikimate kinase	DEG10150310	PA14_66610		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_66190	COG0372C	hypothetical protein	DEG10150307	PA14_66190		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_66090	-	hypothetical protein	DEG10150306	PA14_66090		Pseudomonas aeruginosa UCBPP-PA14
msbA	PA14_66080	COG1132V	transport protein MsbA	DEG10150305	PA14_66080		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_66010	COG0667C	hypothetical protein	DEG10150303	PA14_66010		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_66000	COG0578C	hypothetical protein	DEG10150302	PA14_66000		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_65690	COG1409R	hypothetical protein	DEG10150300	PA14_65690		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_65260	COG3242S	hypothetical protein	DEG10150295	PA14_65260		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_63820	-	hypothetical protein	DEG10150292	PA14_63820		Pseudomonas aeruginosa UCBPP-PA14
omlA	PA14_63030	COG2913J	outer membrane lipoprotein OmlA precursor	DEG10150291	PA14_63030		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_62780	COG0779S	hypothetical protein	DEG10150287	PA14_62780		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_61890	-	hypothetical protein	DEG10150284	PA14_61890		Pseudomonas aeruginosa UCBPP-PA14
lolB	PA14_61740	COG3017M	outer membrane lipoprotein LolB	DEG10150281	PA14_61740		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_61360	COG2937I	hypothetical protein	DEG10150276	PA14_61360		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_60350	COG1047O	peptidyl-prolyl cis-trans isomerase, FkbP-type	DEG10150269	PA14_60350		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_58860	-	hypothetical protein	DEG10150267	PA14_58860		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_58210	COG0797M	hypothetical protein	DEG10150265	PA14_58210		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57920	COG1934S	hypothetical protein	DEG10150260	PA14_57920		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_57250	COG4701S	hypothetical protein	DEG10150248	PA14_57250		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_56910	-	hypothetical protein	DEG10150245	PA14_56910		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_56670	-	hypothetical protein	DEG10150243	PA14_56670		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_54480	COG0354R	hypothetical protein	DEG10150242	PA14_54480		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_53690	-	hypothetical protein	DEG10150240	PA14_53690		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_52530	COG2932K	transcriptional regulator	DEG10150239	PA14_52530		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_52500	-	hypothetical protein	DEG10150238	PA14_52500		Pseudomonas aeruginosa UCBPP-PA14
tolR	PA14_51740	COG0848U	TolR protein	DEG10150235	PA14_51740		Pseudomonas aeruginosa UCBPP-PA14
tolA	PA14_51730	COG3064M	TolA protein	DEG10150234	PA14_51730		Pseudomonas aeruginosa UCBPP-PA14
tolB	PA14_51720	COG0823U	translocation protein TolB	DEG10150233	PA14_51720		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_50510	COG5626S	hypothetical protein	DEG10150230	PA14_50510		Pseudomonas aeruginosa UCBPP-PA14
pcpS	PA14_49340	COG2977Q	protein Pcprotein PS	DEG10150227	PA14_49340		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_48750	COG1765O	hypothetical protein	DEG10150226	PA14_48750		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_48620	-	clavaminic acid synthetase	DEG10150225	PA14_48620		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_48550	COG3319Q	hypothetical protein	DEG10150224	PA14_48550		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_47420	COG1937S	hypothetical protein	DEG10150223	PA14_47420		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_47010	-	hypothetical protein	DEG10150222	PA14_47010		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_46740	COG2606S	hypothetical protein	DEG10150221	PA14_46740		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_46390	-	hypothetical protein	DEG10150220	PA14_46390		Pseudomonas aeruginosa UCBPP-PA14
cheY	PA14_45620	COG2204T	two-component response regulator CheY	DEG10150219	PA14_45620		Pseudomonas aeruginosa UCBPP-PA14
ccmH	PA14_45290	COG3088O	cytochrome C-type biogenesis protein CcmH	DEG10150215	PA14_45290		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_44780	COG1802K	transcriptional regulator	DEG10150214	PA14_44780		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_44170	-	hypothetical protein	DEG10150211	PA14_44170		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_44140	COG3123S	hypothetical protein	DEG10150210	PA14_44140		Pseudomonas aeruginosa UCBPP-PA14
sucA	PA14_44010	COG0567C	2-oxoglutarate dehydrogenase E1	DEG10150205	PA14_44010		Pseudomonas aeruginosa UCBPP-PA14
sucB	PA14_44000	COG0508C	dihydrolipoamide succinyltransferase	DEG10150204	PA14_44000		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_43600	COG2050Q	hypothetical protein	DEG10150202	PA14_43600		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_43580	COG2207K	transcriptional regulator	DEG10150201	PA14_43580		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_43570	COG1280E	hypothetical protein	DEG10150200	PA14_43570		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_43230	-	hypothetical protein	DEG10150199	PA14_43230		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_42180	COG0518F	hypothetical protein	DEG10150194	PA14_42180		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_41960	-	hypothetical protein	DEG10150193	PA14_41960		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_40210	COG1709K	hypothetical protein	DEG10150186	PA14_40210		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_40150	COG1396K	transcriptional regulator	DEG10150185	PA14_40150		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_39630	COG0811U	hypothetical protein	DEG10150184	PA14_39630		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_39100	COG3232E	hypothetical protein	DEG10150182	PA14_39100		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_38880	COG1357S	hypothetical protein	DEG10150181	PA14_38880		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_38270	-	hypothetical protein	DEG10150180	PA14_38270		Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
-	PA14_38020	COG1359S	ntibiotic biosynthesis monooxygenase	DEG10150179	PA14_38020		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_37910	COG0583K	LysR family transcriptional regulator	DEG10150178	PA14_37910		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_37420	COG3712PT	transmembrane sensor protein	DEG10150177	PA14_37420		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_36850	-	hypothetical protein	DEG10150176	PA14_36850		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_36770	-	hypothetical protein	DEG10150175	PA14_36770		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_36560	-	hypothetical protein	DEG10150174	PA14_36560		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_36530	-	hypothetical protein	DEG10150173	PA14_36530		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_35200	COG3153R	acetyltransferase	DEG10150172	PA14_35200		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_35170	COG0789K	redox-sensing activator of soxS	DEG10150171	PA14_35170		Pseudomonas aeruginosa UCBPP-PA14
arsC	PA14_35100	COG0394T	arsenate reductase	DEG10150170	PA14_35100		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_35040	-	hypothetical protein	DEG10150169	PA14_35040		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_35000	-	hypothetical protein	DEG10150168	PA14_35000		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34740	-	hypothetical protein	DEG10150167	PA14_34740		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34700	COG1680V	beta lactamase	DEG10150166	PA14_34700		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34580	COG1960I	hypothetical protein	DEG10150165	PA14_34580		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34500	COG1116P	ABC transporter ATP-binding protein	DEG10150164	PA14_34500		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34370	COG3839G	ABC maltose/mannitol transporter ATP-binding protein	DEG10150163	PA14_34370		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_34030	COG3157S	hypothetical protein	DEG10150162	PA14_34030		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_33920	COG2197TK	transcriptional regulator	DEG10150161	PA14_33920		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_32420	COG0604CR	oxidoreductase	DEG10150158	PA14_32420		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_31750	COG0204I	acyltransferase	DEG10150157	PA14_31750		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_31360	-	hypothetical protein	DEG10150156	PA14_31360		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_30770	COG1522K	AsnC family transcriptional regulator	DEG10150155	PA14_30770		Pseudomonas aeruginosa UCBPP-PA14
lolA	PA14_30310	COG2834M	outer-membrane lipoprotein carrier protein	DEG10150148	PA14_30310		Pseudomonas aeruginosa UCBPP-PA14
aat	PA14_30270	COG2360O	leucyl/phenylalanyl-tRNA--protein transferase	DEG10150147	PA14_30270		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_29750	-	hypothetical protein	DEG10150143	PA14_29750		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_29190	-	hypothetical protein	DEG10150141	PA14_29190		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_28500	-	hypothetical protein	DEG10150137	PA14_28500		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_27170	-	hypothetical protein	DEG10150136	PA14_27170		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25930	COG2073H	hypothetical protein	DEG10150135	PA14_25930		Pseudomonas aeruginosa UCBPP-PA14
etfB	PA14_25860	COG2086C	electron transfer flavoprotein subunit beta	DEG10150133	PA14_25860		Pseudomonas aeruginosa UCBPP-PA14
acpP	PA14_25670	COG0236IQ	acyl carrier protein	DEG10150131	PA14_25670		Pseudomonas aeruginosa UCBPP-PA14
ptpA	PA14_25540	COG0394T	phosphotyrosine protein phosphatase	DEG10150128	PA14_25540		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_25520	COG2835S	hypothetical protein	DEG10150126	PA14_25520		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_20460	-	hypothetical protein	DEG10150114	PA14_20460		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_19590	COG3585H	molybdopterin-binding protein	DEG10150113	PA14_19590		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_18930	COG2878C	electron transport complex protein RnfB	DEG10150112	PA14_18930		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_18800	COG2608P	hypothetical protein	DEG10150111	PA14_18800		Pseudomonas aeruginosa UCBPP-PA14
fdxA	PA14_17490	COG1146C	ferredoxin I	DEG10150109	PA14_17490		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_17330	COG2919D	hypothetical protein	DEG10150108	PA14_17330		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_17280	COG0037D	hypothetical protein	DEG10150106	PA14_17280		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_17150	COG4775M	outer membrane antigen	DEG10150100	PA14_17150		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_16920	COG2166R	hypothetical protein	DEG10150092	PA14_16920		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_16710	COG1214O	hypothetical protein	DEG10150091	PA14_16710		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_15680	COG0590FJ	hypothetical protein	DEG10150087	PA14_15680		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_15110	-	hypothetical protein	DEG10150085	PA14_15110		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14750	COG0316S	iron-binding protein IscA	DEG10150079	PA14_14750		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14740	COG0822C	scaffold protein	DEG10150078	PA14_14740		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14250	COG4276S	hypothetical protein	DEG10150074	PA14_14250		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_14160	COG0110R	acetyltransferase	DEG10150073	PA14_14160		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_13680	COG0300R	short chain dehydrogenase	DEG10150072	PA14_13680		Pseudomonas aeruginosa UCBPP-PA14
tauD	PA14_12970	COG2175Q	taurine dioxygenase	DEG10150071	PA14_12970		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_12310	COG0319R	metalloprotease	DEG10150070	PA14_12310		Pseudomonas aeruginosa UCBPP-PA14
lnt	PA14_12280	COG0815M	apolipoprotein N-acyltransferase	DEG10150069	PA14_12280		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_12210	COG2980M	hypothetical protein	DEG10150068	PA14_12210		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_12110	COG2921S	hypothetical protein	DEG10150064	PA14_12110		Pseudomonas aeruginosa UCBPP-PA14
thiL	PA14_11460	COG0611H	thiamine monophosphate kinase	DEG10150060	PA14_11460		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11150	COG1476K	transcriptional regulator	DEG10150055|D	PA14_11150		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_11010	COG3553S	hypothetical protein	DEG10150054	PA14_11010		Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain
-	PA14_08510	COG0316S	iron-sulfur cluster insertion protein ErpA	DEG10150028	PA14_08510		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08470	COG1981S	hypothetical protein	DEG10150027	PA14_08470		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08250	COG4718S	hypothetical protein	DEG10150025	PA14_08250		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_08190	-	hypothetical protein	DEG10150024	PA14_08190		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_07970	COG1734T	hypothetical protein	DEG10150023	PA14_07970		Pseudomonas aeruginosa UCBPP-PA14
gcp	PA14_07570	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10150020	PA14_07570		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_06860	-	hypothetical protein	DEG10150017	PA14_06860		Pseudomonas aeruginosa UCBPP-PA14
nirC	PA14_06730	COG2010C	c-type cytochrome	DEG10150016	PA14_06730		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_06580	-	hypothetical protein	DEG10150015	PA14_06580		Pseudomonas aeruginosa UCBPP-PA14
yqgF	PA14_05280	COG0816L	Holliday junction resolvase-like protein	DEG10150014	PA14_05280		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_01560	COG2824P	hypothetical protein	DEG10150009	PA14_01560		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_00630	-	hypothetical protein	DEG10150008	PA14_00630		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_46610	COG2020O	hypothetical protein	DEG10050071	PA14_46610		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_27150	COG4181Q	ABC transporter ATP-binding protein	DEG10030734	PA14_27150		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_18180	COG1359S	hypothetical protein	DEG10030716	PA14_18180		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_21970	COG2188K	transcriptional regulator	DEG10030707	PA14_21970		Pseudomonas aeruginosa UCBPP-PA14
-	PA14_58830	COG0456R	hypothetical protein	DEG10030672	PA14_58830		Pseudomonas aeruginosa UCBPP-PA14

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
						PA5570	Pseudomonas aeruginosa PAO1
ddlB	PA4410	COG1181M	D-alanine--D-alanine ligase	DEG10300078	**PA5560**	PA5560	Pseudomonas aeruginosa PAO1
-	PA0170	-	hypothetical protein			PA5559	Pseudomonas aeruginosa PAO1
-	PA4404	COG0739M	hypothetical protein	DEG10300077	**PA5558**	PA5558	Pseudomonas aeruginosa PAO1
-	PA4398	COG5000T	two-component sensor	DEG10300076	**PA5557**	PA5557	Pseudomonas aeruginosa PAO1
-	PA4387	COG3030R	FxsA protein	DEG10300075	**PA5556**	PA5556	Pseudomonas aeruginosa PAO1
pykA	PA4329	COG0469G	pyruvate kinase	DEG10300074	**PA5555**	PA5555	Pseudomonas aeruginosa PAO1
sbcB	PA4316	COG2925L	exonuclease I	DEG10300073	**PA5554**	PA5554	Pseudomonas aeruginosa PAO1
-	PA0169	COG2199T	hypothetical protein			PA5553	Pseudomonas aeruginosa PAO1
mvaT	PA4315	-	transcriptional regulator MvaT	DEG10300072	**PA5552**	PA5552	Pseudomonas aeruginosa PAO1
-	PA4223	COG1132V	ABC transporter ATP-binding protein	DEG10300071	**PA5549**	PA5549	Pseudomonas aeruginosa PAO1
algC	PA5322	-	phosphomannomutase			PA5524	Pseudomonas aeruginosa PAO1
dut	PA5321	COG0756F	deoxyuridine 5'-triphosphate nucleotidohydrolase			PA5523	Pseudomonas aeruginosa PAO1
-	PA5313	COG0161H	omega amino acid--pyruvate transaminase			PA5516	Pseudomonas aeruginosa PAO1
-	PA5290	COG0606O	hypothetical protein			PA5493	Pseudomonas aeruginosa PAO1
-	PA4222	COG1132V	ABC transporter ATP-binding protein	DEG10300070	**PA5492**	PA5492	Pseudomonas aeruginosa PAO1
-	PA5237	COG0043H	hypothetical protein			PA5445	Pseudomonas aeruginosa PAO1
pgpA	PA4050	COG1267I	phosphatidylglycerophosphatase A	DEG10300068	**PA5358**	PA5358	Pseudomonas aeruginosa PAO1
mutY	PA5147	COG1194L	A / G specific adenine glycosylase			PA5357	Pseudomonas aeruginosa PAO1
-	PA5126	-	hypothetical protein			PA5337	Pseudomonas aeruginosa PAO1
prfC	PA3903	COG4108J	peptide chain release factor 3	DEG10300067	**PA5336**	PA5336	Pseudomonas aeruginosa PAO1
gloA3	PA5111	COG0346E	lactoylglutathione lyase			PA5322	Pseudomonas aeruginosa PAO1
pcs	PA3857	COG1183I	phosphatidylcholine synthase	DEG10300066	**PA5321**	PA5321	Pseudomonas aeruginosa PAO1
queA	PA3824	COG0809J	S-adenosylmethionine--tRNA ribosyltransferase-isomerase	DEG10300065	**PA5320**	PA5320	Pseudomonas aeruginosa PAO1
-	PA0166	COG2233F	transporter			PA5316	Pseudomonas aeruginosa PAO1
blc	PA5107	COG3040M	outer membrane lipoprotein Blc			PA5315	Pseudomonas aeruginosa PAO1
-	PA5090	COG3501S	hypothetical protein			PA5298	Pseudomonas aeruginosa PAO1
tgt	PA3823	COG0343J	queuine tRNA-ribosyltransferase	DEG10300064	**PA5296**	**PA5296**	Pseudomonas aeruginosa PAO1
thrC	PA3735	COG0498E	threonine synthase	DEG10300063	**PA5278**	PA5278	Pseudomonas aeruginosa PAO1
-	PA3733	COG1804C	hypothetical protein	DEG10300062	**PA5260**	PA5260	Pseudomonas aeruginosa PAO1
map	PA3657	COG0024J	methionine aminopeptidase	DEG10300061	**PA5259**	PA5259	Pseudomonas aeruginosa PAO1
-	PA5047	COG4784R	hypothetical protein			PA5255	Pseudomonas aeruginosa PAO1
-	PA3649	COG0750M	hypothetical protein	DEG10300060	**PA5243**	PA5243	Pseudomonas aeruginosa PAO1
hemE	PA5034	COG0407H	uroporphyrinogen decarboxylase			PA5242	Pseudomonas aeruginosa PAO1
-	PA0164	COG0405E	gamma-glutamyltranspeptidase			PA5240	Pseudomonas aeruginosa PAO1
trkH	PA3210	COG0168P	potassium uptake protein TrkH	DEG10300057	**PA5223**	PA5223	Pseudomonas aeruginosa PAO1
edd	PA3194	COG0129EG	phosphogluconate dehydratase	DEG10300056	**PA5221**	PA5221	Pseudomonas aeruginosa PAO1
-	PA3086	COG0705R	hypothetical protein	DEG10300054	**PA5164**	PA5164	Pseudomonas aeruginosa PAO1
pyrD	PA3050	COG0167F	dihydroorotate dehydrogenase	DEG10300053	**PA5163**	PA5163	Pseudomonas aeruginosa PAO1
-	PA3018	-	hypothetical protein	DEG10300052	**PA5162**	PA5162	Pseudomonas aeruginosa PAO1
-	PA3016	-	hypothetical protein	DEG10300051	**PA5161**	PA5161	Pseudomonas aeruginosa PAO1
-	PA4925	COG0668M	hypothetical protein			PA5128	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
faoA	PA3014	COG1250I	multifunctional fatty acid oxidation complex subunit alpha	DEG10300050	**PA5119**	PA5119	Pseudomonas aeruginosa PAO1
foaB	PA3013	COG0183I	3-ketoacyl-CoA thiolase	DEG10300049	**PA5110**	PA5110	Pseudomonas aeruginosa PAO1
-	PA4870	COG1734T	hypothetical protein			PA5071	Pseudomonas aeruginosa PAO1
-	PA4869	-	hypothetical protein			PA5070	Pseudomonas aeruginosa PAO1
ureC	PA4868	COG0804E	urease subunit alpha			PA5069	Pseudomonas aeruginosa PAO1
ureB	PA4867	COG0832E	urease subunit beta			PA5068	Pseudomonas aeruginosa PAO1
pyrF	PA2876	COG0284F	orotidine 5'-phosphate decarboxylase	DEG10300047	**PA5063**	PA5063	Pseudomonas aeruginosa PAO1
-	PA2840	COG0513LKJ	ATP-dependent RNA helicase	DEG10300046	**PA5051**	PA5051	Pseudomonas aeruginosa PAO1
opdC	PA0162	-	histidine porin OpdC			PA5050	Pseudomonas aeruginosa PAO1
-	PA4852	COG0042J	hypothetical protein			PA5049	Pseudomonas aeruginosa PAO1
aroQ1	PA4846	COG0757E	3-dehydroquinate dehydratase			PA5045	Pseudomonas aeruginosa PAO1
-	PA2812	COG1131V	ABC transporter ATP-binding protein	DEG10300045	**PA5034**	PA5034	Pseudomonas aeruginosa PAO1
-	PA2811	COG1682GM	ABC transporter permease	DEG10300044	**PA5012**	PA5012	Pseudomonas aeruginosa PAO1
-	PA2806	COG2904S	7-cyano-7-deazaguanine reductase	DEG10300043	**PA5011**	PA5011	Pseudomonas aeruginosa PAO1
-	PA2737	-	hypothetical protein	DEG10300042	**PA5010**	PA5010	Pseudomonas aeruginosa PAO1
-	PA2658	COG3212S	hypothetical protein	DEG10300040	**PA5009**	PA5009	Pseudomonas aeruginosa PAO1
-	PA2491	COG0604CR	oxidoreductase	DEG10300035	**PA4996**	PA4996	Pseudomonas aeruginosa PAO1
ppiC1	PA1996	COG0760O	peptidyl-prolyl cis-trans isomerase C1	DEG10300032	**PA4988**	PA4988	Pseudomonas aeruginosa PAO1
ppiD	PA1805	COG0760O	peptidyl-prolyl cis-trans isomerase D	DEG10300031	**PA4967**	PA4967	Pseudomonas aeruginosa PAO1
tig	PA1800	COG0544O	trigger factor	DEG10300030	**PA4964**	PA4964	Pseudomonas aeruginosa PAO1
cmpX	PA1775	COG0668M	hypothetical protein	DEG10300029	**PA4957**	PA4957	Pseudomonas aeruginosa PAO1
omlA	PA4765	COG2913J	outer membrane lipoprotein OmlA			PA4944	Pseudomonas aeruginosa PAO1
dctA	PA1183	COG1301C	C4-dicarboxylate transporter DctA	DEG10300028	**PA4938**	PA4938	Pseudomonas aeruginosa PAO1
-	PA4757	COG1280E	leucine export protein LeuE			PA4937	Pseudomonas aeruginosa PAO1
ruvB	PA0967	COG2255L	Holliday junction DNA helicase RuvB	DEG10300027	**PA4935**	PA4935	Pseudomonas aeruginosa PAO1
-	PA0156	COG0845M	resistance-nodulation-cell division (RND) efflux membrane fusion protein			PA4934	Pseudomonas aeruginosa PAO1
-	PA4754	-	hypothetical protein			PA4932	Pseudomonas aeruginosa PAO1
ruvA	PA0966	COG0632L	Holliday junction DNA helicase RuvA	DEG10300026	**PA4931**	PA4931	Pseudomonas aeruginosa PAO1
-	PA4677	COG4690E	hypothetical protein			PA4854	Pseudomonas aeruginosa PAO1
-	PA0858	COG1054R	hypothetical protein	DEG10300024	**PA4848**	PA4848	Pseudomonas aeruginosa PAO1
algU	PA0762	COG1595K	RNA polymerase sigma factor AlgU	DEG10300023	**PA4847**	PA4847	Pseudomonas aeruginosa PAO1
pcaR	PA0155	COG1414K	transcriptional regulator PcaR			PA4840	Pseudomonas aeruginosa PAO1
-	PA4612	COG0666R	hypothetical protein			PA4786	Pseudomonas aeruginosa PAO1
pcaG	PA0154	COG3485Q	protocatechuate 3,4-dioxygenase subunit alpha			PA4762	Pseudomonas aeruginosa PAO1
glyS	PA0008	COG0751J	glycyl-tRNA synthetase subunit beta		**PA4761**	PA4761	Pseudomonas aeruginosa PAO1
-	PA0664	COG1664M	hypothetical protein	DEG10300021	**PA4759**	PA4759	Pseudomonas aeruginosa PAO1
-	PA0663	-	hypothetical protein	DEG10300020	**PA4751**	**PA4751**	Pseudomonas aeruginosa PAO1
argC	PA0662	COG0002E	N-acetyl-gamma-glutamyl-phosphate reductase	DEG10300019	**PA4750**	PA4750	Pseudomonas aeruginosa PAO1
ksgA	PA0592	COG0030J	dimethyladenosine transferase	DEG10300018	**PA4749**	PA4749	Pseudomonas aeruginosa PAO1
pcaH	PA0153	COG3485Q	protocatechuate 3,4-dioxygenase subunit beta			PA4747	Pseudomonas aeruginosa PAO1
mexR	PA0424	COG1846K	multidrug resistance operon repressor MexR	DEG10300015	**PA4744**	PA4744	Pseudomonas aeruginosa PAO1
pcaQ	PA0152	COG0583K	transcriptional regulator PcaQ			PA4741	Pseudomonas aeruginosa PAO1
chpA	PA0413	COG0643NT	chemotactic signal transduction system protein	DEG10300014	**PA4740**	PA4740	Pseudomonas aeruginosa PAO1
-	PA4575	-	hypothetical protein			PA4732	Pseudomonas aeruginosa PAO1
pilJ	PA0411	COG0840NT	twitching motility protein PilJ	DEG10300013	**PA4728**	PA4728	Pseudomonas aeruginosa PAO1
-	PA4571	COG3258C	cytochrome C			PA4727	Pseudomonas aeruginosa PAO1
-	PA4539	COG1485R	hypothetical protein			PA4700	Pseudomonas aeruginosa PAO1
-	PA0151	COG1629P	TonB-dependent receptor			PA4693	Pseudomonas aeruginosa PAO1
-	PA0392	COG0762S	hypothetical protein	DEG10300011	**PA4672**	PA4672	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA4513	COG0369P	oxidoreductase			PA4671	Pseudomonas aeruginosa PAO1
ftsX	PA0375	COG2177D	cell division protein FtsX	DEG10300010	**PA4670**	PA4670	Pseudomonas aeruginosa PAO1
ftsE	PA0374	COG2884D	cell division protein FtsE	DEG10300009	**PA4669**	PA4669	Pseudomonas aeruginosa PAO1
-	PA0149	COG1595K	ECF subfamily sigma-70 factor			PA4666	Pseudomonas aeruginosa PAO1
spuB	PA0298	COG0174E	glutamine synthetase	DEG10300007	**PA4665**	PA4665	Pseudomonas aeruginosa PAO1
-	PA0148	COG1816F	adenosine deaminase			PA4662	Pseudomonas aeruginosa PAO1
coIII	PA0108	COG1845C	cytochrome C oxidase subunit III	DEG10300006	**PA4655**	PA4655	Pseudomonas aeruginosa PAO1
-	PA4496	COG0747E	ABC transporter			PA4646	Pseudomonas aeruginosa PAO1
trkA	PA0016	COG0569P	potassium transporter peripheral membrane protein	DEG10300004	**PA4602**	PA4602	Pseudomonas aeruginosa PAO1
-	PA0014	-	hypothetical protein	DEG10300003	**PA4569**	PA4569	Pseudomonas aeruginosa PAO1
-	PA0147	COG3491R	oxidoreductase			PA4568	Pseudomonas aeruginosa PAO1
-	PA0146	COG1744R	hypothetical protein			PA4567	Pseudomonas aeruginosa PAO1
-	PA0145	COG3613F	hypothetical protein			PA4563	Pseudomonas aeruginosa PAO1
-	PA0013	COG1738S	hypothetical protein	DEG10300002	**PA4562**	PA4562	Pseudomonas aeruginosa PAO1
-	PA0011	COG1560M	lipid A biosynthesis lauroyl acyltransferase	DEG10300001	**PA4561**	PA4561	Pseudomonas aeruginosa PAO1
atpE	PA5559	COG0636C	ATP synthase F0F1 subunit C	DEG10150335	**PA4560**	PA4560	Pseudomonas aeruginosa PAO1
atpA	PA5556	COG0056C	ATP synthase F0F1 subunit alpha	DEG10150334	**PA4559**	PA4559	Pseudomonas aeruginosa PAO1
-	PA5461	-	hypothetical protein	DEG10150331	**PA4557**	PA4557	Pseudomonas aeruginosa PAO1
-	PA5408	-	hypothetical protein	DEG10150330	**PA4529**	PA4529	Pseudomonas aeruginosa PAO1
-	PA4355	COG2814G	major facilitator superfamily (MFS) transporter			PA4517	Pseudomonas aeruginosa PAO1
-	PA5407	COG3027S	hypothetical protein	DEG10150329	**PA4484**	PA4484	Pseudomonas aeruginosa PAO1
-	PA0144	COG3613F	hypothetical protein			PA4482	Pseudomonas aeruginosa PAO1
lppL	PA5276	COG5567N	Lipopeptide LppL	DEG10150324	**PA4481**	PA4481	Pseudomonas aeruginosa PAO1
dnaN	PA0002	COG0592L	DNA polymerase III subunit beta		**PA4479**	PA4479	Pseudomonas aeruginosa PAO1
nuh	PA0143	COG1957F	nonspecific ribonucleoside hydrolase			PA4462	Pseudomonas aeruginosa PAO1
hemD	PA5259	COG1587H	uroporphyrinogen-III synthase	DEG10150322	**PA4461**	PA4461	Pseudomonas aeruginosa PAO1
rcpC	PA4305	COG3745U	RcpC protein			PA4458	Pseudomonas aeruginosa PAO1
-	PA5071	COG1385S	16S ribosomal RNA methyltransferase RsmE	DEG10150316	**PA4457**	PA4457	Pseudomonas aeruginosa PAO1
-	PA0142	COG0402FR	hydroxydechloroatrazine ethylaminohydrolase			PA4456	Pseudomonas aeruginosa PAO1
-	PA0141	COG2326S	hypothetical protein			PA4455	Pseudomonas aeruginosa PAO1
ahpF	PA0140	COG3634O	alkyl hydroperoxide reductase			PA4454	Pseudomonas aeruginosa PAO1
ahpC	PA0139	COG0450O	alkyl hydroperoxide reductase			PA4453	Pseudomonas aeruginosa PAO1
-	PA0138	COG1079R	ABC transporter permease			PA4452	Pseudomonas aeruginosa PAO1
tatB	PA5069	COG1826U	sec-independent translocase	DEG10150315	**PA4450**	PA4450	Pseudomonas aeruginosa PAO1
tatA	PA5068	COG1826U	twin-arginine translocation protein TatA	DEG10150314	**PA4439**	PA4439	Pseudomonas aeruginosa PAO1
ubiE	PA5063	COG2226H	ubiquinone/menaquinone biosynthesis methyltransferase	DEG10150312	**PA4433**	PA4433	Pseudomonas aeruginosa PAO1
aroK	PA5039	COG0703E	shikimate kinase	DEG10150310	**PA4432**	PA4432	Pseudomonas aeruginosa PAO1
waaA	PA4988	COG1519M	3-deoxy-D-manno-octulosonic-acid transferase	DEG10150301	**PA4425**	PA4425	Pseudomonas aeruginosa PAO1
-	PA0136	COG3845R	ABC transporter ATP-binding protein			PA4419	Pseudomonas aeruginosa PAO1
parC	PA4964	COG0188L	DNA topoisomerase IV subunit A	DEG10150298	**PA4418**	PA4418	Pseudomonas aeruginosa PAO1
hfq	PA4944	COG1923R	RNA-binding protein Hfq	DEG10150296	**PA4417**	PA4417	Pseudomonas aeruginosa PAO1
-	PA4940	COG3242S	hypothetical protein	DEG10150295	**PA4416**	PA4416	Pseudomonas aeruginosa PAO1
accC	PA4848	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	DEG10150294	**PA4415**	PA4415	Pseudomonas aeruginosa PAO1
accB	PA4847	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	DEG10150293	**PA4414**	PA4414	Pseudomonas aeruginosa PAO1
grpE	PA4762	COG0576O	heat shock protein GrpE	DEG10150290	**PA4413**	PA4413	Pseudomonas aeruginosa PAO1
polA	PA5493	COG0749L	DNA polymerase I	DEG10300115	**PA4412**	PA4412	Pseudomonas aeruginosa PAO1
dapB	PA4759	COG0289E	dihydrodipicolinate reductase	DEG10150289	**PA4411**	PA4411	Pseudomonas aeruginosa PAO1
-	PA0135	-	hypothetical protein			PA4409	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA4746	COG0779S	hypothetical protein	DEG10150287	**PA4408**	PA4408	Pseudomonas aeruginosa PAO1
rpsO	PA4741	COG0184J	30S ribosomal protein S15	DEG10150285	**PA4407**	**PA4407**	Pseudomonas aeruginosa PAO1
-	PA4672	COG0193J	peptidyl-tRNA hydrolase	DEG10150283	**PA4406**	PA4406	Pseudomonas aeruginosa PAO1
hemA	PA4666	COG0373H	glutamyl-tRNA reductase	DEG10150280	**PA4403**	PA4403	Pseudomonas aeruginosa PAO1
rplB	PA4260	COG0090J	50S ribosomal protein L2			PA4389	Pseudomonas aeruginosa PAO1
-	PA0134	COG0402FR	guanine deaminase			PA4386	Pseudomonas aeruginosa PAO1
rpmA	PA4567	COG0211J	50S ribosomal protein L27	DEG10150274	**PA4385**	PA4385	Pseudomonas aeruginosa PAO1
rpsT	PA4563	COG0268J	30S ribosomal protein S20	DEG10150273	**PA4366**	PA4366	Pseudomonas aeruginosa PAO1
mexH	PA4206	COG0845M	resistance-nodulation-cell division (RND) efflux membrane fusion protein			PA4351	Pseudomonas aeruginosa PAO1
-	PA0665	COG0316S	iron-sulfur cluster insertion protein ErpA	DEG10150028	**PA4279**	PA4279	Pseudomonas aeruginosa PAO1
-	PA4279	COG1521K	pantothenate kinase	DEG10150029	**PA4276**	PA4276	Pseudomonas aeruginosa PAO1
rplA	PA4273	COG0081J	50S ribosomal protein L1	DEG10150031	**PA4274**	PA4274	Pseudomonas aeruginosa PAO1
rplL	PA4271	COG0222J	50S ribosomal protein L7/L12	DEG10150032	**PA4273**	PA4273	Pseudomonas aeruginosa PAO1
rpsG	PA4267	COG0049J	30S ribosomal protein S7	DEG10150034	**PA4272**	PA4272	Pseudomonas aeruginosa PAO1
rpsJ	PA4264	COG0051J	30S ribosomal protein S10	DEG10150035	**PA4271**	PA4271	Pseudomonas aeruginosa PAO1
rpsS	PA4259	COG0185J	30S ribosomal protein S19	DEG10150036	**PA4270**	PA4270	Pseudomonas aeruginosa PAO1
rplV	PA4258	COG0091J	50S ribosomal protein L22	DEG10150037	**PA4269**	PA4269	Pseudomonas aeruginosa PAO1
rpsC	PA4257	COG0092J	30S ribosomal protein S3	DEG10150038	**PA4268**	PA4268	Pseudomonas aeruginosa PAO1
rplP	PA4256	COG0197J	50S ribosomal protein L16	DEG10150039	**PA4267**	PA4267	Pseudomonas aeruginosa PAO1
-	PA0040	COG2831U	hypothetical protein			PA4264	Pseudomonas aeruginosa PAO1
rpsQ	PA4254	COG0186J	30S ribosomal protein S17	DEG10150041	**PA4263**	PA4263	Pseudomonas aeruginosa PAO1
rplN	PA4253	COG0093J	50S ribosomal protein L14	DEG10150042	**PA4262**	PA4262	Pseudomonas aeruginosa PAO1
-	PA0041	COG2911S	hemagglutinin			PA4261	Pseudomonas aeruginosa PAO1
rplX	PA4252	COG0198J	50S ribosomal protein L24	DEG10150043	**PA4260**	PA4260	Pseudomonas aeruginosa PAO1
-	PA0041a	-	transposase			PA4259	Pseudomonas aeruginosa PAO1
-	PA0042	-	hypothetical protein			PA4258	Pseudomonas aeruginosa PAO1
rplE	PA4251	COG0094J	50S ribosomal protein L5	DEG10150044	**PA4257**	PA4257	Pseudomonas aeruginosa PAO1
rpsN	PA4250	COG0199J	30S ribosomal protein S14	DEG10150045	**PA4256**	PA4256	Pseudomonas aeruginosa PAO1
-	PA0043	COG3174S	hypothetical protein			PA4255	Pseudomonas aeruginosa PAO1
exoT	PA0044	COG5585T	exoenzyme T			PA4254	Pseudomonas aeruginosa PAO1
-	PA0045	COG1462M	hypothetical protein			PA4253	Pseudomonas aeruginosa PAO1
-	PA0046	COG4259S	hypothetical protein			PA4252	Pseudomonas aeruginosa PAO1
rplF	PA4248	COG0097J	50S ribosomal protein L6	DEG10150046	**PA4251**	PA4251	Pseudomonas aeruginosa PAO1
-	PA0048	COG1396K	transcriptional regulator			PA4250	Pseudomonas aeruginosa PAO1
rplR	PA4247	COG0256J	50S ribosomal protein L18	DEG10150047	**PA4249**	PA4249	Pseudomonas aeruginosa PAO1
rpmD	PA4245	COG1841J	50S ribosomal protein L30	DEG10150048	**PA4248**	PA4248	Pseudomonas aeruginosa PAO1
-	PA0049	-	hypothetical protein			PA4247	Pseudomonas aeruginosa PAO1
rplO	PA4244	COG0200J	50S ribosomal protein L15	DEG10150049	**PA4246**	PA4246	Pseudomonas aeruginosa PAO1
phzH	PA0051	COG0367E	phenazine-modifying protein			PA4245	Pseudomonas aeruginosa PAO1
rpmJ	PA4242	COG0257J	50S ribosomal protein L36	DEG10150050	**PA4244**	PA4244	Pseudomonas aeruginosa PAO1
rpsM	PA4241	COG0099J	30S ribosomal protein S13	DEG10150051	**PA4243**	PA4243	Pseudomonas aeruginosa PAO1
-	PA0814	COG0251J	hypothetical protein			PA4242	Pseudomonas aeruginosa PAO1
rpsK	PA4240	COG0100J	30S ribosomal protein S11	DEG10150052	**PA4241**	PA4241	Pseudomonas aeruginosa PAO1
rplQ	PA4237	COG0203J	50S ribosomal protein L17	DEG10150053	**PA4240**	PA4240	Pseudomonas aeruginosa PAO1
-	PA4090	COG3553S	hypothetical protein	DEG10150054	**PA4239**	PA4239	Pseudomonas aeruginosa PAO1
-	PA4077	COG1476K	transcriptional regulator	DEG10150055	**PA4238**	PA4238	Pseudomonas aeruginosa PAO1
ribC	PA4055	COG0307H	riboflavin synthase subunit alpha	DEG10150058	**PA4237**	PA4237	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA0910	-	hypothetical protein			PA4138	Pseudomonas aeruginosa PAO1
-	PA0952	-	hypothetical protein			PA4089	Pseudomonas aeruginosa PAO1
-	PA0953	COG0526OC	thioredoxin			PA4088	Pseudomonas aeruginosa PAO1
nusB	PA4052	COG0781K	transcription antitermination protein NusB	DEG10150059	**PA4068**	PA4068	Pseudomonas aeruginosa PAO1
-	PA0984	-	colicin immunity protein			PA4061	Pseudomonas aeruginosa PAO1
-	PA0054	COG1859J	RNA 2'-phosphotransferase-like protein			PA4056	Pseudomonas aeruginosa PAO1
-	PA0055	COG3812S	hypothetical protein			PA4055	Pseudomonas aeruginosa PAO1
-	PA0056	COG0583K	transcriptional regulator			PA4053	Pseudomonas aeruginosa PAO1
dxs	PA4044	COG1154HI	1-deoxy-D-xylulose-5-phosphate synthase	DEG10150062	**PA4052**	PA4052	Pseudomonas aeruginosa PAO1
-	PA0989	-	hypothetical protein			PA4050	Pseudomonas aeruginosa PAO1
-	PA0057	COG0491R	hypothetical protein			PA4047	Pseudomonas aeruginosa PAO1
-	PA3998	COG2921S	hypothetical protein	DEG10150064	**PA4044**	PA4044	Pseudomonas aeruginosa PAO1
lipB	PA3997	COG0321H	lipoate-protein ligase B	DEG10150065	**PA4043**	PA4043	Pseudomonas aeruginosa PAO1
-	PA3988	COG2980M	hypothetical protein	DEG10150068	**PA4019**	PA4019	Pseudomonas aeruginosa PAO1
-	PA3982	COG0319R	metalloprotease	DEG10150070	**PA4003**	PA4003	Pseudomonas aeruginosa PAO1
-	PA1034	COG0653U	hypothetical protein			PA3999	Pseudomonas aeruginosa PAO1
iscU	PA3813	COG0822C	scaffold protein	DEG10150078	**PA3997**	PA3997	Pseudomonas aeruginosa PAO1
-	PA0058	COG3531O	hypothetical protein			PA3996	Pseudomonas aeruginosa PAO1
iscA	PA3812	COG0316S	iron-binding protein IscA	DEG10150079	**PA3989**	PA3989	Pseudomonas aeruginosa PAO1
hscB	PA3811	COG1076O	co-chaperone HscB	DEG10150080	**PA3987**	PA3987	Pseudomonas aeruginosa PAO1
gcpE	PA3803	COG0821I	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	DEG10150083	**PA3977**	PA3977	Pseudomonas aeruginosa PAO1
-	PA1112	COG2133G	hypothetical protein			PA3910	Pseudomonas aeruginosa PAO1
-	PA1117	-	hypothetical protein			PA3903	Pseudomonas aeruginosa PAO1
guaB	PA3770	COG0516F	inosine 5'-monophosphate dehydrogenase	DEG10150086	**PA3834**	PA3834	Pseudomonas aeruginosa PAO1
-	PA1189	COG3091S	hypothetical protein			PA3832	Pseudomonas aeruginosa PAO1
-	PA3767	COG0590FJ	hypothetical protein	DEG10150087	**PA3828**	PA3828	Pseudomonas aeruginosa PAO1
-	PA3668	COG2166R	hypothetical protein	DEG10150092	**PA3827**	PA3827	Pseudomonas aeruginosa PAO1
-	PA0060	-	hypothetical protein			PA3822	Pseudomonas aeruginosa PAO1
-	PA0061	-	hypothetical protein			PA3820	Pseudomonas aeruginosa PAO1
pyrH	PA3654	COG0528F	uridylate kinase	DEG10150095	**PA3814**	PA3814	Pseudomonas aeruginosa PAO1
-	PA4960	COG0560E	phosphoserine phosphatase	DEG10300087	**PA3811**	PA3811	Pseudomonas aeruginosa PAO1
-	PA0063	COG4324R	hypothetical protein			PA3809	Pseudomonas aeruginosa PAO1
-	PA1203	COG1765O	hypothetical protein			PA3807	Pseudomonas aeruginosa PAO1
fabZ	PA3645	COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	DEG10150101	**PA3803**	PA3803	Pseudomonas aeruginosa PAO1
lpxA	PA3644	COG1043M	UDP-N-acetylglucosamine acyltransferase	DEG10150102	**PA3802**	PA3802	Pseudomonas aeruginosa PAO1
dnaE	PA3640	COG0587L	DNA polymerase III subunit alpha	DEG10150104	**PA3799**	PA3799	Pseudomonas aeruginosa PAO1
accA	PA3639	COG0825I	acetyl-CoA carboxylase carboxyltransferase subunit alpha	DEG10150105	**PA3770**	PA3770	Pseudomonas aeruginosa PAO1
pyrG	PA3637	COG0504F	CTP synthetase	DEG10150107	**PA3769**	PA3769	Pseudomonas aeruginosa PAO1
aprE	PA1247	COG1566V	alkaline protease secretion protein AprE			PA3759	Pseudomonas aeruginosa PAO1
-	PA0065	COG0546R	hypothetical protein			PA3746	Pseudomonas aeruginosa PAO1
-	PA0066	COG0663R	hypothetical protein			PA3745	Pseudomonas aeruginosa PAO1
-	PA3634	COG2919D	hypothetical protein	DEG10150108	**PA3744**	PA3744	Pseudomonas aeruginosa PAO1
prlC	PA0067	COG0339E	oligopeptidase A			PA3742	Pseudomonas aeruginosa PAO1
rnt	PA3528	COG0847L	ribonuclease T	DEG10150110	**PA3700**	PA3700	Pseudomonas aeruginosa PAO1
-	PA0068	COG3529R	hypothetical protein			PA3686	Pseudomonas aeruginosa PAO1
-	PA1324	-	hypothetical protein			PA3673	Pseudomonas aeruginosa PAO1
-	PA3441	COG3585H	molybdopterin-binding protein	DEG10150113	**PA3666**	PA3666	Pseudomonas aeruginosa PAO1
ansB	PA1337	COG0252EJ	glutaminase-asparaginase			PA3659	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA1339	COG1126E	amino acid ABC transporter ATP binding protein			PA3657	Pseudomonas aeruginosa PAO1
-	PA0069	COG1533L	hypothetical protein			PA3656	Pseudomonas aeruginosa PAO1
cmk	PA3163	COG0283F	cytidylate kinase	DEG10150118	**PA3654**	PA3654	Pseudomonas aeruginosa PAO1
asd	PA3117	COG0136E	aspartate-semialdehyde dehydrogenase	DEG10150120	**PA3653**	PA3653	Pseudomonas aeruginosa PAO1
-	PA5130	COG0607P	hypothetical protein	DEG10300091	**PA3652**	PA3652	Pseudomonas aeruginosa PAO1
accD	PA3112	COG0777I	acetyl-CoA carboxylase subunit beta	DEG10150121	**PA3651**	PA3651	Pseudomonas aeruginosa PAO1
-	PA2988	COG4591M	hypothetical protein	DEG10150122	**PA3650**	PA3650	Pseudomonas aeruginosa PAO1
-	PA2980	COG2835S	hypothetical protein	DEG10150126	**PA3646**	PA3646	Pseudomonas aeruginosa PAO1
fabG	PA2967	COG1028IQ	3-ketoacyl-ACP reductase	DEG10150130	**PA3645**	PA3645	Pseudomonas aeruginosa PAO1
acpP	PA2966	COG0236IQ	acyl carrier protein	DEG10150131	**PA3644**	PA3644	Pseudomonas aeruginosa PAO1
etfB	PA2952	COG2086C	electron transfer flavoprotein subunit beta	DEG10150133	**PA3643**	PA3643	Pseudomonas aeruginosa PAO1
-	PA1341	COG0765E	amino acid ABC transporter membrane protein			PA3642	Pseudomonas aeruginosa PAO1
-	PA2855	-	hypothetical protein	DEG10150136	**PA3640**	PA3640	Pseudomonas aeruginosa PAO1
-	PA2753	-	hypothetical protein	DEG10150137	**PA3639**	PA3639	Pseudomonas aeruginosa PAO1
-	PA2666	COG0720H	6-pyruvoyl tetrahydrobiopterin synthase	DEG10150142|	**PA3637**	PA3637	Pseudomonas aeruginosa PAO1
trmU	PA2626	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10150145	**PA3636**	PA3636	Pseudomonas aeruginosa PAO1
-	PA0073	COG1136V	ABC transporter ATP-binding protein			PA3633	Pseudomonas aeruginosa PAO1
infA	PA2619	COG0361J	translation initiation factor IF-1	DEG10150146	**PA3627**	PA3627	Pseudomonas aeruginosa PAO1
-	PA1349	COG3795S	hypothetical protein			PA3625	Pseudomonas aeruginosa PAO1
-	PA1352	COG2814G	hypothetical protein			PA3622	Pseudomonas aeruginosa PAO1
fabF2	PA1373	COG0304IQ	3-oxoacyl-ACP synthase			PA3601	Pseudomonas aeruginosa PAO1
fliO	PA1445	COG3190N	flagellar protein FliO			PA3528	Pseudomonas aeruginosa PAO1
-	PA1473	COG2257S	hypothetical protein			PA3482	Pseudomonas aeruginosa PAO1
-	PA1474	-	hypothetical protein			PA3480	Pseudomonas aeruginosa PAO1
-	PA1509	-	hypothetical protein			PA3446	Pseudomonas aeruginosa PAO1
anr	PA1544	COG0664T	transcriptional regulator Anr			PA3410	Pseudomonas aeruginosa PAO1
-	PA1624	-	hypothetical protein			PA3337	Pseudomonas aeruginosa PAO1
-	PA1665	COG3456T	hypothetical protein			PA3296	Pseudomonas aeruginosa PAO1
-	PA1676	-	hypothetical protein			PA3285	Pseudomonas aeruginosa PAO1
-	PA0078	COG3455S	hypothetical protein			PA3245	Pseudomonas aeruginosa PAO1
pscF	PA1719	-	type III export protein PscF			PA3242	Pseudomonas aeruginosa PAO1
-	PA5133	COG4942D	hypothetical protein	DEG10300092	**PA3171**	PA3171	Pseudomonas aeruginosa PAO1
-	PA2607	COG2168P	hypothetical protein	DEG10150151	**PA3168**	PA3168	Pseudomonas aeruginosa PAO1
-	PA0079	COG3522S	hypothetical protein			PA3163	Pseudomonas aeruginosa PAO1
-	PA2606	COG2923P	sulfur relay protein TusC	DEG10150152	**PA3162**	PA3162	Pseudomonas aeruginosa PAO1
-	PA0021	COG0758LU	hypothetical protein		**PA3150**	**PA3150**	Pseudomonas aeruginosa PAO1
-	PA2605	COG1553P	sulfur transfer complex subunit TusD	DEG10150153	**PA3134**	PA3134	Pseudomonas aeruginosa PAO1
pgsA	PA2584	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	DEG10150154	**PA3117**	PA3117	Pseudomonas aeruginosa PAO1
foxI	PA2468	COG1595K	ECF sigma factor FoxI	DEG10150159	**PA3112**	PA3112	Pseudomonas aeruginosa PAO1
-	PA0080	COG3521S	hypothetical protein			PA3111	Pseudomonas aeruginosa PAO1
polB	PA1886	COG0417L	DNA polymerase II			PA3047	Pseudomonas aeruginosa PAO1
nrdG	PA1919	COG1180O	class III (anaerobic) ribonucleoside-triphosphate reductase activating protein NrdG			PA3014	Pseudomonas aeruginosa PAO1
-	PA2329	COG1116P	ABC transporter ATP-binding protein	DEG10150164	**PA2988**	PA2988	Pseudomonas aeruginosa PAO1
-	PA2311	-	hypothetical protein	DEG10150167	**PA2987**	PA2987	Pseudomonas aeruginosa PAO1
arsC	PA2279	COG0394T	ArsC protein	DEG10150170	**PA2986**	PA2986	Pseudomonas aeruginosa PAO1
soxR	PA2273	COG0789K	SoxR protein	DEG10150171	**PA2981**	PA2981	Pseudomonas aeruginosa PAO1
-	PA2149	-	hypothetical protein	DEG10150175	**PA2979**	PA2979	Pseudomonas aeruginosa PAO1
-	PA1931	COG2080C	ferredoxin	DEG10150183	**PA2977**	PA2977	Pseudomonas aeruginosa PAO1
-	PA1951	COG1729S	hypothetical protein			PA2976	Pseudomonas aeruginosa PAO1
-	PA1958	COG3201H	transporter			PA2969	Pseudomonas aeruginosa PAO1
-	PA0084	COG3517S	hypothetical protein			PA2968	Pseudomonas aeruginosa PAO1
-	PA1924	COG0811U	hypothetical protein	DEG10150184	**PA2967**	PA2967	Pseudomonas aeruginosa PAO1
bacA	PA1959	COG1968V	undecaprenyl pyrophosphate phosphatase			PA2965	Pseudomonas aeruginosa PAO1
-	PA1879	COG1709K	hypothetical protein	DEG10150186	**PA2962**	PA2962	Pseudomonas aeruginosa PAO1
-	PA0086	COG4455R	hypothetical protein			PA2961	Pseudomonas aeruginosa PAO1
ppx	PA5241	COG0248FP	exopolyphosphatase	DEG10300098	**PA2950**	PA2950	Pseudomonas aeruginosa PAO1
-	PA1747	-	hypothetical protein	DEG10150193	**PA2744**	PA2744	Pseudomonas aeruginosa PAO1
clpV1	PA0090	COG0542O	ClpV1 protein			PA2742	Pseudomonas aeruginosa PAO1
-	PA1699	-	hypothetical protein	DEG10150197	**PA2741**	PA2741	Pseudomonas aeruginosa PAO1

Gene	Gene locu	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA1645	-	hypothetical protein	DEG10150199	**PA2740**	PA2740	Pseudomonas aeruginosa PAO1
pslA	PA2231	COG2148M	protein PslA			PA2666	Pseudomonas aeruginosa PAO1
fabA	PA1610	COG0764I	3-hydroxydecanoyl-ACP dehydratase	DEG10150203	**PA2629**	PA2629	Pseudomonas aeruginosa PAO1
sucA	PA1585	COG0567C	2-oxoglutarate dehydrogenase E1	DEG10150205	**PA2626**	PA2626	Pseudomonas aeruginosa PAO1
-	PA0092	-	hypothetical protein			PA2619	Pseudomonas aeruginosa PAO1
-	PA2280	COG0431R	hypothetical protein			PA2616	Pseudomonas aeruginosa PAO1
sdhB	PA1584	COG0479C	succinate dehydrogenase iron-sulfur subunit	DEG10150206	**PA2615**	**PA2615**	Pseudomonas aeruginosa PAO1
sdhD	PA1582	COG2142C	succinate dehydrogenase subunit D	DEG10150208	**PA2612**	PA2612	Pseudomonas aeruginosa PAO1
-	PA2285	-	hypothetical protein			PA2608	Pseudomonas aeruginosa PAO1
-	PA0093	COG4104S	hypothetical protein			PA2607	Pseudomonas aeruginosa PAO1
-	PA0094	COG5435S	hypothetical protein			PA2606	Pseudomonas aeruginosa PAO1
sdhC	PA1581	COG2009C	succinate dehydrogenase subunit C	DEG10150209	**PA2605**	PA2605	Pseudomonas aeruginosa PAO1
-	PA1574	COG3123S	hypothetical protein	DEG10150210	**PA2584**	PA2584	Pseudomonas aeruginosa PAO1
-	PA2427	-	hypothetical protein			PA2468	Pseudomonas aeruginosa PAO1
-	PA2506	-	hypothetical protein			PA2387	Pseudomonas aeruginosa PAO1
-	PA2531	COG0079E	aminotransferase			PA2357	Pseudomonas aeruginosa PAO1
-	PA2613	COG2256L	recombination factor protein RarA			PA2272	Pseudomonas aeruginosa PAO1
-	PA2786	COG2203T	hypothetical protein			PA2062	Pseudomonas aeruginosa PAO1
-	PA2829	-	hypothetical protein			PA2023	Pseudomonas aeruginosa PAO1
-	PA2919	-	hypothetical protein			PA1931	Pseudomonas aeruginosa PAO1
-	PA2930	COG0583K	transcriptional regulator			PA1920	Pseudomonas aeruginosa PAO1
-	PA2938	COG2233F	transporter			PA1912	Pseudomonas aeruginosa PAO1
snr1	PA3032	COG1858P	cytochrome C Snr1			PA1827	Pseudomonas aeruginosa PAO1
-	PA1564	COG0425O	sulfur transfer protein SirA	DEG10150212	**PA1816**	PA1816	Pseudomonas aeruginosa PAO1
-	PA1520	COG1802K	transcriptional regulator	DEG10150214	**PA1815**	PA1815	Pseudomonas aeruginosa PAO1
-	PA3052	-	hypothetical protein			PA1806	Pseudomonas aeruginosa PAO1
-	PA1478	COG3114U	hypothetical protein	DEG10150216	**PA1796**	PA1796	Pseudomonas aeruginosa PAO1
ccmC	PA1477	COG0755O	heme exporter protein CcmC	DEG10150217	**PA1795**	PA1795	Pseudomonas aeruginosa PAO1
cheY	PA1456	COG2204T	chemotaxis protein CheY	DEG10150219	**PA1794**	PA1794	Pseudomonas aeruginosa PAO1
-	PA1357	COG2606S	hypothetical protein	DEG10150221	**PA1792**	PA1792	Pseudomonas aeruginosa PAO1
-	PA3128	COG1028IQ	short-chain dehydrogenase			PA1725	Pseudomonas aeruginosa PAO1
-	PA3130	COG0824R	hypothetical protein			PA1723	Pseudomonas aeruginosa PAO1
-	PA3132	COG1506E	hydrolase			PA1721	Pseudomonas aeruginosa PAO1
-	PA3133	COG1309K	transcriptional regulator			PA1720	Pseudomonas aeruginosa PAO1
-	PA3137	COG2814G	major facilitator superfamily (MFS) transporter			PA1716	Pseudomonas aeruginosa PAO1
hisF2	PA3151	COG0107E	imidazole glycerol phosphate synthase subunit HisF			PA1703	Pseudomonas aeruginosa PAO1
wbpE	PA3155	COG0399M	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase WbpE			PA1699	Pseudomonas aeruginosa PAO1
wbpD	PA3156	COG1045E	UDP-2-acetamido-3-amino-23-dideoxy-d-glucuronic acid N-acetyltransferase WbpD			PA1698	Pseudomonas aeruginosa PAO1
-	PA3157	COG1835I	acetyltransferase			PA1697	Pseudomonas aeruginosa PAO1
wbpB	PA3158	COG0673R	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase WbpB			PA1696	Pseudomonas aeruginosa PAO1
wzz	PA3160	COG3765M	O-antigen chain length regulator			PA1694	Pseudomonas aeruginosa PAO1
himD	PA3161	COG0776L	integration host factor subunit beta			PA1693	Pseudomonas aeruginosa PAO1
rpsA	PA3162	COG0539J	30S ribosomal protein S1			PA1692	Pseudomonas aeruginosa PAO1
hisC2	PA3165	COG0079E	histidinol-phosphate aminotransferase			PA1691	Pseudomonas aeruginosa PAO1
pheA	PA3166	COG0077E	chorismate mutase			PA1690	Pseudomonas aeruginosa PAO1
-	PA1219	COG3319Q	hypothetical protein	DEG10150224	**PA1610**	PA1610	Pseudomonas aeruginosa PAO1
-	PA1213	-	hypothetical protein	DEG10150225	**PA1609**	PA1609	Pseudomonas aeruginosa PAO1
-	PA3262	COG0545O	FkbP-type peptidyl-prolyl cis-trans isomerase			PA1596	Pseudomonas aeruginosa PAO1
nrdA	PA1156	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10150228	**PA1589**	PA1589	Pseudomonas aeruginosa PAO1
pstA	PA5367	COG4985P	phosphate ABC transporter membrane protein	DEG10300106	**PA1588**	PA1588	Pseudomonas aeruginosa PAO1
tolR	PA0970	COG0848U	TolR protein	DEG10150235	**PA1584**	PA1584	Pseudomonas aeruginosa PAO1
-	PA0947	COG0593L	DNA replication initiation factor	DEG10150237	**PA1583**	PA1583	Pseudomonas aeruginosa PAO1
-	PA0909	-	hypothetical protein	DEG10150238	**PA1582**	PA1582	Pseudomonas aeruginosa PAO1
-	PA0906	COG2932K	transcriptional regulator	DEG10150239	**PA1581**	PA1581	Pseudomonas aeruginosa PAO1
-	PA3284	COG3767S	hypothetical protein			PA1564	Pseudomonas aeruginosa PAO1
fadD1	PA3299	COG0318IQ	long-chain-fatty-acid--CoA ligase			PA1546	Pseudomonas aeruginosa PAO1
era	PA0771	COG1159R	GTP-binding protein Era	DEG10150241	**PA1532**	PA1532	Pseudomonas aeruginosa PAO1
sodB	PA4366	COG0605P	superoxide dismutase	DEG10150244	**PA1529**	PA1529	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	PA4377	-	hypothetical protein	DEG10150245	**PA1528**	**PA1528**	Pseudomonas aeruginosa PAO1
-	PA3320	COG3238S	hypothetical protein			PA1521	Pseudomonas aeruginosa PAO1
-	PA3362	-	hypothetical protein			PA1478	Pseudomonas aeruginosa PAO1
amiR	PA3363	COG3707T	aliphatic amidase regulator			PA1477	Pseudomonas aeruginosa PAO1
-	PA0120	COG2186K	transcriptional regulator			PA1476	Pseudomonas aeruginosa PAO1
pstC	PA5368	COG4590R	phosphate ABC transporter membrane protein	DEG10300107	**PA1475**	PA1475	Pseudomonas aeruginosa PAO1
-	PA3445	COG0715P	hypothetical protein			PA1373	Pseudomonas aeruginosa PAO1
-	PA3449	COG0715P	hypothetical protein			PA1363	Pseudomonas aeruginosa PAO1
-	PA3461	COG1363G	hypothetical protein			PA1351	Pseudomonas aeruginosa PAO1
-	PA3514	COG1116P	ABC transporter ATP-binding protein			PA1300	Pseudomonas aeruginosa PAO1
groES	PA4386	COG0234O	co-chaperonin GroES	DEG10150246	**PA1162**	PA1162	Pseudomonas aeruginosa PAO1
ftsA	PA4408	COG0849D	cell division protein FtsA	DEG10150249	**PA1156**	PA1156	Pseudomonas aeruginosa PAO1
murC	PA4411	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10150250	**PA1155**	PA1155	Pseudomonas aeruginosa PAO1
-	PA0124	COG3668R	hypothetical protein			PA1049	Pseudomonas aeruginosa PAO1
murG	PA4412	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	DEG10150251	**PA1010**	PA1010	Pseudomonas aeruginosa PAO1
-	PA0126	-	hypothetical protein			PA0967	Pseudomonas aeruginosa PAO1
-	PA0127	COG5608S	hypothetical protein			PA0966	Pseudomonas aeruginosa PAO1
rplM	PA4433	COG0102J	50S ribosomal protein L13	DEG10150258	**PA0963**	PA0963	Pseudomonas aeruginosa PAO1
-	PA4460	COG1934S	hypothetical protein	DEG10150260	**PA0956**	PA0956	Pseudomonas aeruginosa PAO1
mreD	PA4479	COG2891M	rod shape-determining protein MreD	DEG10150261	**PA0947**	PA0947	Pseudomonas aeruginosa PAO1
nhaP	PA3887	COG0025P	Na+/H+ antiporter NhaP			PA0935	Pseudomonas aeruginosa PAO1
mreB	PA4481	COG1077D	rod shape-determining protein MreB	DEG10150262	**PA0904**	PA0904	Pseudomonas aeruginosa PAO1
gatC	PA4482	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10150263	**PA0903**	PA0903	Pseudomonas aeruginosa PAO1
-	PA3925	COG0183I	acyl-CoA thiolase			PA0895	Pseudomonas aeruginosa PAO1
-	PA5471	COG1690S	hypothetical protein	DEG10300112	**PA0773**	PA0773	Pseudomonas aeruginosa PAO1
-	PA4537	-	hypothetical protein	DEG10150267	**PA0771**	PA0771	Pseudomonas aeruginosa PAO1
-	PA4064	COG1136V	ABC transporter ATP-binding protein			PA0762	Pseudomonas aeruginosa PAO1
-	PA4133	COG3278O	cbb3-type cytochrome C oxidase subunit I			PA0675	Pseudomonas aeruginosa PAO1
-	PA0809	COG1914P	manganese transporter MntH			PA0668	Pseudomonas aeruginosa PAO1
-	PA0637	COG4718S	hypothetical protein	DEG10150025	**PA0655**	PA0655	Pseudomonas aeruginosa PAO1
rpe	PA0607	COG0036G	ribulose-phosphate 3-epimerase	DEG10150022	**PA0607**	PA0607	Pseudomonas aeruginosa PAO1
-	PA0735	-	hypothetical protein			PA0583	Pseudomonas aeruginosa PAO1
rpoD	PA0576	COG0568K	RNA polymerase sigma factor RpoD	DEG10150019	**PA0582**	PA0582	Pseudomonas aeruginosa PAO1
-	PA0734	-	hypothetical protein			PA0581	Pseudomonas aeruginosa PAO1
-	PA0733	COG1187J	pseudouridylate synthase			PA0579	Pseudomonas aeruginosa PAO1
-	PA4823	-	hypothetical protein	DEG10300084	**PA0577**	PA0577	Pseudomonas aeruginosa PAO1
nirC	PA0517	COG2010C	cytochrome C	DEG10150016	**PA0576**	PA0576	Pseudomonas aeruginosa PAO1
-	PA0404	COG0816L	Holliday junction resolvase-like protein	DEG10150014	**PA0555**	PA0555	Pseudomonas aeruginosa PAO1
coaD	PA0363	COG0669H	phosphopantetheine adenylyltransferase	DEG10150013	**PA0548**	PA0548	Pseudomonas aeruginosa PAO1
-	PA0690	-	hypothetical protein			PA0530	Pseudomonas aeruginosa PAO1
trpC	PA0651	COG0134E	indole-3-glycerol phosphate synthase			PA0494	Pseudomonas aeruginosa PAO1
-	PA0583	COG0801H	hypothetical protein			PA0428	Pseudomonas aeruginosa PAO1
-	PA0560	COG1451R	hypothetical protein			PA0403	Pseudomonas aeruginosa PAO1
-	PA0542	COG0525J	hypothetical protein			PA0386	Pseudomonas aeruginosa PAO1
dsbB	PA0538	COG1495O	disulfide bond formation protein			PA0382	Pseudomonas aeruginosa PAO1
-	PA0534	COG0665E	hypothetical protein			PA0378	Pseudomonas aeruginosa PAO1
thyA	PA0342	COG0207F	thymidylate synthase	DEG10150011	**PA0376**	PA0376	Pseudomonas aeruginosa PAO1
-	PA0532	-	hypothetical protein			PA0375	Pseudomonas aeruginosa PAO1
-	PA0531	COG0518F	glutamine amidotransferase			PA0374	Pseudomonas aeruginosa PAO1
-	PA0032a	-	DOPA 4,5-dioxygenase			PA0373	Pseudomonas aeruginosa PAO1
rpiA	PA0330	COG0120G	ribose-5-phosphate isomerase A	DEG10150010	**PA0363**	PA0363	Pseudomonas aeruginosa PAO1
-	PA0128	COG2824P	hypothetical protein	DEG10150009	**PA0350**	PA0350	Pseudomonas aeruginosa PAO1
-	PA0050	-	hypothetical protein	DEG10150008	**PA0342**	PA0342	Pseudomonas aeruginosa PAO1
-	PA0022	COG0009J	hypothetical protein	DEG10150006	**PA0330**	PA0330	Pseudomonas aeruginosa PAO1
lgt	PA0341	COG0682M	prolipoprotein diacylglyceryl transferase			PA0182	Pseudomonas aeruginosa PAO1
-	PA0306a	-	transcriptional regulator			PA0149	Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
spuE	PA0301	COG0687E	polyamine transporter			PA0143	Pseudomonas aeruginosa PAO1
aguA	PA0292	COG2957E	agmatine deiminase			PA0134	Pseudomonas aeruginosa PAO1
-	PA0257	COG2801L	hypothetical protein			PA0098	Pseudomonas aeruginosa PAO1
glyQ	PA0009	COG0752J	glycyl-tRNA synthetase subunit alpha	DEG10150003	**PA0024**	PA0024	Pseudomonas aeruginosa PAO1
-	PA4636	COG2937I	hypothetical protein	DEG10030755	**PA0019**	PA0019	Pseudomonas aeruginosa PAO1
-	PA2857	COG4181Q	ABC transporter ATP-binding protein	DEG10030734	**PA0018**	PA0018	Pseudomonas aeruginosa PAO1
aer2	PA0176	COG0840NT	aerotaxis transducer Aer2			PA0011	Pseudomonas aeruginosa PAO1
-	PA3566	COG1359S	hypothetical protein	DEG10030716	**PA0009**	PA0009	Pseudomonas aeruginosa PAO1
-	PA3249	COG2188K	transcriptional regulator	DEG10030707	**PA0008**	PA0008	Pseudomonas aeruginosa PAO1
-	PA4426	COG2823R	hypothetical protein	DEG10300080	**PA0006**	PA0006	Pseudomonas aeruginosa PAO1
-	PA0173	COG2201NT	chemotaxis-specific methylesterase			PA0005	Pseudomonas aeruginosa PAO1
-	PA4534	COG0456R	hypothetical protein	DEG10030672	**PA0004**	PA0004	Pseudomonas aeruginosa PAO1
rpmI	PA2742	COG0291J	50S ribosomal protein L35	DEG10030596|	**PA0002**	PA0002	Pseudomonas aeruginosa PAO1
-	PA2950	COG3007S	trans-2-enoyl-CoA reductase	DEG10030340|	**PA0001**	PA0001	Pseudomonas aeruginosa PAO1
fmt	PA0018	COG0223J	methionyl-tRNA formyltransferase		**PA5569**		Pseudomonas aeruginosa PAO1
-	PA4422	COG0313R	hypothetical protein	DEG10300079	**PA5568**		Pseudomonas aeruginosa PAO1
-	PA3485	-	hypothetical protein	DEG10300059	**PA5239**		Pseudomonas aeruginosa PAO1
-	PA3237	COG3205S	hypothetical protein	DEG10300058	**PA5237**		Pseudomonas aeruginosa PAO1
-	PA3169	COG0182J	methylthioribose-1-phosphate isomerase	DEG10300055	**PA5174**		Pseudomonas aeruginosa PAO1
sth	PA2991	COG1249C	soluble pyridine nucleotide transhydrogenase	DEG10300048	**PA5065**		Pseudomonas aeruginosa PAO1
-	PA2656	COG0642T	two-component sensor	DEG10300039	**PA5008**		Pseudomonas aeruginosa PAO1
-	PA2627	COG2915R	hypothetical protein	DEG10300038	**PA5006**		Pseudomonas aeruginosa PAO1
-	PA0017	COG0144J	hypothetical protein		**PA4999**		Pseudomonas aeruginosa PAO1
-	PA2604	COG0670R	hypothetical protein	DEG10300037	**PA4998**		Pseudomonas aeruginosa PAO1
oprN	PA2495	COG1538MU	Multidrug efflux outer membrane protein OprN	DEG10300036	**PA4997**		Pseudomonas aeruginosa PAO1
-	PA2019	COG0845M	periplasmic multidrug efflux lipoprotein	DEG10300034	**PA4992**		Pseudomonas aeruginosa PAO1
-	PA2018	COG0841V	multidrug efflux protein	DEG10300033	**PA4991**		Pseudomonas aeruginosa PAO1
-	PA0015	COG4783R	hypothetical protein		**PA4969**		Pseudomonas aeruginosa PAO1
relA	PA0934	COG0317TK	GTP pyrophosphokinase	DEG10300025	**PA4920**		Pseudomonas aeruginosa PAO1
-	PA0012	-	hypothetical protein		**PA4767**		Pseudomonas aeruginosa PAO1
-	PA0667	COG0739M	hypothetical protein	DEG10300022	**PA4765**		Pseudomonas aeruginosa PAO1
tag	PA0010	COG2818L	DNA-3-methyladenine glycosidase I		**PA4764**		Pseudomonas aeruginosa PAO1
-	PA0007	-	hypothetical protein		**PA4752**		Pseudomonas aeruginosa PAO1
-	PA0006	COG0241E	D,D-heptose 1,7-bisphosphate phosphatase		**PA4748**		Pseudomonas aeruginosa PAO1
-	PA0502	COG0596R	biotin biosynthesis protein bioH	DEG10300017	**PA4746**		Pseudomonas aeruginosa PAO1
oprM	PA0427	COG1538MU	multidrug ABC transporter	DEG10300016	**PA4745**		Pseudomonas aeruginosa PAO1
lptA	PA0005	COG0204I	lysophosphatidic acid acyltransferase, LptA		**PA4685**		Pseudomonas aeruginosa PAO1
pilG	PA0408	COG0745TK	twitching motility protein PilG	DEG10300012	**PA4679**		Pseudomonas aeruginosa PAO1
-	PA0332	COG5528S	hypothetical protein	DEG10300008	**PA4668**		Pseudomonas aeruginosa PAO1
gyrB	PA0004	COG0187L	DNA gyrase subunit B		**PA4664**		Pseudomonas aeruginosa PAO1
-	PA0047	COG4380S	hypothetical protein	DEG10300005	**PA4636**		Pseudomonas aeruginosa PAO1
rpmB	PA5316	COG0227J	50S ribosomal protein L28	DEG10150325	**PA4483**		Pseudomonas aeruginosa PAO1
recF	PA0003	COG1195L	recombination protein F		**PA4480**		Pseudomonas aeruginosa PAO1
trxA	PA5240	COG3118O	thioredoxin	DEG10150321	**PA4460**		Pseudomonas aeruginosa PAO1
glnA	PA5119	COG0174E	glutamine synthetase	DEG10150318	**PA4459**		Pseudomonas aeruginosa PAO1
-	PA5551	COG0739M	hypothetical protein	DEG10300117	**PA4429**		Pseudomonas aeruginosa PAO1
-	PA5528	COG4395S	hypothetical protein	DEG10300116	**PA4420**		Pseudomonas aeruginosa PAO1
-	PA4668	COG3017M	molecular chaperone LolB	DEG10150281	**PA4405**		Pseudomonas aeruginosa PAO1
gltP	PA5479	COG1301C	glutamate/aspartate:proton symporter	DEG10300114	**PA4333**		Pseudomonas aeruginosa PAO1
rplK	PA4274	COG0080J	50S ribosomal protein L11	DEG10150030	**PA4275**		Pseudomonas aeruginosa PAO1
rpmC	PA4255	COG0255J	50S ribosomal protein L29	DEG10150040	**PA4266**		Pseudomonas aeruginosa PAO1
hflK	PA4942	COG0330O	protease subunit HflK	DEG10300086	**PA4093**		Pseudomonas aeruginosa PAO1
-	PA4019	COG0163H	aromatic acid decarboxylase	DEG10150063	**PA4051**		Pseudomonas aeruginosa PAO1
lis	PA3996	COG0320H	lipoyl synthase	DEG10150066	**PA4031**		Pseudomonas aeruginosa PAO1
-	PA3827	COG0795R	hypothetical protein	DEG10150076	**PA4002**		Pseudomonas aeruginosa PAO1
fdx2	PA3809	COG0633C	(2Fe-2S) ferredoxin	DEG10150081	**PA3984**		Pseudomonas aeruginosa PAO1
ndk	PA3807	COG0105F	nucleoside diphosphate kinase	DEG10150082	**PA3982**		Pseudomonas aeruginosa PAO1
rpsB	PA3656	COG0052J	30S ribosomal protein S2	DEG10150094	**PA3821**		Pseudomonas aeruginosa PAO1

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
frr	PA3653	COG0233J	ribosome recycling factor	DEG10150096	PA3813		Pseudomonas aeruginosa PAO1
cdsA	PA3651	COG0575I	phosphatidate cytidylyltransferase	DEG10150098	PA3810		Pseudomonas aeruginosa PAO1
hslV	PA5053	COG5405O	ATP-dependent protease peptidase subunit	DEG10300088	PA3767		Pseudomonas aeruginosa PAO1
hslU	PA5054	COG1220O	ATP-dependent protease ATP-binding subunit HslU	DEG10300089	PA3721		Pseudomonas aeruginosa PAO1
fdxA	PA3621	COG1146C	ferredoxin I	DEG10150109	PA3703		Pseudomonas aeruginosa PAO1
-	PA0030	COG2113E	hypothetical protein		PA3701		Pseudomonas aeruginosa PAO1
-	PA3520	COG2608P	hypothetical protein	DEG10150111	PA3685		Pseudomonas aeruginosa PAO1
minE	PA3245	COG0851D	cell division topological specificity factor MinE	DEG10150115	PA3655		Pseudomonas aeruginosa PAO1
lpxK	PA2981	COG1663M	tetraacyldisaccharide 4'-kinase	DEG10150125	PA3648		Pseudomonas aeruginosa PAO1
rplT	PA2741	COG0292J	50S ribosomal protein L20	DEG10150139	PA3638		Pseudomonas aeruginosa PAO1
lolA	PA2614	COG2834M	outer-membrane lipoprotein carrier protein	DEG10150148	PA3481		Pseudomonas aeruginosa PAO1
serS	PA2612	COG0172J	seryl-tRNA synthetase	DEG10150149	PA3397		Pseudomonas aeruginosa PAO1
cysQ	PA5175	COG1218P	3,5-bisphosphate nucleotidase CysQ	DEG10300093	PA3167		Pseudomonas aeruginosa PAO1
amgS	PA5199	COG0642T	protein AmgS	DEG10300095	PA3159		Pseudomonas aeruginosa PAO1
-	PA0029	COG0659P	sulfate transporter		PA3158		Pseudomonas aeruginosa PAO1
-	PA0028	-	hypothetical protein		PA3156		Pseudomonas aeruginosa PAO1
-	PA0027	COG0760O	hypothetical protein		PA3155		Pseudomonas aeruginosa PAO1
plcB	PA0026	-	phospholipase C, PlcB		PA3154		Pseudomonas aeruginosa PAO1
aroE	PA0025	COG0169E	shikimate 5-dehydrogenase		PA3153		Pseudomonas aeruginosa PAO1
qor	PA0023	COG0604CR	quinone oxidoreductase		PA3151		Pseudomonas aeruginosa PAO1
-	PA0020	COG1652S	hypothetical protein		PA3149		Pseudomonas aeruginosa PAO1
-	PA5194	-	hypothetical protein	DEG10300094	PA3148		Pseudomonas aeruginosa PAO1
def	PA0019	COG0242J	peptide deformylase		PA3147		Pseudomonas aeruginosa PAO1
amgR	PA5200	COG0745TK	osmolarity response regulator	DEG10300096	PA3145		Pseudomonas aeruginosa PAO1
-	PA5227	COG3027S	hypothetical protein	DEG10300097	PA3141		Pseudomonas aeruginosa PAO1
fpvI	PA2387	COG1595K	RNA polymerase sigma factor	DEG10150160	PA3088		Pseudomonas aeruginosa PAO1
-	PA2367	COG3157S	hypothetical protein	DEG10150162	PA3011		Pseudomonas aeruginosa PAO1
rnhA	PA1815	COG0328L	ribonuclease H	DEG10150188	PA2953		Pseudomonas aeruginosa PAO1
folD	PA1796	COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	DEG10150189	PA2952		Pseudomonas aeruginosa PAO1
-	PA1792	COG2908S	UDP-2,3-diacylglucosamine hydrolase	DEG10150192	PA2951		Pseudomonas aeruginosa PAO1
dsbH	PA5256	COG1495O	disulfide bond formation protein	DEG10300099	PA2798		Pseudomonas aeruginosa PAO1
pscH	PA1721	-	type III export protein PscH	DEG10150195	PA2743		Pseudomonas aeruginosa PAO1
-	PA1618	COG2050Q	hypothetical protein	DEG10150202	PA2739		Pseudomonas aeruginosa PAO1
algR	PA5261	COG3279KT	alginate biosynthesis regulatory protein AlgR	DEG10300100	PA2726		Pseudomonas aeruginosa PAO1
sdhA	PA1583	COG1053C	succinate dehydrogenase flavoprotein subunit	DEG10150207	PA2614		Pseudomonas aeruginosa PAO1
-	PA5285	-	hypothetical protein	DEG10300101	PA2156		Pseudomonas aeruginosa PAO1
pyrE	PA5331	COG0461F	orotate phosphoribosyltransferase	DEG10300102	PA2024		Pseudomonas aeruginosa PAO1
oxyR	PA5344	COG0583K	OxyR protein	DEG10300103	PA1969		Pseudomonas aeruginosa PAO1
-	PA1298	COG1937S	hypothetical protein	DEG10150223	PA1787		Pseudomonas aeruginosa PAO1
rubA1	PA5351	COG1773C	rubredoxin	DEG10300104	PA1776		Pseudomonas aeruginosa PAO1
pstB	PA5366	COG1117P	phosphate transporter ATP-binding protein	DEG10300105	PA1681		Pseudomonas aeruginosa PAO1
nrdB	PA1155	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10150229	PA1587		Pseudomonas aeruginosa PAO1
-	PA1075	COG5626S	hypothetical protein	DEG10150230	PA1586		Pseudomonas aeruginosa PAO1
dapA	PA1010	COG0329EM	dihydrodipicolinate synthase	DEG10150232	PA1585		Pseudomonas aeruginosa PAO1
pstS	PA5369	COG0226P	phosphate ABC transporter substrate-binding protein	DEG10300108	PA1375		Pseudomonas aeruginosa PAO1
-	PA5406	-	hypothetical protein	DEG10300109	PA1059		Pseudomonas aeruginosa PAO1
-	PA5428	COG0583K	transcriptional regulator	DEG10300110	PA1056		Pseudomonas aeruginosa PAO1
ftsW	PA4413	COG0772D	cell division protein FtsW	DEG10150252	PA0972		Pseudomonas aeruginosa PAO1

Gene	**Gene locus**	**COG**	**Product**	**DEG code**	**Experimental EG**	**Predicted EG**	**Strain name**
mraY	PA4415	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10150253	**PA0971**		Pseudomonas aeruginosa PAO1
ftsL	PA4419	COG3116D	cell division protein FtsL	DEG10150256	**PA0970**		Pseudomonas aeruginosa PAO1
-	PA4425	COG0279G	phosphoheptose isomerase	DEG10150257	**PA0969**		Pseudomonas aeruginosa PAO1
aspA	PA5429	COG1027E	aspartate ammonia-lyase	DEG10300111	**PA0906**		Pseudomonas aeruginosa PAO1
-	PA4558	COG1047O	FkbP-type peptidyl-prolyl cis-trans isomerase	DEG10150269	**PA0768**		Pseudomonas aeruginosa PAO1
-	PA4562	COG0728R	hypothetical protein	DEG10150272	**PA0759**		Pseudomonas aeruginosa PAO1
-	PA5475	COG1247M	hypothetical protein	DEG10300113	**PA0678**		Pseudomonas aeruginosa PAO1
-	PA0655	COG2941H	hypothetical protein	DEG10150026	**PA0665**		Pseudomonas aeruginosa PAO1
ptrB	PA0612	COG1734T	repressor PtrB	DEG10150023	**PA0611**		Pseudomonas aeruginosa PAO1
folB	PA0582	COG1539H	dihydroneopterin aldolase	DEG10150021	**PA0594**		Pseudomonas aeruginosa PAO1
hflC	PA4941	COG0330O	protease subunit HflC	DEG10300085	**PA0593**		Pseudomonas aeruginosa PAO1
fda	PA0555	COG0191G	fructose-1,6-bisphosphate aldolase	DEG10150018	**PA0580**		Pseudomonas aeruginosa PAO1
smpB	PA4768	COG0691O	SsrA-binding protein	DEG10300083	**PA0551**		Pseudomonas aeruginosa PAO1
-	PA4698	COG3098S	hypothetical protein	DEG10300082	**PA0438**		Pseudomonas aeruginosa PAO1
folA	PA0350	COG0262H	dihydrofolate reductase	DEG10150012	**PA0404**		Pseudomonas aeruginosa PAO1
hemF	PA0024	COG0408H	coproporphyrinogen III oxidase	DEG10150007	**PA0341**		Pseudomonas aeruginosa PAO1
sspB	PA4427	COG2969R	ClpXP protease specificity-enhancing factor	DEG10300081	**PA0123**		Pseudomonas aeruginosa PAO1
dnaA	PA0001	COG0593L	chromosome replication initiator DnaA	DEG10150001	**PA0022**		Pseudomonas aeruginosa PAO1

Gene	**Gene locus**	**COG**	**Product**	**DEG code**	**Experimental EG**	**Predicted EG**	Strain name
rpsN	SSA_2391	COG0199J	30S ribosomal protein S14	DEG10210218	SSA_2391	SSA_2391	Streptococcus sanguinis SK36
trpS	SSA_2375	COG0180J	tryptophanyl-tRNA synthetase II	DEG10210217	SSA_2375	SSA_2375	Streptococcus sanguinis SK36
pgsA	SSA_2368	COG0558I	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	DEG10210216	SSA_2368	SSA_2368	Streptococcus sanguinis SK36
mnmA	SSA_2360	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10210215	SSA_2360	SSA_2360	Streptococcus sanguinis SK36
dnaC	SSA_2356	COG0305L	replicative DNA helicase	DEG10210214	SSA_2356	SSA_2356	Streptococcus sanguinis SK36
rpsD	SSA_2350	COG0522J	30S ribosomal protein S4	DEG10210213	SSA_2350	SSA_2350	Streptococcus sanguinis SK36
hisS	SSA_2284	COG0124J	histidyl-tRNA synthetase	DEG10210212	SSA_2284	SSA_2284	Streptococcus sanguinis SK36
nrdI	SSA_2263	COG1780F	flavoprotein NrdI	DEG10210211	SSA_2263	SSA_2263	Streptococcus sanguinis SK36
argS	SSA_2262	COG0018J	arginyl-tRNA synthetase	DEG10210210	SSA_2262	SSA_2262	Streptococcus sanguinis SK36
-	SSA_2240	COG0816L	Holliday junction resolvase-like protein	DEG10210209	SSA_2240	SSA_2240	Streptococcus sanguinis SK36
secE	SSA_2208	COG0690U	preprotein translocase subunit SecE	DEG10210208	SSA_2208	SSA_2208	Streptococcus sanguinis SK36
rpsB	SSA_2203	COG0052J	30S ribosomal protein S2	DEG10210207	SSA_2203	SSA_2203	Streptococcus sanguinis SK36
tsf	SSA_2202	COG0264J	elongation factor Ts	DEG10210206	SSA_2202	SSA_2202	Streptococcus sanguinis SK36
pgi	SSA_2183	COG0166G	glucose-6-phosphate isomerase	DEG10210205	SSA_2183	SSA_2183	Streptococcus sanguinis SK36
galU	SSA_2169	COG1210M	glucose-1-phosphate uridylyltransferase	DEG10210204	SSA_2169	SSA_2169	Streptococcus sanguinis SK36
gltX	SSA_2144	COG0008J	glutamyl-tRNA synthetase	DEG10210203	SSA_2144	SSA_2144	Streptococcus sanguinis SK36
rnpA	SSA_2140	COG0594J	ribonuclease P protein component	DEG10210202	SSA_2140	SSA_2140	Streptococcus sanguinis SK36
rpmH	SSA_2136	-	50S ribosomal protein L34	DEG10210201	SSA_2136	SSA_2136	Streptococcus sanguinis SK36
rpsL	SSA_2111	COG0048J	30S ribosomal protein S12	DEG10210200	SSA_2111	SSA_2111	Streptococcus sanguinis SK36
rpsG	SSA_2110	COG0049J	30S ribosomal protein S7	DEG10210199	SSA_2110	SSA_2110	Streptococcus sanguinis SK36
fusA	SSA_2109	COG0480J	elongation factor G	DEG10210198	SSA_2109	SSA_2109	Streptococcus sanguinis SK36
gapA	SSA_2108	COG0057G	glyceraldehyde 3-phosphate dehydrogenase	DEG10210197	SSA_2108	SSA_2108	Streptococcus sanguinis SK36
glmS	SSA_2107	COG0449M	glucosamine--fructose-6-phosphate aminotransferase	DEG10210196	SSA_2107	SSA_2107	Streptococcus sanguinis SK36
uppS	SSA_2073	COG0020I	undecaprenyl pyrophosphate synthase	DEG10210195	SSA_2073	SSA_2073	Streptococcus sanguinis SK36
cdsA	SSA_2072	COG0575I	phosphatidate cytidylyltransferase	DEG10210194	SSA_2072	SSA_2072	Streptococcus sanguinis SK36
proS	SSA_2069	COG0442J	prolyl-tRNA synthetase	DEG10210193	SSA_2069	SSA_2069	Streptococcus sanguinis SK36
polC	SSA_2066	COG2176L	DNA polymerase III PolC	DEG10210192	SSA_2066	SSA_2066	Streptococcus sanguinis SK36
def	SSA_2061	COG0242J	peptide deformylase	DEG10210191	SSA_2061	SSA_2061	Streptococcus sanguinis SK36
cysS	SSA_2044	COG0215J	cysteinyl-tRNA synthetase	DEG10210190	SSA_2044	SSA_2044	Streptococcus sanguinis SK36
rplM	SSA_2034	COG0102J	50S ribosomal protein L13	DEG10210189	SSA_2034	SSA_2034	Streptococcus sanguinis SK36
dnaK	SSA_2007	COG0443O	molecular chaperone DnaK	DEG10210188	SSA_2007	SSA_2007	Streptococcus sanguinis SK36
dnaJ	SSA_2005	COG0484O	molecular chaperone DnaJ	DEG10210187	SSA_2005	SSA_2005	Streptococcus sanguinis SK36
fba	SSA_1992	COG0191G	fructose-bisphosphate aldolase	DEG10210186	SSA_1992	SSA_1992	Streptococcus sanguinis SK36
fabH	SSA_1940	COG0332I	3-oxoacyl-ACP synthase	DEG10210185	SSA_1940	SSA_1940	Streptococcus sanguinis SK36
acpP	SSA_1939	COG0236IQ	acyl carrier protein	DEG10210184	SSA_1939	SSA_1939	Streptococcus sanguinis SK36
fabK	SSA_1938	COG2070R	enoyl-acyl carrier protein(ACP) reductase	DEG10210183	SSA_1938	SSA_1938	Streptococcus sanguinis SK36
fabD	SSA_1937	COG0331I	malonyl-CoA:ACP transacylase	DEG10210182	SSA_1937	SSA_1937	Streptococcus sanguinis SK36
fabG	SSA_1936	COG1028IQR	3-ketoacyl-ACP reductase	DEG10210181	SSA_1936	SSA_1936	Streptococcus sanguinis SK36
fabF	SSA_1935	COG0304IQ	3-oxoacyl-ACP synthase	DEG10210180	SSA_1935	SSA_1935	Streptococcus sanguinis SK36

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
accB	SSA_1934	COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	DEG10210179	SSA_1934	SSA_1934	Streptococcus sanguinis SK36
fabZ	SSA_1933	COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	DEG10210178	SSA_1933	SSA_1933	Streptococcus sanguinis SK36
accC	SSA_1932	COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	DEG10210177	SSA_1932	SSA_1932	Streptococcus sanguinis SK36
accD	SSA_1931	COG0777I	acetyl-CoA carboxylase subunit beta	DEG10210176	SSA_1931	SSA_1931	Streptococcus sanguinis SK36
accA	SSA_1930	COG0825I	acetyl-CoA carboxylase subunit alpha	DEG10210175	SSA_1930	SSA_1930	Streptococcus sanguinis SK36
serS	SSA_1925	COG0172J	seryl-tRNA synthetase	DEG10210174	SSA_1925	SSA_1925	Streptococcus sanguinis SK36
glyQ	SSA_1880	COG0752J	glycyl-tRNA synthetase subunit alpha	DEG10210172	SSA_1880	SSA_1880	Streptococcus sanguinis SK36
glyS	SSA_1879	COG0751J	glycyl-tRNA synthetase subunit beta	DEG10210171	SSA_1879	SSA_1879	Streptococcus sanguinis SK36
ftsL	SSA_1872	COG4839D	cell division protein	DEG10210170	SSA_1872	SSA_1872	Streptococcus sanguinis SK36
pbpX	SSA_1871	COG0768M	penicillin-binding protein 2X	DEG10210169	SSA_1871	SSA_1871	Streptococcus sanguinis SK36
mraY	SSA_1870	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10210168	SSA_1870	SSA_1870	Streptococcus sanguinis SK36
-	SSA_1865	COG0492O	thioredoxin reductase	DEG10210167	SSA_1865	SSA_1865	Streptococcus sanguinis SK36
pncB	SSA_1864	COG1488H	nicotinate phosphoribosyltransferase	DEG10210166	SSA_1864	SSA_1864	Streptococcus sanguinis SK36
nadE	SSA_1863	COG0171H	NAD synthetase	DEG10210165	SSA_1863	SSA_1863	Streptococcus sanguinis SK36
gmk	SSA_1851	COG0194F	guanylate kinase	DEG10210164	SSA_1851	SSA_1851	Streptococcus sanguinis SK36
fmt	SSA_1848	COG0223J	methionyl-tRNA formyltransferase	DEG10210163	SSA_1848	SSA_1848	Streptococcus sanguinis SK36
valS	SSA_1819	COG0525J	valyl-tRNA synthetase	DEG10210162	SSA_1819	SSA_1819	Streptococcus sanguinis SK36
gnd	SSA_1811	COG0362G	6-phosphogluconate dehydrogenase	DEG10210161	SSA_1811	SSA_1811	Streptococcus sanguinis SK36
dnaB	SSA_1806	COG3611L	replication initiation/membrane attachment protein DnaB	DEG10210160	SSA_1806	SSA_1806	Streptococcus sanguinis SK36
dnaI	SSA_1805	COG1484L	primosomal protein DnaI	DEG10210159	SSA_1805	SSA_1805	Streptococcus sanguinis SK36
engA	SSA_1803	COG1160R	GTP-binding protein EngA	DEG10210158	SSA_1803	SSA_1803	Streptococcus sanguinis SK36
murC	SSA_1800	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10210157	SSA_1800	SSA_1800	Streptococcus sanguinis SK36
murI	SSA_1784	COG0796M	glutamate racemase	DEG10210156	SSA_1784	SSA_1784	Streptococcus sanguinis SK36
ppx	SSA_1748	COG1227C	manganese-dependent inorganic pyrophosphatase	DEG10210155	SSA_1748	SSA_1748	Streptococcus sanguinis SK36
murE	SSA_1739	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase	DEG10210154	SSA_1739	SSA_1739	Streptococcus sanguinis SK36
-	SSA_1738	COG2244R	polysaccharide biosynthesis protein	DEG10210153	SSA_1738	SSA_1738	Streptococcus sanguinis SK36
tmk	SSA_1722	COG0125F	thymidylate kinase	DEG10210152	SSA_1722	SSA_1722	Streptococcus sanguinis SK36
holB	SSA_1721	COG0470L	DNA polymerase III subunit delta'	DEG10210151	SSA_1721	SSA_1721	Streptococcus sanguinis SK36
metS	SSA_1703	COG0143J	methionyl-tRNA synthetase	DEG10210150	SSA_1703	SSA_1703	Streptococcus sanguinis SK36
glmU	SSA_1642	COG1207M	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	DEG10210149	SSA_1642	SSA_1642	Streptococcus sanguinis SK36
rplK	SSA_1623	COG0080J	50S ribosomal protein L11	DEG10210148	SSA_1623	SSA_1623	Streptococcus sanguinis SK36
rplA	SSA_1622	COG0081J	50S ribosomal protein L1	DEG10210147	SSA_1622	SSA_1622	Streptococcus sanguinis SK36
pyrH	SSA_1620	COG0528F	uridylate kinase	DEG10210146	SSA_1620	SSA_1620	Streptococcus sanguinis SK36
frr	SSA_1619	COG0233J	ribosome recycling factor	DEG10210145	SSA_1619	SSA_1619	Streptococcus sanguinis SK36
coaE	SSA_1606	COG0237H	dephospho-CoA kinase	DEG10210144	SSA_1606	SSA_1606	Streptococcus sanguinis SK36
secG	SSA_1604	COG1314U	preprotein translocase subunit SecG	DEG10210143	SSA_1604	SSA_1604	Streptococcus sanguinis SK36
thrS	SSA_1571	COG0441J	threonyl-tRNA synthetase	DEG10210142	SSA_1571	SSA_1571	Streptococcus sanguinis SK36
-	SSA_1565	COG0745TK	two-component response transcriptional regulator	DEG10210141	SSA_1565	SSA_1565	Streptococcus sanguinis SK36
ftsY	SSA_1557	COG0552U	SRPR, signal recognition particle-docking protein	DEG10210140	SSA_1557	SSA_1557	Streptococcus sanguinis SK36
gdh	SSA_1555	COG0364G	glucose-6-phosphate 1-dehydrogenase	DEG10210139	SSA_1555	SSA_1555	Streptococcus sanguinis SK36
lysS	SSA_1529	COG1190J	lysyl-tRNA synthetase	DEG10210138	SSA_1529	SSA_1529	Streptococcus sanguinis SK36
ftsW	SSA_1522	COG0772D	cell division protein FtsW	DEG10210137	SSA_1522	SSA_1522	Streptococcus sanguinis SK36
tuf	SSA_1520	COG0050J	elongation factor Tu	DEG10210136	SSA_1520	SSA_1520	Streptococcus sanguinis SK36
infC	SSA_1500	COG0290J	translation initiation factor IF-3	DEG10210135	SSA_1500	SSA_1500	Streptococcus sanguinis SK36
rplT	SSA_1498	COG0292J	50S ribosomal protein L20	DEG10210134	SSA_1498	SSA_1498	Streptococcus sanguinis SK36
metK	SSA_1495	COG0192H	S-adenosylmethionine synthetase	DEG10210133	SSA_1495	SSA_1495	Streptococcus sanguinis SK36
map	SSA_1491	COG0024J	methionine aminopeptidase	DEG10210132	SSA_1491	SSA_1491	Streptococcus sanguinis SK36
ligA	SSA_1484	COG0272L	NAD-dependent DNA ligase LigA	DEG10210131	SSA_1484	SSA_1484	Streptococcus sanguinis SK36
rexB	SSA_1452	COG3857L	second subunit of major exonuclease	DEG10210130	SSA_1452	SSA_1452	Streptococcus sanguinis SK36
elaC	SSA_1430	COG1234R	ribonuclease Z	DEG10210129	SSA_1430	SSA_1430	Streptococcus sanguinis SK36
dnaD	SSA_1419	COG3935L	hypothetical protein	DEG10210128	SSA_1419	SSA_1419	Streptococcus sanguinis SK36
rpsP	SSA_1310	COG0228J	30S ribosomal protein S16	DEG10210127	SSA_1310	SSA_1310	Streptococcus sanguinis SK36
trmD	SSA_1302	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10210126	SSA_1302	SSA_1302	Streptococcus sanguinis SK36
rplS	SSA_1265	COG0335J	50S ribosomal protein L19	DEG10210125	SSA_1265	SSA_1265	Streptococcus sanguinis SK36
-	SSA_1233	COG0344S	glycerol-3-phosphate acyltransferase PlsY	DEG10210124	SSA_1233	SSA_1233	Streptococcus sanguinis SK36
parE	SSA_1232	COG0187L	DNA topoisomerase IV subunit B	DEG10210123	SSA_1232	SSA_1232	Streptococcus sanguinis SK36
parC	SSA_1226	COG0188L	DNA topoisomerase IV subunit A	DEG10210122	SSA_1226	SSA_1226	Streptococcus sanguinis SK36
rpsA	SSA_1223	COG0539J	30S ribosomal protein S1	DEG10210121	SSA_1223	SSA_1223	Streptococcus sanguinis SK36
gyrA	SSA_1220	COG0188L	DNA gyrase subunit A	DEG10210120	SSA_1220	SSA_1220	Streptococcus sanguinis SK36

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
-	SSA_1213	COG1104E	pyridoxal-phosphate dependent aminotransferase	DEG10210119	SSA_1213	SSA_1213	Streptococcus sanguinis SK36
ppnK	SSA_1209	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10210118	SSA_1209	SSA_1209	Streptococcus sanguinis SK36
rbgA	SSA_1189	COG1161R	ribosomal biogenesis GTPase	DEG10210117	SSA_1189	SSA_1189	Streptococcus sanguinis SK36
topA	SSA_1184	COG0550L	DNA topoisomerase I	DEG10210116	SSA_1184	SSA_1184	Streptococcus sanguinis SK36
ffh	SSA_1167	COG0541U	SRP54, signal recognition particle GTPase protein	DEG10210115	SSA_1167	SSA_1167	Streptococcus sanguinis SK36
prfA	SSA_1152	COG0216J	peptide chain release factor 1	DEG10210114	SSA_1152	SSA_1152	Streptococcus sanguinis SK36
rplL	SSA_1105	COG0222J	50S ribosomal protein L7/L12	DEG10210113	SSA_1105	SSA_1105	Streptococcus sanguinis SK36
rplJ	SSA_1104	COG0244J	50S ribosomal protein L10	DEG10210112	SSA_1104	SSA_1104	Streptococcus sanguinis SK36
engB	SSA_1094	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10210111	SSA_1094	SSA_1094	Streptococcus sanguinis SK36
dfrA	SSA_1092	COG0262H	dihydrofolate reductase	DEG10210110	SSA_1092	SSA_1092	Streptococcus sanguinis SK36
thyA	SSA_1091	COG0207F	thymidylate synthase	DEG10210109	SSA_1091	SSA_1091	Streptococcus sanguinis SK36
papS	SSA_1086	COG0617J	tRNA CCA-pyrophosphorylase	DEG10210108	SSA_1086	SSA_1086	Streptococcus sanguinis SK36
rpmA	SSA_1062	COG0211J	50S ribosomal protein L27	DEG10210107	SSA_1062	SSA_1062	Streptococcus sanguinis SK36
murB	SSA_1047	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10210106	SSA_1047	SSA_1047	Streptococcus sanguinis SK36
birA	SSA_0999	COG0340H	biotin--protein ligase	DEG10210105	SSA_0999	SSA_0999	Streptococcus sanguinis SK36
dnaX	SSA_0997	COG2812L	DNA polymerase III subunits gamma and tau	DEG10210104	SSA_0997	SSA_0997	Streptococcus sanguinis SK36
pstB2	SSA_0944	COG1117P	phosphate ABC transporter ATP-binding protein	DEG10210103	SSA_0944	SSA_0944	Streptococcus sanguinis SK36
pstC	SSA_0943	COG0581P	phosphate ABC transporter permease	DEG10210102	SSA_0943	SSA_0943	Streptococcus sanguinis SK36
pstS	SSA_0941	COG0226P	phosphate ABC transporter substrate-binding protein	DEG10210101	SSA_0941	SSA_0941	Streptococcus sanguinis SK36
mreA	SSA_0936	COG0196H	bifunctional riboflavin kinase/FMN adenylyltransferase	DEG10210100	SSA_0936	SSA_0936	Streptococcus sanguinis SK36
pheT	SSA_0914	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10210099	SSA_0914	SSA_0914	Streptococcus sanguinis SK36
pheS	SSA_0912	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10210098	SSA_0912	SSA_0912	Streptococcus sanguinis SK36
eno	SSA_0886	COG0148G	phosphopyruvate hydratase	DEG10210097	SSA_0886	SSA_0886	Streptococcus sanguinis SK36
gyrB	SSA_0878	COG0187L	DNA gyrase subunit B	DEG10210096	SSA_0878	SSA_0878	Streptococcus sanguinis SK36
ftsX	SSA_0871	COG2177D	cell division protein FtsX	DEG10210095	SSA_0871	SSA_0871	Streptococcus sanguinis SK36
ftsE	SSA_0870	COG2884D	cell division protein FtsE	DEG10210094	SSA_0870	SSA_0870	Streptococcus sanguinis SK36
prfB	SSA_0869	COG1186J	peptide chain release factor 2	DEG10210093	SSA_0869	SSA_0869	Streptococcus sanguinis SK36
murM	SSA_0862	COG2348V	MurM protein	DEG10210092	SSA_0862	SSA_0862	Streptococcus sanguinis SK36
tpiA	SSA_0859	COG0149G	triosephosphate isomerase	DEG10210091	SSA_0859	SSA_0859	Streptococcus sanguinis SK36
pykF	SSA_0848	COG0469G	pyruvate kinase	DEG10210090	SSA_0848	SSA_0848	Streptococcus sanguinis SK36
pfk	SSA_0847	COG0205G	6-phosphofructokinase	DEG10210089	SSA_0847	SSA_0847	Streptococcus sanguinis SK36
dnaE	SSA_0846	COG0587L	DNA polymerase III DnaE	DEG10210088	SSA_0846	SSA_0846	Streptococcus sanguinis SK36
rpoD	SSA_0825	COG0568K	RNA polymerase sigma factor RpoD	DEG10210087	SSA_0825	SSA_0825	Streptococcus sanguinis SK36
dnaG	SSA_0824	COG0358L	DNA primase	DEG10210086	SSA_0824	SSA_0824	Streptococcus sanguinis SK36
obgE	SSA_0807	COG0536R	GTPase ObgE	DEG10210085	SSA_0807	SSA_0807	Streptococcus sanguinis SK36
glmM	SSA_0804	COG1109G	phosphoglucosamine mutase	DEG10210084	SSA_0804	SSA_0804	Streptococcus sanguinis SK36
-	SSA_0801	COG0769M	Mur ligase family protein	DEG10210083	SSA_0801	SSA_0801	Streptococcus sanguinis SK36
atpC	SSA_0789	COG0355C	ATP synthase F0F1 subunit epsilon	DEG10210081	SSA_0789	SSA_0789	Streptococcus sanguinis SK36
uncD	SSA_0788	COG0055C	ATP synthase F0F1 subunit beta	DEG10210080	SSA_0788	SSA_0788	Streptococcus sanguinis SK36
uncG	SSA_0787	COG0224C	ATP synthase F0F1 subunit gamma	DEG10210079	SSA_0787	SSA_0787	Streptococcus sanguinis SK36
uncA	SSA_0786	COG0056C	proton-translocating ATPase, F1 sector subunit alpha	DEG10210078	SSA_0786	SSA_0786	Streptococcus sanguinis SK36
uncH	SSA_0785	COG0712C	ATP synthase F0F1 subunit delta	DEG10210077	SSA_0785	SSA_0785	Streptococcus sanguinis SK36
uncF	SSA_0784	COG0711C	ATP synthase F0F1 subunit B	DEG10210076	SSA_0784	SSA_0784	Streptococcus sanguinis SK36
uncB	SSA_0783	COG0356C	ATP synthase F0F1 subunit A	DEG10210075	SSA_0783	SSA_0783	Streptococcus sanguinis SK36
uncE	SSA_0782	COG0636C	ATP synthase F0F1 subunit C	DEG10210074	SSA_0782	SSA_0782	Streptococcus sanguinis SK36
nrdH	SSA_0771	COG0695O	glutaredoxin-like protein	DEG10210073	SSA_0771	SSA_0771	Streptococcus sanguinis SK36
nrdE	SSA_0770	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10210072	SSA_0770	SSA_0770	Streptococcus sanguinis SK36
nrdF	SSA_0768	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10210071	SSA_0768	SSA_0768	Streptococcus sanguinis SK36
alaS	SSA_0756	COG0013J	alanyl-tRNA synthetase	DEG10210070	SSA_0756	SSA_0756	Streptococcus sanguinis SK36
holA	SSA_0720	COG1466L	DNA polymerase III subunit delta	DEG10210069	SSA_0720	SSA_0720	Streptococcus sanguinis SK36
plsC	SSA_0713	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	DEG10210068	SSA_0713	SSA_0713	Streptococcus sanguinis SK36
murF	SSA_0692	COG0770M	D-Ala-D-Ala adding enzyme	DEG10210067	SSA_0692	SSA_0692	Streptococcus sanguinis SK36
ddl	SSA_0691	COG1181M	D-alanyl-alanine synthetase A	DEG10210066	SSA_0691	SSA_0691	Streptococcus sanguinis SK36
gpmA	SSA_0688	COG0588G	phosphoglyceromutase	DEG10210065	SSA_0688	SSA_0688	Streptococcus sanguinis SK36
-	SSA_0683	COG0776L	DNA-binding protein HU	DEG10210064	SSA_0683	SSA_0683	Streptococcus sanguinis SK36
ileS	SSA_0661	COG0060J	isoleucyl-tRNA synthetase	DEG10210063	SSA_0661	SSA_0661	Streptococcus sanguinis SK36
ftsZ	SSA_0656	COG0206D	cell division protein FtsZ	DEG10210062	SSA_0656	SSA_0656	Streptococcus sanguinis SK36

Gene	Gene locus	COG	Product	DEG code	Experimental EG	Predicted EG	Strain name
murG	SSA_0653	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	DEG10210061	SSA_0653	SSA_0653	Streptococcus sanguinis SK36
murD	SSA_0652	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	DEG10210060	SSA_0652	SSA_0652	Streptococcus sanguinis SK36
coaD	SSA_0625	COG0669H	phosphopantetheine adenylyltransferase	DEG10210059	SSA_0625	SSA_0625	Streptococcus sanguinis SK36
gatB	SSA_0571	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10210057	SSA_0571	SSA_0571	Streptococcus sanguinis SK36
gatA	SSA_0570	COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A	DEG10210056	SSA_0570	SSA_0570	Streptococcus sanguinis SK36
gatC	SSA_0569	COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	DEG10210055	SSA_0569	SSA_0569	Streptococcus sanguinis SK36
alr	SSA_0548	COG0787M	alanine racemase	DEG10210054	SSA_0548	SSA_0548	Streptococcus sanguinis SK36
acpS	SSA_0547	COG0736I	4'-phosphopantetheinyl transferase	DEG10210053	SSA_0547	SSA_0547	Streptococcus sanguinis SK36
secA	SSA_0543	COG0653U	preprotein translocase subunit SecA	DEG10210052	SSA_0543	SSA_0543	Streptococcus sanguinis SK36
rpsR	SSA_0440	COG0238J	30S ribosomal protein S18	DEG10210051	SSA_0440	SSA_0440	Streptococcus sanguinis SK36
ssb	SSA_0438	COG0629L	single-stranded DNA-binding protein	DEG10210050	SSA_0438	SSA_0438	Streptococcus sanguinis SK36
rpsF	SSA_0437	COG0360J	30S ribosomal protein S6	DEG10210049	SSA_0437	SSA_0437	Streptococcus sanguinis SK36
mvaS	SSA_0338	COG3425I	hydroxymethylglutaryl-CoA synthase	DEG10210048	SSA_0338	SSA_0338	Streptococcus sanguinis SK36
mvaA	SSA_0337	COG1257I	hydroxymethylglutaryl-CoA reductase	DEG10210047	SSA_0337	SSA_0337	Streptococcus sanguinis SK36
-	SSA_0336	COG1304C	isopentenyl pyrophosphate isomerase	DEG10210046	SSA_0336	SSA_0336	Streptococcus sanguinis SK36
mvaK2	SSA_0335	COG1577I	phosphomevalonate kinase	DEG10210045	SSA_0335	SSA_0335	Streptococcus sanguinis SK36
mvaD	SSA_0334	COG3407I	diphosphomevalonate decarboxylase	DEG10210044	SSA_0334	SSA_0334	Streptococcus sanguinis SK36
mvaK1	SSA_0333	COG1577I	mevalonate kinase	DEG10210043	SSA_0333	SSA_0333	Streptococcus sanguinis SK36
-	SSA_0312	COG0595R	metallo-beta-lactamase superfamily hydrolase	DEG10210042	SSA_0312	SSA_0312	Streptococcus sanguinis SK36
pgk	SSA_0302	COG0126G	phosphoglycerate kinase	DEG10210041	SSA_0302	SSA_0302	Streptococcus sanguinis SK36
leuS	SSA_0289	COG0495J	leucyl-tRNA synthetase	DEG10210040	SSA_0289	SSA_0289	Streptococcus sanguinis SK36
groEL	SSA_0226	COG0459O	molecular chaperone GroEL	DEG10210039	SSA_0226	SSA_0226	Streptococcus sanguinis SK36
groES	SSA_0225	COG0234O	co-chaperonin GroES	DEG10210038	SSA_0225	SSA_0225	Streptococcus sanguinis SK36
folK	SSA_0200	COG0801H	bifunctional folate synthesis protein	DEG10210037	SSA_0200	SSA_0200	Streptococcus sanguinis SK36
folE	SSA_0199	COG0302H	GTP cyclohydrolase I	DEG10210036	SSA_0199	SSA_0199	Streptococcus sanguinis SK36
-	SSA_0198	COG0285H	dihydrofolate synthetase	DEG10210035	SSA_0198	SSA_0198	Streptococcus sanguinis SK36
folP	SSA_0197	COG0294H	dihydropteroate synthase	DEG10210034	SSA_0197	SSA_0197	Streptococcus sanguinis SK36
rpoC	SSA_0177	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10210033	SSA_0177	SSA_0177	Streptococcus sanguinis SK36
rpoB	SSA_0176	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10210032	SSA_0176	SSA_0176	Streptococcus sanguinis SK36
tyrS	SSA_0174	COG0162J	tyrosyl-tRNA synthetase	DEG10210031	SSA_0174	SSA_0174	Streptococcus sanguinis SK36
rplQ	SSA_0133	COG0203J	50S ribosomal protein L17	DEG10210030	SSA_0133	SSA_0133	Streptococcus sanguinis SK36
rpoA	SSA_0132	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10210029	SSA_0132	SSA_0132	Streptococcus sanguinis SK36
rpsK	SSA_0131	COG0100J	30S ribosomal protein S11	DEG10210028	SSA_0131	SSA_0131	Streptococcus sanguinis SK36
infA	SSA_0129	COG0361J	translation initiation factor IF-1	DEG10210027	SSA_0129	SSA_0129	Streptococcus sanguinis SK36
adk	SSA_0128	COG0563F	adenylate kinase	DEG10210026	SSA_0128	SSA_0128	Streptococcus sanguinis SK36
secY	SSA_0127	COG0201U	preprotein translocase subunit SecY	DEG10210025	SSA_0127	SSA_0127	Streptococcus sanguinis SK36
rpsE	SSA_0124	COG0098J	30S ribosomal protein S5	DEG10210024	SSA_0124	SSA_0124	Streptococcus sanguinis SK36
rplR	SSA_0123	COG0256J	50S ribosomal protein L18	DEG10210023	SSA_0123	SSA_0123	Streptococcus sanguinis SK36
rplF	SSA_0122	COG0097J	50S ribosomal protein L6	DEG10210022	SSA_0122	SSA_0122	Streptococcus sanguinis SK36
rpsH	SSA_0120	COG0096J	30S ribosomal protein S8	DEG10210021	SSA_0120	SSA_0120	Streptococcus sanguinis SK36
rplE	SSA_0119	COG0094J	50S ribosomal protein L5	DEG10210020	SSA_0119	SSA_0119	Streptococcus sanguinis SK36
rplN	SSA_0117	COG0093J	50S ribosomal protein L14	DEG10210019	SSA_0117	SSA_0117	Streptococcus sanguinis SK36
rpsQ	SSA_0116	COG0186J	30S ribosomal protein S17	DEG10210018	SSA_0116	SSA_0116	Streptococcus sanguinis SK36
rplP	SSA_0114	COG0197J	50S ribosomal protein L16	DEG10210017	SSA_0114	SSA_0114	Streptococcus sanguinis SK36
rpsC	SSA_0113	COG0092J	30S ribosomal protein S3	DEG10210016	SSA_0113	SSA_0113	Streptococcus sanguinis SK36
rplV	SSA_0112	COG0091J	50S ribosomal protein L22	DEG10210015	SSA_0112	SSA_0112	Streptococcus sanguinis SK36
rpsS	SSA_0111	COG0185J	30S ribosomal protein S19	DEG10210014	SSA_0111	SSA_0111	Streptococcus sanguinis SK36
rplB	SSA_0110	COG0090J	50S ribosomal protein L2	DEG10210013	SSA_0110	SSA_0110	Streptococcus sanguinis SK36
rplW	SSA_0109	COG0089J	50S ribosomal protein L23	DEG10210012	SSA_0109	SSA_0109	Streptococcus sanguinis SK36
rplD	SSA_0108	COG0088J	50S ribosomal protein L4	DEG10210011	SSA_0108	SSA_0108	Streptococcus sanguinis SK36
rplC	SSA_0107	COG0087J	50S ribosomal protein L3	DEG10210010	SSA_0107	SSA_0107	Streptococcus sanguinis SK36
rpsJ	SSA_0106	COG0051J	30S ribosomal protein S10	DEG10210009	SSA_0106	SSA_0106	Streptococcus sanguinis SK36
polA	SSA_0100	COG0749L	DNA polymerase I	DEG10210008	SSA_0100	SSA_0100	Streptococcus sanguinis SK36
ruvB	SSA_0063	COG2255L	Holliday junction DNA helicase RuvB	DEG10210007	SSA_0063	SSA_0063	Streptococcus sanguinis SK36
prsA	SSA_0020	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10210006	SSA_0020	SSA_0020	Streptococcus sanguinis SK36
mesJ	SSA_0013	COG0037D	PP family ATPase	DEG10210005	SSA_0013	SSA_0013	Streptococcus sanguinis SK36
divIC	SSA_0010	COG2919D	cell division protein DivIC	DEG10210004	SSA_0010	SSA_0010	Streptococcus sanguinis SK36
pth	SSA_0006	COG0193J	peptidyl-tRNA hydrolase	DEG10210003	SSA_0006	SSA_0006	Streptococcus sanguinis SK36
dnaN	SSA_0002	COG0592L	DNA polymerase III subunit beta	DEG10210002	SSA_0002	SSA_0002	Streptococcus sanguinis SK36
dnaA	SSA_0001	COG0593L	chromosomal replication initiation protein	DEG10210001	SSA_0001	SSA_0001	Streptococcus sanguinis SK36
-	SSA_1903	COG0510M	hypothetical protein	DEG10210173	SSA_1903		
cobQ	SSA_0800	COG3442R	glutamine amidotransferase	DEG10210082	SSA_0800		
-	SSA_0575	COG2179R	HAD superfamily hydrolase	DEG10210058	SSA_0575		

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_2087	COG1216R	glycosyltransferase	DEG10220463	PGN_2087		Porphyromonas gingivalis ATCC 33277
-	PGN_2086	COG1560N	acetyltransferase	DEG10220462	PGN_2086	PGN_2086	Porphyromonas gingivalis ATCC 33277
-	PGN_2085	COG0621J	Fe-S oxidoreductase	DEG10220461	PGN_2085	PGN_2085	Porphyromonas gingivalis ATCC 33277
-	PGN_2081	COG1154H	1-deoxy-D-xylulose-5-phosphate synthase	DEG10220460	PGN_2081	PGN_2081	Porphyromonas gingivalis ATCC 33277
-	PGN_2079	COG0836N	mannose-1-phosphate guanylyltransferase	DEG10220459	PGN_2079	PGN_2079	Porphyromonas gingivalis ATCC 33277
thyA	PGN_2062	COG0207F	thymidylate synthase	DEG10220458	PGN_2062	PGN_2062	Porphyromonas gingivalis ATCC 33277
-	PGN_2061	COG0262H	dihydrofolate reductase	DEG10220457	PGN_2061	PGN_2061	Porphyromonas gingivalis ATCC 33277
hisS	PGN_2060	COG0124J	histidyl-tRNA synthetase	DEG10220456	PGN_2060	PGN_2060	Porphyromonas gingivalis ATCC 33277
-	PGN_2056	-	hypothetical protein	DEG10220455	PGN_2056		Porphyromonas gingivalis ATCC 33277
-	PGN_2055	COG1995H	4-hydroxythreonine-4-phosphate dehydrogenase	DEG10220454	PGN_2055	PGN_2055	Porphyromonas gingivalis ATCC 33277
-	PGN_2054	COG0615N	glycerol-3-phosphate cytidylyltransferase	DEG10220453	PGN_2054	PGN_2054	Porphyromonas gingivalis ATCC 33277
-	PGN_2053	COG1028I	hypothetical protein	DEG10220452	PGN_2053		Porphyromonas gingivalis ATCC 33277
-	PGN_2051	COG3176R	hypothetical protein	DEG10220451	PGN_2051		Porphyromonas gingivalis ATCC 33277
pheT	PGN_2045	COG0072J	phenylalanyl-tRNA synthetase subunit beta	DEG10220450	PGN_2045	PGN_2045	Porphyromonas gingivalis ATCC 33277
-	PGN_2034	COG0794N	sugar isomerase	DEG10220449	PGN_2034		Porphyromonas gingivalis ATCC 33277
-	PGN_2024	COG1705N	hemagglutinin	DEG10220448	PGN_2024		Porphyromonas gingivalis ATCC 33277
-	PGN_2023	COG0150F	phosphoribosylformylglycinamidine cyclo-ligase	DEG10220447	PGN_2023	PGN_2023	Porphyromonas gingivalis ATCC 33277
prfA	PGN_2022	COG0216J	peptide chain release factor 1	DEG10220446	PGN_2022	PGN_2022	Porphyromonas gingivalis ATCC 33277
lpxD	PGN_2020	COG1044N	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	DEG10220445	PGN_2020	PGN_2020	Porphyromonas gingivalis ATCC 33277
-	PGN_2019	COG0774N	bifunctional UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase/(3R)-hydroxymyristoyl-ACP dehydratase	DEG10220444	PGN_2019	PGN_2019	Porphyromonas gingivalis ATCC 33277
-	PGN_2018	COG1043N	UDP-N-acetylglucosamine acyltransferase	DEG10220443	PGN_2018	PGN_2018	Porphyromonas gingivalis ATCC 33277
nadD	PGN_2007	COG1057H	nicotinic acid mononucleotide adenylyltransferase	DEG10220442	PGN_2007	PGN_2007	Porphyromonas gingivalis ATCC 33277
-	PGN_2006	COG1488H	nicotinate phosphoribosyltransferase	DEG10220441	PGN_2006	PGN_2006	Porphyromonas gingivalis ATCC 33277
-	PGN_2005	-	hypothetical protein	DEG10220440	PGN_2005		Porphyromonas gingivalis ATCC 33277
dapA	PGN_1996	COG0329E	dihydrodipicolinate synthase	DEG10220439	PGN_1996	PGN_1996	Porphyromonas gingivalis ATCC 33277
-	PGN_1991	COG0037D	cell-cycle protein	DEG10220438	PGN_1991	PGN_1991	Porphyromonas gingivalis ATCC 33277
-	PGN_1990	COG1579R	hypothetical protein	DEG10220437	PGN_1990		Porphyromonas gingivalis ATCC 33277
fmt	PGN_1969	COG0223J	methionyl-tRNA formyltransferase	DEG10220436	PGN_1969	PGN_1969	Porphyromonas gingivalis ATCC 33277
-	PGN_1968	COG4485S	hypothetical protein	DEG10220435	PGN_1968		Porphyromonas gingivalis ATCC 33277
-	PGN_1955	COG1109G	phosphomannomutase	DEG10220434	PGN_1955	PGN_1955	Porphyromonas gingivalis ATCC 33277
dapB	PGN_1947	COG0289E	dihydrodipicolinate reductase	DEG10220433	PGN_1947	PGN_1947	Porphyromonas gingivalis ATCC 33277
-	PGN_1946	COG0681U	signal peptidase I	DEG10220432	PGN_1946	PGN_1946	Porphyromonas gingivalis ATCC 33277
-	PGN_1934	-	hypothetical protein	DEG10220431	PGN_1934		Porphyromonas gingivalis ATCC 33277
-	PGN_1895	COG0009J	hypothetical protein	DEG10220430	PGN_1895		Porphyromonas gingivalis ATCC 33277
-	PGN_1892	COG0306P	hypothetical protein	DEG10220429	PGN_1892		Porphyromonas gingivalis ATCC 33277
-	PGN_1886	COG0451N	NAD dependent epimerase	DEG10220428	PGN_1886	PGN_1886	Porphyromonas gingivalis ATCC 33277
-	PGN_1885	COG1284S	hypothetical protein	DEG10220427	PGN_1885		Porphyromonas gingivalis ATCC 33277
-	PGN_1884	COG0586S	alkaline phosphatase	DEG10220426	PGN_1884		Porphyromonas gingivalis ATCC 33277
-	PGN_1883	COG0008J	glutaminyl-tRNA synthetase	DEG10220425	PGN_1883	PGN_1883	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
rpsL	PGN_1872	COG0048J	30S ribosomal protein S12	DEG10220424	PGN_1872	PGN_1872	Porphyromonas gingivalis ATCC 33277
rpsG	PGN_1871	COG0049J	30S ribosomal protein S7	DEG10220423	PGN_1871	PGN_1871	Porphyromonas gingivalis ATCC 33277
-	PGN_1870	COG0480J	elongation factor G	DEG10220422	PGN_1870	PGN_1870	Porphyromonas gingivalis ATCC 33277
rpsJ	PGN_1869	COG0051J	30S ribosomal protein S10	DEG10220421	PGN_1869	PGN_1869	Porphyromonas gingivalis ATCC 33277
rplC	PGN_1868	COG0087J	50S ribosomal protein L3	DEG10220420	PGN_1868	PGN_1868	Porphyromonas gingivalis ATCC 33277
rplD	PGN_1867	COG0088J	50S ribosomal protein L4	DEG10220419	PGN_1867	PGN_1867	Porphyromonas gingivalis ATCC 33277
rplW	PGN_1866	COG0089J	50S ribosomal protein L23	DEG10220418	PGN_1866	PGN_1866	Porphyromonas gingivalis ATCC 33277
rplB	PGN_1865	COG0090J	50S ribosomal protein L2	DEG10220417	PGN_1865	PGN_1865	Porphyromonas gingivalis ATCC 33277
rpsS	PGN_1864	COG0185J	30S ribosomal protein S19	DEG10220416	PGN_1864	PGN_1864	Porphyromonas gingivalis ATCC 33277
rplV	PGN_1863	COG0091J	50S ribosomal protein L22	DEG10220415	PGN_1863	PGN_1863	Porphyromonas gingivalis ATCC 33277
rpsC	PGN_1862	COG0092J	30S ribosomal protein S3	DEG10220414	PGN_1862	PGN_1862	Porphyromonas gingivalis ATCC 33277
rplP	PGN_1861	COG0197J	50S ribosomal protein L16	DEG10220413	PGN_1861	PGN_1861	Porphyromonas gingivalis ATCC 33277
rpsQ	PGN_1859	COG0186J	30S ribosomal protein S17	DEG10220412	PGN_1859	PGN_1859	Porphyromonas gingivalis ATCC 33277
rplN	PGN_1858	COG0093J	50S ribosomal protein L14	DEG10220411	PGN_1858	PGN_1858	Porphyromonas gingivalis ATCC 33277
rplX	PGN_1857	COG0198J	50S ribosomal protein L24	DEG10220410	PGN_1857	PGN_1857	Porphyromonas gingivalis ATCC 33277
rplE	PGN_1856	COG0094J	50S ribosomal protein L5	DEG10220409	PGN_1856	PGN_1856	Porphyromonas gingivalis ATCC 33277
rpsN	PGN_1855	COG0199J	30S ribosomal protein S14	DEG10220408	PGN_1855	PGN_1855	Porphyromonas gingivalis ATCC 33277
rpsH	PGN_1854	COG0096J	30S ribosomal protein S8	DEG10220407	PGN_1854	PGN_1854	Porphyromonas gingivalis ATCC 33277
rplF	PGN_1853	COG0097J	50S ribosomal protein L6	DEG10220406	PGN_1853	PGN_1853	Porphyromonas gingivalis ATCC 33277
rplR	PGN_1852	COG0256J	50S ribosomal protein L18	DEG10220405	PGN_1852	PGN_1852	Porphyromonas gingivalis ATCC 33277
rpsE	PGN_1851	COG0098J	30S ribosomal protein S5	DEG10220404	PGN_1851	PGN_1851	Porphyromonas gingivalis ATCC 33277
rpmD	PGN_1850	COG1841J	50S ribosomal protein L30	DEG10220403	PGN_1850	PGN_1850	Porphyromonas gingivalis ATCC 33277
rplO	PGN_1849	COG0200J	50S ribosomal protein L15	DEG10220402	PGN_1849	PGN_1849	Porphyromonas gingivalis ATCC 33277
secY	PGN_1848	COG0201U	preprotein translocase subunit SecY	DEG10220401	PGN_1848	PGN_1848	Porphyromonas gingivalis ATCC 33277
-	PGN_1847	COG0024J	methionine aminopeptidase type I	DEG10220400	PGN_1847	PGN_1847	Porphyromonas gingivalis ATCC 33277
infA	PGN_1846	COG0361J	translation initiation factor IF-1	DEG10220399	PGN_1846	PGN_1846	Porphyromonas gingivalis ATCC 33277
rpmJ	PGN_1845	COG0257J	50S ribosomal protein L36	DEG10220398	PGN_1845	PGN_1845	Porphyromonas gingivalis ATCC 33277
rpsM	PGN_1844	COG0099J	30S ribosomal protein S13	DEG10220397	PGN_1844	PGN_1844	Porphyromonas gingivalis ATCC 33277
rpsK	PGN_1843	COG0100J	30S ribosomal protein S11	DEG10220396	PGN_1843	PGN_1843	Porphyromonas gingivalis ATCC 33277
rpsD	PGN_1842	COG0522J	30S ribosomal protein S4	DEG10220395	PGN_1842	PGN_1842	Porphyromonas gingivalis ATCC 33277
rpoA	PGN_1841	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10220394	PGN_1841	PGN_1841	Porphyromonas gingivalis ATCC 33277
-	PGN_1834	-	hypothetical protein	DEG10220393	PGN_1834		Porphyromonas gingivalis ATCC 33277
pyrH	PGN_1833	COG0528F	uridylate kinase	DEG10220392	PGN_1833	PGN_1833	Porphyromonas gingivalis ATCC 33277
frr	PGN_1832	COG0233J	ribosome recycling factor	DEG10220391	PGN_1832	PGN_1832	Porphyromonas gingivalis ATCC 33277
-	PGN_1829	COG3201H	nicotinamide mononucleotide transporter	DEG10220390	PGN_1829	PGN_1829	Porphyromonas gingivalis ATCC 33277
-	PGN_1827	COG0192H	S-adenosylmethionine synthetase	DEG10220389	PGN_1827	PGN_1827	Porphyromonas gingivalis ATCC 33277
-	PGN_1807	COG1216R	glycosyltransferase	DEG10220388	PGN_1807		Porphyromonas gingivalis ATCC 33277
-	PGN_1806	COG1752R	hypothetical protein	DEG10220387	PGN_1806		Porphyromonas gingivalis ATCC 33277
cysS	PGN_1805	COG0215J	cysteinyl-tRNA synthetase	DEG10220386	PGN_1805	PGN_1805	Porphyromonas gingivalis ATCC 33277
-	PGN_1794	COG1929G	hypothetical protein	DEG10220385	PGN_1794		Porphyromonas gingivalis ATCC 33277
-	PGN_1789	COG2131F	deoxycytidylate deaminase	DEG10220384	PGN_1789	PGN_1789	Porphyromonas gingivalis ATCC 33277
-	PGN_1786	COG0592L	DNA polymerase III beta chain	DEG10220383	PGN_1786	PGN_1786	Porphyromonas gingivalis ATCC 33277
-	PGN_1785	COG0847L	DNA polymerase III epsilon chain	DEG10220382	PGN_1785	PGN_1785	Porphyromonas gingivalis ATCC 33277
-	PGN_1784	COG0452H	DNA/pantothenate metabolism flavoprotein	DEG10220381	PGN_1784	PGN_1784	Porphyromonas gingivalis ATCC 33277
-	PGN_1773	COG0475P	sodium/hydrogen antiporter	DEG10220380	PGN_1773		Porphyromonas gingivalis ATCC 33277
-	PGN_1766	-	hypothetical protein	DEG10220379	PGN_1766		Porphyromonas gingivalis ATCC 33277
-	PGN_1757	COG0317TK	GTP pyrophosphokinase	DEG10220378	PGN_1757	PGN_1757	Porphyromonas gingivalis ATCC 33277
-	PGN_1751	COG0358L	DNA primase	DEG10220377	PGN_1751	PGN_1751	Porphyromonas gingivalis ATCC 33277
-	PGN_1750	COG1212M	3-deoxy-manno-octulosonate cytidylyltransferase	DEG10220376	PGN_1750	PGN_1750	Porphyromonas gingivalis ATCC 33277
-	PGN_1749	COG2249R	NADPH-quinone reductase	DEG10220375	PGN_1749	PGN_1749	Porphyromonas gingivalis ATCC 33277
-	PGN_1736	COG0297G	glycogen synthase	DEG10220374	PGN_1736	PGN_1736	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_1718	COG2908S	UDP-2,3-diacylglucosamine hydrolase	DEG10220373	PGN_1718	PGN_1718	Porphyromonas gingivalis ATCC 33277
-	PGN_1717	COG2151R	hypothetical protein	DEG10220372	PGN_1717		Porphyromonas gingivalis ATCC 33277
dnaJ	PGN_1716	COG0484O	molecular chaperone DnaJ	DEG10220371	PGN_1716	PGN_1716	Porphyromonas gingivalis ATCC 33277
pheS	PGN_1711	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10220370	PGN_1711	PGN_1711	Porphyromonas gingivalis ATCC 33277
acpP	PGN_1705	COG0236IQ	acyl carrier protein	DEG10220369	PGN_1705	PGN_1705	Porphyromonas gingivalis ATCC 33277
-	PGN_1704	COG0304IQ	beta-ketoacyl-acyl-carrier-protein synthase II	DEG10220368	PGN_1704	PGN_1704	Porphyromonas gingivalis ATCC 33277
-	PGN_1702	COG0342U	bifunctional preprotein translocase subunit SecD/SecF	DEG10220367	PGN_1702	PGN_1702	Porphyromonas gingivalis ATCC 33277
rpsO	PGN_1698	COG0184J	30S ribosomal protein S15	DEG10220366	PGN_1698	PGN_1698	Porphyromonas gingivalis ATCC 33277
-	PGN_1695	COG3588G	fructose-1,6-bisphosphate aldolase	DEG10220365	PGN_1695	PGN_1695	Porphyromonas gingivalis ATCC 33277
-	PGN_1689	COG0021G	transketolase	DEG10220364	PGN_1689	PGN_1689	Porphyromonas gingivalis ATCC 33277
-	PGN_1688	COG0698G	ribose 5-phosphate isomerase B	DEG10220363	PGN_1688	PGN_1688	Porphyromonas gingivalis ATCC 33277
-	PGN_1678	-	hypothetical protein	DEG10220362	PGN_1678		Porphyromonas gingivalis ATCC 33277
-	PGN_1660	COG3086T	hypothetical protein	DEG10220361	PGN_1660		Porphyromonas gingivalis ATCC 33277
-	PGN_1659	COG2878C	ferredoxin	DEG10220360	PGN_1659	PGN_1659	Porphyromonas gingivalis ATCC 33277
-	PGN_1658	COG4656C	electron transport complex RnfABCDGE type C subunit	DEG10220359	PGN_1658	PGN_1658	Porphyromonas gingivalis ATCC 33277
-	PGN_1657	COG4658C	electron transport complex RnfABCDGE type D subunit	DEG10220358	PGN_1657	PGN_1657	Porphyromonas gingivalis ATCC 33277
-	PGN_1656	COG4659C	electron transport complex RnfABCDGE type G subunit	DEG10220357	PGN_1656	PGN_1656	Porphyromonas gingivalis ATCC 33277
-	PGN_1655	COG4660C	electron transport complex RsxE subunit	DEG10220356	PGN_1655	PGN_1655	Porphyromonas gingivalis ATCC 33277
-	PGN_1654	COG4657C	electron transport complex RnfABCDGE type A subunit	DEG10220355	PGN_1654	PGN_1654	Porphyromonas gingivalis ATCC 33277
-	PGN_1653	COG1477H	thiamine biosynthesis lipoprotein ApbE	DEG10220354	PGN_1653		Porphyromonas gingivalis ATCC 33277
-	PGN_1652	COG0778C	nitroreductase	DEG10220353	PGN_1652		Porphyromonas gingivalis ATCC 33277
-	PGN_1651	COG0463M	glycosyltransferase	DEG10220352	PGN_1651		Porphyromonas gingivalis ATCC 33277
-	PGN_1650	-	hypothetical protein	DEG10220351	PGN_1650		Porphyromonas gingivalis ATCC 33277
rplU	PGN_1648	COG0261J	50S ribosomal protein L21	DEG10220350	PGN_1648	PGN_1648	Porphyromonas gingivalis ATCC 33277
rpmA	PGN_1647	COG0211J	50S ribosomal protein L27	DEG10220349	PGN_1647	PGN_1647	Porphyromonas gingivalis ATCC 33277
-	PGN_1646	COG0172J	seryl-tRNA synthetase	DEG10220348	PGN_1646	PGN_1646	Porphyromonas gingivalis ATCC 33277
rho	PGN_1630	COG1158K	transcription termination factor Rho	DEG10220347	PGN_1630	PGN_1630	Porphyromonas gingivalis ATCC 33277
engB	PGN_1615	COG0218R	ribosome biogenesis GTP-binding protein YsxC	DEG10220346	PGN_1615	PGN_1615	Porphyromonas gingivalis ATCC 33277
-	PGN_1602	COG1853R	flavoredoxin	DEG10220345	PGN_1602	PGN_1602	Porphyromonas gingivalis ATCC 33277
-	PGN_1601	COG1704S	conserved hypothetical protein with lemA family domain	DEG10220344	PGN_1601		Porphyromonas gingivalis ATCC 33277
-	PGN_1600	COG1512R	hypothetical protein	DEG10220343	PGN_1600		Porphyromonas gingivalis ATCC 33277
-	PGN_1599	-	hypothetical protein	DEG10220342	PGN_1599		Porphyromonas gingivalis ATCC 33277
-	PGN_1594	COG0187L	DNA topoisomerase IV subunit B	DEG10220341	PGN_1594	PGN_1594	Porphyromonas gingivalis ATCC 33277
coaD	PGN_1593	COG0669H	phosphopantetheine adenylyltransferase	DEG10220340	PGN_1593	PGN_1593	Porphyromonas gingivalis ATCC 33277
rplM	PGN_1590	COG0102J	50S ribosomal protein L13	DEG10220339	PGN_1590	PGN_1590	Porphyromonas gingivalis ATCC 33277
rpsI	PGN_1589	COG0103J	30S ribosomal protein S9	DEG10220338	PGN_1589	PGN_1589	Porphyromonas gingivalis ATCC 33277
rpsB	PGN_1588	COG0052J	30S ribosomal protein S2	DEG10220337	PGN_1588	PGN_1588	Porphyromonas gingivalis ATCC 33277
tsf	PGN_1587	COG0264J	elongation factor Ts	DEG10220336	PGN_1587	PGN_1587	Porphyromonas gingivalis ATCC 33277
-	PGN_1578	COG0050J	elongation factor Tu	DEG10220335	PGN_1578	PGN_1578	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_1577	COG0690U	preprotein translocase SecE subunit	DEG10220334	PGN_1577	PGN_1577	Porphyromonas gingivalis ATCC 33277
-	PGN_1576	COG0250K	transcription antitermination protein	DEG10220333	PGN_1576	PGN_1576	Porphyromonas gingivalis ATCC 33277
rplK	PGN_1575	COG0080J	50S ribosomal protein L11	DEG10220332	PGN_1575	PGN_1575	Porphyromonas gingivalis ATCC 33277
rplA	PGN_1574	COG0081J	50S ribosomal protein L1	DEG10220331	PGN_1574	PGN_1574	Porphyromonas gingivalis ATCC 33277
rplJ	PGN_1573	COG0244J	50S ribosomal protein L10	DEG10220330	PGN_1573	PGN_1573	Porphyromonas gingivalis ATCC 33277
rplL	PGN_1572	COG0222J	50S ribosomal protein L7/L12	DEG10220329	PGN_1572	PGN_1572	Porphyromonas gingivalis ATCC 33277
rpoB	PGN_1571	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10220328	PGN_1571	PGN_1571	Porphyromonas gingivalis ATCC 33277
rpoC	PGN_1570	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10220327	PGN_1570	PGN_1570	Porphyromonas gingivalis ATCC 33277
-	PGN_1568	-	hypothetical protein	DEG10220326	PGN_1568		Porphyromonas gingivalis ATCC 33277
-	PGN_1566	-	hypothetical protein	DEG10220325	PGN_1566		Porphyromonas gingivalis ATCC 33277
-	PGN_1565	COG1774S	hypothetical protein	DEG10220324	PGN_1565		Porphyromonas gingivalis ATCC 33277
-	PGN_1564	COG1418R	phosphodiesterase	DEG10220323	PGN_1564	PGN_1564	Porphyromonas gingivalis ATCC 33277
-	PGN_1562	-	hypothetical protein	DEG10220322	PGN_1562		Porphyromonas gingivalis ATCC 33277
-	PGN_1555	COG0323L	DNA mismatch repair protein MutL	DEG10220321	PGN_1555		Porphyromonas gingivalis ATCC 33277
-	PGN_1554	-	hypothetical protein	DEG10220320	PGN_1554		Porphyromonas gingivalis ATCC 33277
-	PGN_1552	COG0760O	peptidyl-prolyl cis-trans isomerase	DEG10220319	PGN_1552	PGN_1552	Porphyromonas gingivalis ATCC 33277
-	PGN_1518	COG1297S	oligopeptide transporter	DEG10220318	PGN_1518		Porphyromonas gingivalis ATCC 33277
-	PGN_1516	COG0476H	molybdopterin biosynthesis MoeB protein	DEG10220317	PGN_1516		Porphyromonas gingivalis ATCC 33277
-	PGN_1515	COG1521K	pantothenate kinase	DEG10220316	PGN_1515	PGN_1515	Porphyromonas gingivalis ATCC 33277
-	PGN_1514	COG2067I	hypothetical protein	DEG10220315	PGN_1514		Porphyromonas gingivalis ATCC 33277
-	PGN_1513	COG4783R	hypothetical protein	DEG10220314	PGN_1513		Porphyromonas gingivalis ATCC 33277
-	PGN_1512	COG1452M	hypothetical protein	DEG10220313	PGN_1512		Porphyromonas gingivalis ATCC 33277
-	PGN_1510	-	peptidyl-prolyl cis-trans isomerase	DEG10220312	PGN_1510	PGN_1510	Porphyromonas gingivalis ATCC 33277
-	PGN_1505	COG0285H	folylpolyglutamate synthase	DEG10220311	PGN_1505	PGN_1505	Porphyromonas gingivalis ATCC 33277
-	PGN_1504	COG0104F	adenylosuccinate synthetase	DEG10220310	PGN_1504	PGN_1504	Porphyromonas gingivalis ATCC 33277
-	PGN_1503	COG0735P	ferric uptake transcriptional regulator	DEG10220309	PGN_1503	PGN_1503	Porphyromonas gingivalis ATCC 33277
-	PGN_1501	COG1482G	mannose-6-phosphate isomerase	DEG10220308	PGN_1501	PGN_1501	Porphyromonas gingivalis ATCC 33277
-	PGN_1500	-	hypothetical protein	DEG10220307	PGN_1500		Porphyromonas gingivalis ATCC 33277
-	PGN_1487	COG0237H	dephospho-CoA kinase	DEG10220306	PGN_1487	PGN_1487	Porphyromonas gingivalis ATCC 33277
-	PGN_1486	COG4856S	hypothetical protein	DEG10220305	PGN_1486		Porphyromonas gingivalis ATCC 33277
-	PGN_1485	COG1862U	hypothetical protein	DEG10220304	PGN_1485	PGN_1485	Porphyromonas gingivalis ATCC 33277
-	PGN_1484	COG0350L	methylated-DNA-protein-cysteine methyltransferase	DEG10220303	PGN_1484	PGN_1484	Porphyromonas gingivalis ATCC 33277
ruvB	PGN_1482	COG2255L	Holliday junction DNA helicase RuvB	DEG10220302	PGN_1482	PGN_1482	Porphyromonas gingivalis ATCC 33277
-	PGN_1481	COG2244R	polysaccharide biosynthesis protein	DEG10220301	PGN_1481		Porphyromonas gingivalis ATCC 33277
-	PGN_1472	COG0343J	queuine tRNA-ribosyltransferase	DEG10220300	PGN_1472	PGN_1472	Porphyromonas gingivalis ATCC 33277
-	PGN_1471	COG0795R	hypothetical protein	DEG10220299	PGN_1471	PGN_1471	Porphyromonas gingivalis ATCC 33277
smpB	PGN_1470	COG0691O	SsrA-binding protein	DEG10220298	PGN_1470		Porphyromonas gingivalis ATCC 33277
-	PGN_1464	COG0560E	HAD-superfamily subfamily IB hydrolase	DEG10220297	PGN_1464		Porphyromonas gingivalis ATCC 33277
-	PGN_1462	COG0319R	hypothetical protein	DEG10220296	PGN_1462		Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	**DEG**	**Exp EG**	**Predicted EG**	Strain name
-	PGN_1461	COG2715R	spore maturation protein A/B	DEG10220295	PGN_1461		Porphyromonas gingivalis ATCC 33277
gmk	PGN_1460	COG0194F	guanylate kinase	DEG10220294	PGN_1460	PGN_1460	Porphyromonas gingivalis ATCC 33277
-	PGN_1459	COG1561S	hypothetical protein	DEG10220293	PGN_1459		Porphyromonas gingivalis ATCC 33277
secA	PGN_1458	COG0653U	preprotein translocase subunit SecA	DEG10220292	PGN_1458	PGN_1458	Porphyromonas gingivalis ATCC 33277
-	PGN_1457	COG1524R	alkaline phosphatase	DEG10220291	PGN_1457		Porphyromonas gingivalis ATCC 33277
groEL	PGN_1452	COG0459O	molecular chaperone GroEL	DEG10220290	PGN_1452	PGN_1452	Porphyromonas gingivalis ATCC 33277
groES	PGN_1451	COG0234O	co-chaperonin GroES	DEG10220289	PGN_1451	PGN_1451	Porphyromonas gingivalis ATCC 33277
-	PGN_1449	COG0516F	inosine 5-monophosphate dehydrogenase	DEG10220288	PGN_1449	PGN_1449	Porphyromonas gingivalis ATCC 33277
pyrG	PGN_1447	COG0504F	CTP synthetase	DEG10220287	PGN_1447	PGN_1447	Porphyromonas gingivalis ATCC 33277
-	PGN_1446	COG0706U	inner membrane protein translocase component YidC	DEG10220286	PGN_1446	PGN_1446	Porphyromonas gingivalis ATCC 33277
nadE	PGN_1441	COG0171H	NAD synthetase	DEG10220285	PGN_1441	PGN_1441	Porphyromonas gingivalis ATCC 33277
-	PGN_1393	COG0776L	DNA-binding protein HU	DEG10220284	PGN_1393	PGN_1393	Porphyromonas gingivalis ATCC 33277
-	PGN_1391	COG1530J	ribonuclease E	DEG10220283	PGN_1391	PGN_1391	Porphyromonas gingivalis ATCC 33277
recR	PGN_1390	COG0353L	recombination protein RecR	DEG10220282	PGN_1390	PGN_1390	Porphyromonas gingivalis ATCC 33277
-	PGN_1389	COG1670J	acetyltransferase	DEG10220281	PGN_1389		Porphyromonas gingivalis ATCC 33277
-	PGN_1388	COG0272L	DNA ligase	DEG10220280	PGN_1388	PGN_1388	Porphyromonas gingivalis ATCC 33277
-	PGN_1387	COG4591M	ABC transporter permease protein	DEG10220279	PGN_1387	PGN_1387	Porphyromonas gingivalis ATCC 33277
alaS	PGN_1381	COG0013J	alanyl-tRNA synthetase	DEG10220278	PGN_1381	PGN_1381	Porphyromonas gingivalis ATCC 33277
-	PGN_1378	COG0305L	replicative DNA helicase	DEG10220277	PGN_1378	PGN_1378	Porphyromonas gingivalis ATCC 33277
-	PGN_1377	COG0481M	GTP-binding protein LepA	DEG10220276	PGN_1377	PGN_1377	Porphyromonas gingivalis ATCC 33277
-	PGN_1376	COG1309K	transcriptional regulator	DEG10220275	PGN_1376	PGN_1376	Porphyromonas gingivalis ATCC 33277
-	PGN_1375	COG1028IQ	beta-ketoacyl-acyl carrier protein reductase	DEG10220274	PGN_1375	PGN_1375	Porphyromonas gingivalis ATCC 33277
-	PGN_1367	COG0334E	glutamate dehydrogenase	DEG10220273	PGN_1367	PGN_1367	Porphyromonas gingivalis ATCC 33277
-	PGN_1359	COG0111HE	erythronate-4-phosphate dehydrogenase	DEG10220272	PGN_1359	PGN_1359	Porphyromonas gingivalis ATCC 33277
-	PGN_1358	-	hypothetical protein	DEG10220271	PGN_1358		Porphyromonas gingivalis ATCC 33277
-	PGN_1357	-	hypothetical protein	DEG10220270	PGN_1357		Porphyromonas gingivalis ATCC 33277
-	PGN_1356	COG0857R	hypothetical protein	DEG10220269	PGN_1356		Porphyromonas gingivalis ATCC 33277
-	PGN_1315	-	hypothetical protein	DEG10220268	PGN_1315		Porphyromonas gingivalis ATCC 33277
-	PGN_1312	COG1438K	transcriptional regulator	DEG10220267	PGN_1312	PGN_1312	Porphyromonas gingivalis ATCC 33277
-	PGN_1301	COG0789K	transcriptional regulator	DEG10220266	PGN_1301	PGN_1301	Porphyromonas gingivalis ATCC 33277
-	PGN_1251	COG0438M	glycosyltransferase	DEG10220265	PGN_1251		Porphyromonas gingivalis ATCC 33277
-	PGN_1250	-	hypothetical protein	DEG10220264	PGN_1250		Porphyromonas gingivalis ATCC 33277
-	PGN_1244	COG1186J	peptide chain release factor 2	DEG10220263	PGN_1244	PGN_1244	Porphyromonas gingivalis ATCC 33277
-	PGN_1242	-	hypothetical protein	DEG10220262	PGN_1242		Porphyromonas gingivalis ATCC 33277
-	PGN_1241	-	hypothetical protein	DEG10220261	PGN_1241		Porphyromonas gingivalis ATCC 33277
-	PGN_1240	COG0438M	hypothetical protein	DEG10220260	PGN_1240		Porphyromonas gingivalis ATCC 33277
-	PGN_1232	COG0492O	thioredoxin reductase	DEG10220259	PGN_1232	PGN_1232	Porphyromonas gingivalis ATCC 33277
valS	PGN_1229	COG0525J	valyl-tRNA synthetase	DEG10220258	PGN_1229	PGN_1229	Porphyromonas gingivalis ATCC 33277
-	PGN_1223	COG2233F	uracil permease	DEG10220257	PGN_1223	PGN_1223	Porphyromonas gingivalis ATCC 33277
-	PGN_1222	-	hypothetical protein	DEG10220256	PGN_1222		Porphyromonas gingivalis ATCC 33277
-	PGN_1220	COG0015F	adenylosuccinate lyase	DEG10220255	PGN_1220	PGN_1220	Porphyromonas gingivalis ATCC 33277
-	PGN_1219	COG1187J	ribosomal large subunit pseudouridine synthase B	DEG10220254	PGN_1219	PGN_1219	Porphyromonas gingivalis ATCC 33277
asnC	PGN_1218	COG0017J	asparaginyl-tRNA synthetase	DEG10220253	PGN_1218	PGN_1218	Porphyromonas gingivalis ATCC 33277
-	PGN_1215	-	hypothetical protein	DEG10220252	PGN_1215		Porphyromonas gingivalis ATCC 33277
-	PGN_1205	COG0541U	signal recognition particle protein	DEG10220251	PGN_1205	PGN_1205	Porphyromonas gingivalis ATCC 33277
-	PGN_1204	COG0853H	aspartate alpha-decarboxylase	DEG10220250	PGN_1204	PGN_1204	Porphyromonas gingivalis ATCC 33277
-	PGN_1203	COG0770M	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	DEG10220249	PGN_1203	PGN_1203	Porphyromonas gingivalis ATCC 33277
rpoN	PGN_1202	COG1508K	RNA polymerase sigma-54 factor	DEG10220248	PGN_1202	PGN_1202	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_1194	COG0787M	bifunctional UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase/alanine racemase	DEG10220247	PGN_1194	PGN_1194	Porphyromonas gingivalis ATCC 33277
-	PGN_1189	COG1109G	phosphoglucomutase/phosphomannomutase	DEG10220246	PGN_1189	PGN_1189	Porphyromonas gingivalis ATCC 33277
-	PGN_1188	-	hypothetical protein	DEG10220245	PGN_1188		Porphyromonas gingivalis ATCC 33277
-	PGN_1187	COG0618R	hypothetical protein	DEG10220244	PGN_1187		Porphyromonas gingivalis ATCC 33277
-	PGN_1179	COG0280C	phosphotransacetylase	DEG10220243	PGN_1179	PGN_1179	Porphyromonas gingivalis ATCC 33277
-	PGN_1178	COG0282C	acetate kinase	DEG10220242	PGN_1178	PGN_1178	Porphyromonas gingivalis ATCC 33277
-	PGN_1173	COG2086C	electron transfer flavoprotein beta subunit	DEG10220241	PGN_1173	PGN_1173	Porphyromonas gingivalis ATCC 33277
lysS	PGN_1157	COG1190J	lysyl-tRNA synthetase	DEG10220240	PGN_1157	PGN_1157	Porphyromonas gingivalis ATCC 33277
-	PGN_1156	COG0240C	glycerol-3-phosphate dehydrogenase	DEG10220239	PGN_1156	PGN_1156	Porphyromonas gingivalis ATCC 33277
pgi	PGN_1155	COG0166G	glucose-6-phosphate isomerase	DEG10220238	PGN_1155	PGN_1155	Porphyromonas gingivalis ATCC 33277
-	PGN_1154	-	hypothetical protein	DEG10220237	PGN_1154		Porphyromonas gingivalis ATCC 33277
-	PGN_1153	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	DEG10220236	PGN_1153	PGN_1153	Porphyromonas gingivalis ATCC 33277
rimM	PGN_1152	COG0806J	16S rRNA-processing protein RimM	DEG10220235	PGN_1152	PGN_1152	Porphyromonas gingivalis ATCC 33277
-	PGN_1151	COG0743I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	DEG10220234	PGN_1151	PGN_1151	Porphyromonas gingivalis ATCC 33277
-	PGN_1134	COG0438M	hypothetical protein	DEG10220233	PGN_1134		Porphyromonas gingivalis ATCC 33277
murB	PGN_1130	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	DEG10220232	PGN_1130	PGN_1130	Porphyromonas gingivalis ATCC 33277
-	PGN_1129	COG3087D	hypothetical protein	DEG10220231	PGN_1129		Porphyromonas gingivalis ATCC 33277
-	PGN_1079	COG0451M	GDP-fucose synthetase	DEG10220230	PGN_1079	PGN_1079	Porphyromonas gingivalis ATCC 33277
-	PGN_1078	COG1089M	GDP-mannose 4,6-dehydratase	DEG10220229	PGN_1078	PGN_1078	Porphyromonas gingivalis ATCC 33277
bcp	PGN_1058	COG1225O	bacterioferritin comigratory protein	DEG10220228	PGN_1058		Porphyromonas gingivalis ATCC 33277
-	PGN_1038	COG1945S	hypothetical protein	DEG10220227	PGN_1038	PGN_1038	Porphyromonas gingivalis ATCC 33277
-	PGN_1033	COG2244R	polysaccharide transport protein	DEG10220226	PGN_1033		Porphyromonas gingivalis ATCC 33277
-	PGN_1026	COG0463M	glycosyl transferase family 2	DEG10220225	PGN_1026		Porphyromonas gingivalis ATCC 33277
-	PGN_1025	COG4591M	hypothetical protein	DEG10220224	PGN_1025	PGN_1025	Porphyromonas gingivalis ATCC 33277
-	PGN_1024	COG0858J	ribosome-binding factor A	DEG10220223	PGN_1024	PGN_1024	Porphyromonas gingivalis ATCC 33277
-	PGN_1023	COG2503R	acid phosphatase OlpA	DEG10220222	PGN_1023		Porphyromonas gingivalis ATCC 33277
-	PGN_1022	COG1435F	thymidine kinase	DEG10220221	PGN_1022	PGN_1022	Porphyromonas gingivalis ATCC 33277
-	PGN_1020	COG0802R	ATP/GTP-binding transmembrane protein	DEG10220220	PGN_1020		Porphyromonas gingivalis ATCC 33277
-	PGN_1019	COG2204T	response regulator	DEG10220219	PGN_1019		Porphyromonas gingivalis ATCC 33277
-	PGN_1012	COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	DEG10220218	PGN_1012	PGN_1012	Porphyromonas gingivalis ATCC 33277
-	PGN_1011	COG2252R	xanthine/uracil/vitamin C permease	DEG10220217	PGN_1011		Porphyromonas gingivalis ATCC 33277
-	PGN_1010	-	hypothetical protein	DEG10220216	PGN_1010		Porphyromonas gingivalis ATCC 33277
-	PGN_1005	COG1668CP	ABC transporter permease protein	DEG10220215	PGN_1005		Porphyromonas gingivalis ATCC 33277
-	PGN_1003	-	hypothetical protein	DEG10220214	PGN_1003		Porphyromonas gingivalis ATCC 33277
-	PGN_1002	COG0775F	AMP nucleosidase	DEG10220213	PGN_1002	PGN_1002	Porphyromonas gingivalis ATCC 33277
-	PGN_1001	COG1466L	hypothetical protein	DEG10220212	PGN_1001	PGN_1001	Porphyromonas gingivalis ATCC 33277
-	PGN_1000	COG0509E	glycine cleavage system protein H	DEG10220211	PGN_1000		Porphyromonas gingivalis ATCC 33277
-	PGN_0999	COG0041F	phosphoribosylaminoimidazole carboxylase	DEG10220210	PGN_0999	PGN_0999	Porphyromonas gingivalis ATCC 33277
-	PGN_0998	COG0821I	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	DEG10220209	PGN_0998	PGN_0998	Porphyromonas gingivalis ATCC 33277
dut	PGN_0997	COG0756F	deoxyuridine 5'-triphosphate nucleotidohydrolase	DEG10220208	PGN_0997	PGN_0997	Porphyromonas gingivalis ATCC 33277
-	PGN_0994	-	hypothetical protein	DEG10220207	PGN_0994		Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	**DEG**	**Exp EG**	**Predicted EG**	Strain name
-	PGN_0993	COG4942D	peptidase M23/M37 family	DEG10220206	PGN_0993	PGN_0993	Porphyromonas gingivalis ATCC 33277
-	PGN_0992	COG0196H	riboflavin biosynthesis protein	DEG10220205	PGN_0992	PGN_0992	Porphyromonas gingivalis ATCC 33277
-	PGN_0988	-	hypothetical protein	DEG10220204	PGN_0988		Porphyromonas gingivalis ATCC 33277
-	PGN_0987	COG0442J	prolyl-tRNA synthetase	DEG10220203	PGN_0987	PGN_0987	Porphyromonas gingivalis ATCC 33277
-	PGN_0985	COG1183I	phosphatidylserine synthase	DEG10220202	PGN_0985	PGN_0985	Porphyromonas gingivalis ATCC 33277
-	PGN_0984	COG0688I	phosphatidylserine decarboxylase	DEG10220201	PGN_0984	PGN_0984	Porphyromonas gingivalis ATCC 33277
-	PGN_0970	COG1595K	RNA polymerase sigma-70 factor ECF subfamily	DEG10220200	PGN_0970	PGN_0970	Porphyromonas gingivalis ATCC 33277
rplT	PGN_0965	COG0292J	50S ribosomal protein L20	DEG10220199	PGN_0965	PGN_0965	Porphyromonas gingivalis ATCC 33277
rpmI	PGN_0964	COG0291J	50S ribosomal protein L35	DEG10220198	PGN_0964	PGN_0964	Porphyromonas gingivalis ATCC 33277
infC	PGN_0963	COG0290J	translation initiation factor IF-3	DEG10220197	PGN_0963	PGN_0963	Porphyromonas gingivalis ATCC 33277
thrS	PGN_0962	COG0441J	threonyl-tRNA synthetase	DEG10220196	PGN_0962	PGN_0962	Porphyromonas gingivalis ATCC 33277
-	PGN_0919	-	hypothetical protein	DEG10220195	PGN_0919		Porphyromonas gingivalis ATCC 33277
dnaK	PGN_0916	COG0443O	molecular chaperone DnaK	DEG10220194	PGN_0916	PGN_0916	Porphyromonas gingivalis ATCC 33277
-	PGN_0907	COG3093R	hypothetical protein	DEG10220193	PGN_0907		Porphyromonas gingivalis ATCC 33277
-	PGN_0902	COG1729S	hypothetical protein	DEG10220192	PGN_0902		Porphyromonas gingivalis ATCC 33277
ribH	PGN_0901	COG0054H	6,7-dimethyl-8-ribityllumazine synthase	DEG10220191	PGN_0901	PGN_0901	Porphyromonas gingivalis ATCC 33277
-	PGN_0894	COG2812L	DNA polymerase III, gamma and tau subunits	DEG10220190	PGN_0894	PGN_0894	Porphyromonas gingivalis ATCC 33277
-	PGN_0884	COG1452M	organic solvent tolerance protein OstA	DEG10220189	PGN_0884		Porphyromonas gingivalis ATCC 33277
-	PGN_0883	COG0705R	hypothetical protein	DEG10220188	PGN_0883		Porphyromonas gingivalis ATCC 33277
gyrA	PGN_0875	COG0188L	DNA gyrase A subunit	DEG10220187	PGN_0875	PGN_0875	Porphyromonas gingivalis ATCC 33277
-	PGN_0870	COG0772D	rod shape-determining protein RodA	DEG10220186	PGN_0870	PGN_0870	Porphyromonas gingivalis ATCC 33277
-	PGN_0868	-	hypothetical protein	DEG10220185	PGN_0868		Porphyromonas gingivalis ATCC 33277
-	PGN_0867	COG1792M	rod shape-determining protein MreC	DEG10220184	PGN_0867	PGN_0867	Porphyromonas gingivalis ATCC 33277
-	PGN_0866	COG1077D	rod shape-determining protein MreB	DEG10220183	PGN_0866	PGN_0866	Porphyromonas gingivalis ATCC 33277
purH	PGN_0865	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	DEG10220182	PGN_0865	PGN_0865	Porphyromonas gingivalis ATCC 33277
-	PGN_0851	-	hypothetical protein	DEG10220181	PGN_0851		Porphyromonas gingivalis ATCC 33277
ispD	PGN_0841	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	DEG10220180	PGN_0841	PGN_0841	Porphyromonas gingivalis ATCC 33277
ruvA	PGN_0833	COG0632L	Holliday junction DNA helicase RuvA	DEG10220179	PGN_0833	PGN_0833	Porphyromonas gingivalis ATCC 33277
-	PGN_0831	COG0781K	nitrogen utilization substance protein	DEG10220178	PGN_0831		Porphyromonas gingivalis ATCC 33277
-	PGN_0830	COG1712R	meso-diaminopimelate D-dehydrogenase	DEG10220177	PGN_0830	PGN_0830	Porphyromonas gingivalis ATCC 33277
-	PGN_0829	COG0682M	prolipoprotein diacylglyceryl transferase	DEG10220176	PGN_0829		Porphyromonas gingivalis ATCC 33277
-	PGN_0828	COG0426C	flavoprotein	DEG10220175	PGN_0828	PGN_0828	Porphyromonas gingivalis ATCC 33277
nagB	PGN_0827	COG0363G	glucosamine-6-phosphate deaminase	DEG10220174	PGN_0827	PGN_0827	Porphyromonas gingivalis ATCC 33277
-	PGN_0824	COG0617J	tRNA nucleotidyltransferase	DEG10220173	PGN_0824	PGN_0824	Porphyromonas gingivalis ATCC 33277
-	PGN_0820	-	hypothetical protein	DEG10220172	PGN_0820		Porphyromonas gingivalis ATCC 33277
leuS	PGN_0819	COG0495J	leucyl-tRNA synthetase	DEG10220171	PGN_0819	PGN_0819	Porphyromonas gingivalis ATCC 33277
-	PGN_0817	COG5009M	penicillin-binding protein 1A	DEG10220170	PGN_0817	PGN_0817	Porphyromonas gingivalis ATCC 33277
-	PGN_0816	COG3855G	fructose-1,6-bisphosphatase	DEG10220169	PGN_0816	PGN_0816	Porphyromonas gingivalis ATCC 33277
-	PGN_0815	COG0634F	hypoxanthine phosphoribosyltransferase	DEG10220168	PGN_0815	PGN_0815	Porphyromonas gingivalis ATCC 33277
adk	PGN_0814	COG0563F	adenylate kinase	DEG10220167	PGN_0814	PGN_0814	Porphyromonas gingivalis ATCC 33277
obgE	PGN_0813	COG0536R	GTPase ObgE	DEG10220166	PGN_0813	PGN_0813	Porphyromonas gingivalis ATCC 33277
-	PGN_0809	COG0810M	TonB protein	DEG10220165	PGN_0809		Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_0806	COG0811U	MotA/TolQ/ExbB proton channel protein	DEG10220164	PGN_0806		Porphyromonas gingivalis ATCC 33277
-	PGN_0805	-	hypothetical protein	DEG10220163	PGN_0805		Porphyromonas gingivalis ATCC 33277
-	PGN_0804	-	hypothetical protein	DEG10220162	PGN_0804		Porphyromonas gingivalis ATCC 33277
-	PGN_0803	COG0848U	hypothetical protein	DEG10220161	PGN_0803		Porphyromonas gingivalis ATCC 33277
-	PGN_0801	COG2086C	electron transfer flavoprotein beta subunit	DEG10220160	PGN_0801	PGN_0801	Porphyromonas gingivalis ATCC 33277
-	PGN_0800	COG2025C	electron transfer flavoprotein alpha subunit	DEG10220159	PGN_0800	PGN_0800	Porphyromonas gingivalis ATCC 33277
-	PGN_0799	COG1960I	acyl-CoA dehydrogenase	DEG10220158	PGN_0799	PGN_0799	Porphyromonas gingivalis ATCC 33277
-	PGN_0781	COG0550L	DNA topoisomerase I	DEG10220157	PGN_0781	PGN_0781	Porphyromonas gingivalis ATCC 33277
-	PGN_0777	COG0463M	glycosyl transferase	DEG10220156	PGN_0777		Porphyromonas gingivalis ATCC 33277
-	PGN_0766	COG0520E	aminotransferase class V	DEG10220155	PGN_0766	PGN_0766	Porphyromonas gingivalis ATCC 33277
-	PGN_0765	COG0778C	nitroreductase	DEG10220154	PGN_0765		Porphyromonas gingivalis ATCC 33277
-	PGN_0764	COG0307H	riboflavin synthase subunit alpha	DEG10220153	PGN_0764	PGN_0764	Porphyromonas gingivalis ATCC 33277
-	PGN_0762	COG2815S	hypothetical protein	DEG10220152	PGN_0762		Porphyromonas gingivalis ATCC 33277
-	PGN_0761	COG0564J	ribosomal large subunit pseudouridine synthase	DEG10220151	PGN_0761	PGN_0761	Porphyromonas gingivalis ATCC 33277
ddl	PGN_0760	COG1181M	D-alanyl-alanine synthetase A	DEG10220150	PGN_0760	PGN_0760	Porphyromonas gingivalis ATCC 33277
-	PGN_0759	COG0204I	hypothetical protein	DEG10220149	PGN_0759		Porphyromonas gingivalis ATCC 33277
-	PGN_0734	-	hypothetical protein	DEG10220148	PGN_0734		Porphyromonas gingivalis ATCC 33277
-	PGN_0726	COG0694O	hypothetical protein	DEG10220147	PGN_0726		Porphyromonas gingivalis ATCC 33277
-	PGN_0723	COG1012C	succinate-semialdehyde dehydrogenase	DEG10220146	PGN_0723		Porphyromonas gingivalis ATCC 33277
-	PGN_0717	-	hypothetical protein	DEG10220145	PGN_0717		Porphyromonas gingivalis ATCC 33277
-	PGN_0713	COG1748E	saccharopine dehydrogenase	DEG10220144	PGN_0713	PGN_0713	Porphyromonas gingivalis ATCC 33277
-	PGN_0680	COG0616O	signal peptide peptidase SppA 67K type	DEG10220143	PGN_0680	PGN_0680	Porphyromonas gingivalis ATCC 33277
-	PGN_0679	COG1663M	tetraacyldisaccharide 4'-kinase	DEG10220142	PGN_0679	PGN_0679	Porphyromonas gingivalis ATCC 33277
-	PGN_0671	COG0854H	pyridoxine 5'-phosphate synthase	DEG10220141	PGN_0671	PGN_0671	Porphyromonas gingivalis ATCC 33277
ppnK	PGN_0670	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10220140	PGN_0670	PGN_0670	Porphyromonas gingivalis ATCC 33277
-	PGN_0669	COG1137R	ABC transporter ATP-binding protein	DEG10220139	PGN_0669	PGN_0669	Porphyromonas gingivalis ATCC 33277
folE	PGN_0667	COG0302H	GTP cyclohydrolase I	DEG10220138	PGN_0667	PGN_0667	Porphyromonas gingivalis ATCC 33277
-	PGN_0666	-	hypothetical protein	DEG10220137	PGN_0666		Porphyromonas gingivalis ATCC 33277
tpiA	PGN_0665	COG0149G	triosephosphate isomerase	DEG10220136	PGN_0665	PGN_0665	Porphyromonas gingivalis ATCC 33277
-	PGN_0664	COG2259S	hypothetical protein	DEG10220135	PGN_0664		Porphyromonas gingivalis ATCC 33277
-	PGN_0663	-	hypothetical protein	DEG10220134	PGN_0663		Porphyromonas gingivalis ATCC 33277
-	PGN_0662	COG0466O	ATP-dependent protease La	DEG10220133	PGN_0662		Porphyromonas gingivalis ATCC 33277
ispH	PGN_0647	COG0761IM	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	DEG10220132	PGN_0647	PGN_0647	Porphyromonas gingivalis ATCC 33277
cmk	PGN_0646	COG0283F	cytidylate kinase	DEG10220131	PGN_0646	PGN_0646	Porphyromonas gingivalis ATCC 33277
-	PGN_0645	COG2067I	hypothetical protein	DEG10220130	PGN_0645		Porphyromonas gingivalis ATCC 33277
-	PGN_0643	COG0108H	3,4-dihydroxy-2-butanone 4-phosphate synthase	DEG10220129	PGN_0643	PGN_0643	Porphyromonas gingivalis ATCC 33277
-	PGN_0642	COG0795R	hypothetical protein	DEG10220128	PGN_0642	PGN_0642	Porphyromonas gingivalis ATCC 33277
rpsF	PGN_0639	COG0360J	30S ribosomal protein S6	DEG10220127	PGN_0639	PGN_0639	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
rpoD	PGN_0638	COG0568K	RNA polymerase sigma factor RpoD	DEG10220126	PGN_0638	PGN_0638	Porphyromonas gingivalis ATCC 33277
guaA	PGN_0635	COG0519F	GMP synthase	DEG10220125	PGN_0635	PGN_0635	Porphyromonas gingivalis ATCC 33277
-	PGN_0630	COG0849D	cell division protein FtsA	DEG10220124	PGN_0630	PGN_0630	Porphyromonas gingivalis ATCC 33277
-	PGN_0629	-	cell division protein FtsQ	DEG10220123	PGN_0629	PGN_0629	Porphyromonas gingivalis ATCC 33277
murC	PGN_0628	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10220122	PGN_0628	PGN_0628	Porphyromonas gingivalis ATCC 33277
murG	PGN_0627	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	DEG10220121	PGN_0627	PGN_0627	Porphyromonas gingivalis ATCC 33277
-	PGN_0626	COG0772D	rod shape-determining protein RodA	DEG10220120	PGN_0626	PGN_0626	Porphyromonas gingivalis ATCC 33277
-	PGN_0625	COG0771M	UDP-N-acetylmuramoylalanine--D-glutamate ligase	DEG10220119	PGN_0625	PGN_0625	Porphyromonas gingivalis ATCC 33277
mraY	PGN_0624	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10220118	PGN_0624	PGN_0624	Porphyromonas gingivalis ATCC 33277
murE	PGN_0623	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	DEG10220117	PGN_0623	PGN_0623	Porphyromonas gingivalis ATCC 33277
-	PGN_0622	COG0768M	penicillin-binding protein	DEG10220116	PGN_0622	PGN_0622	Porphyromonas gingivalis ATCC 33277
-	PGN_0621	-	hypothetical protein	DEG10220115	PGN_0621		Porphyromonas gingivalis ATCC 33277
mraW	PGN_0620	COG0275M	S-adenosyl-methyltransferase MraW	DEG10220114	PGN_0620	PGN_0620	Porphyromonas gingivalis ATCC 33277
-	PGN_0618	COG0136E	aspartate-semialdehyde dehydrogenase	DEG10220113	PGN_0618	PGN_0618	Porphyromonas gingivalis ATCC 33277
-	PGN_0612	COG1932HE	phosphoserine aminotransferase	DEG10220112	PGN_0612	PGN_0612	Porphyromonas gingivalis ATCC 33277
-	PGN_0611	COG0111HE	D-3-phosphoglycerate dehydrogenase	DEG10220111	PGN_0611	PGN_0611	Porphyromonas gingivalis ATCC 33277
-	PGN_0610	COG4198S	hypothetical protein	DEG10220110	PGN_0610		Porphyromonas gingivalis ATCC 33277
-	PGN_0573	COG2177D	cell division protein FtsX	DEG10220109	PGN_0573	PGN_0573	Porphyromonas gingivalis ATCC 33277
-	PGN_0572	-	hypothetical protein	DEG10220108	PGN_0572		Porphyromonas gingivalis ATCC 33277
queA	PGN_0569	COG0809J	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	DEG10220107	PGN_0569	PGN_0569	Porphyromonas gingivalis ATCC 33277
-	PGN_0568	COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	DEG10220106	PGN_0568	PGN_0568	Porphyromonas gingivalis ATCC 33277
-	PGN_0549	COG1088M	dTDP-glucose 4,6-dehydratase	DEG10220105	PGN_0549	PGN_0549	Porphyromonas gingivalis ATCC 33277
-	PGN_0548	COG1091M	dTDP-4-dehydrorhamnose reductase	DEG10220104	PGN_0548	PGN_0548	Porphyromonas gingivalis ATCC 33277
-	PGN_0547	COG1898M	dTDP-4-dehydrorhamnose 3,5-epimerase	DEG10220103	PGN_0547	PGN_0547	Porphyromonas gingivalis ATCC 33277
-	PGN_0546	COG1209M	glucose-1-phosphate thymidylyltransferase	DEG10220102	PGN_0546	PGN_0546	Porphyromonas gingivalis ATCC 33277
-	PGN_0544	COG1519M	3-deoxy-D-manno-octulosonic-acid transferase	DEG10220101	PGN_0544	PGN_0544	Porphyromonas gingivalis ATCC 33277
gltX	PGN_0543	COG0008J	glutamyl-tRNA synthetase	DEG10220100	PGN_0543	PGN_0543	Porphyromonas gingivalis ATCC 33277
-	PGN_0540	COG0607P	hypothetical protein	DEG10220099	PGN_0540		Porphyromonas gingivalis ATCC 33277
-	PGN_0523	COG1624S	hypothetical protein	DEG10220098	PGN_0523		Porphyromonas gingivalis ATCC 33277
-	PGN_0522	COG0294H	dihydropteroate synthase	DEG10220097	PGN_0522	PGN_0522	Porphyromonas gingivalis ATCC 33277
-	PGN_0518	COG0036G	ribulose-phosphate 3-epimerase	DEG10220096	PGN_0518	PGN_0518	Porphyromonas gingivalis ATCC 33277
ileS	PGN_0517	COG0060J	isoleucyl-tRNA synthetase	DEG10220095	PGN_0517	PGN_0517	Porphyromonas gingivalis ATCC 33277
-	PGN_0516	COG1734T	DnaK suppressor protein	DEG10220094	PGN_0516	PGN_0516	Porphyromonas gingivalis ATCC 33277
-	PGN_0515	COG0597MU	lipoprotein signal peptidase	DEG10220093	PGN_0515	PGN_0515	Porphyromonas gingivalis ATCC 33277
-	PGN_0512	COG0340H	biotin--acetyl-CoA-carboxylase ligase	DEG10220092	PGN_0512	PGN_0512	Porphyromonas gingivalis ATCC 33277
-	PGN_0511	COG2315S	hypothetical protein	DEG10220091	PGN_0511		Porphyromonas gingivalis ATCC 33277
-	PGN_0510	COG0127F	deoxyribonucleoside-triphosphatase	DEG10220090	PGN_0510	PGN_0510	Porphyromonas gingivalis ATCC 33277
-	PGN_0503	COG0511I	biotin carboxyl carrier protein	DEG10220089	PGN_0503	PGN_0503	Porphyromonas gingivalis ATCC 33277
-	PGN_0502	-	hypothetical protein	DEG10220088	PGN_0502		Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_0501	-	hypothetical protein	DEG10220087	PGN_0501		Porphyromonas gingivalis ATCC 33277
-	PGN_0500	COG4799I	methylmalonyl-CoA decarboxylase alpha subunit	DEG10220086	PGN_0500	PGN_0500	Porphyromonas gingivalis ATCC 33277
-	PGN_0499	COG3185ER	hypothetical protein	DEG10220085	PGN_0499		Porphyromonas gingivalis ATCC 33277
-	PGN_0487	COG1674D	DNA translocase FtsK	DEG10220084	PGN_0487	PGN_0487	Porphyromonas gingivalis ATCC 33277
-	PGN_0473	COG0348C	hypothetical protein	DEG10220083	PGN_0473		Porphyromonas gingivalis ATCC 33277
-	PGN_0472	COG0188L	DNA topoisomerase IV subunit A	DEG10220082	PGN_0472	PGN_0472	Porphyromonas gingivalis ATCC 33277
-	PGN_0449	-	hypothetical protein	DEG10220081	PGN_0449		Porphyromonas gingivalis ATCC 33277
pgk	PGN_0433	COG0126G	phosphoglycerate kinase	DEG10220080	PGN_0433	PGN_0433	Porphyromonas gingivalis ATCC 33277
-	PGN_0420	COG1136V	lipoprotein releasing system ATP-binding protein	DEG10220079	PGN_0420	PGN_0420	Porphyromonas gingivalis ATCC 33277
-	PGN_0419	COG1179H	dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	DEG10220078	PGN_0419		Porphyromonas gingivalis ATCC 33277
-	PGN_0418	COG1559R	hypothetical protein	DEG10220077	PGN_0418		Porphyromonas gingivalis ATCC 33277
gyrB	PGN_0413	COG0187L	DNA gyrase B subunit	DEG10220076	PGN_0413	PGN_0413	Porphyromonas gingivalis ATCC 33277
-	PGN_0408	COG2919D	hypothetical protein	DEG10220075	PGN_0408		Porphyromonas gingivalis ATCC 33277
-	PGN_0403	COG0259H	pyridoxamine-phosphate oxidase	DEG10220074	PGN_0403	PGN_0403	Porphyromonas gingivalis ATCC 33277
-	PGN_0398	COG1132V	ABC transporter ATP-binding protein MsbA family	DEG10220073	PGN_0398		Porphyromonas gingivalis ATCC 33277
-	PGN_0393	COG0533O	DNA-binding/iron metalloprotein/AP endonuclease	DEG10220072	PGN_0393	PGN_0393	Porphyromonas gingivalis ATCC 33277
-	PGN_0376	COG2877M	2-dehydro-3-deoxyphosphooctonate aldolase	DEG10220071	PGN_0376	PGN_0376	Porphyromonas gingivalis ATCC 33277
-	PGN_0374	-	hypothetical protein	DEG10220070	PGN_0374		Porphyromonas gingivalis ATCC 33277
-	PGN_0371	COG2091H	hypothetical protein	DEG10220069	PGN_0371		Porphyromonas gingivalis ATCC 33277
-	PGN_0370	COG1253R	hypothetical protein	DEG10220068	PGN_0370		Porphyromonas gingivalis ATCC 33277
-	PGN_0369	COG0629L	single-stranded binding protein	DEG10220067	PGN_0369	PGN_0369	Porphyromonas gingivalis ATCC 33277
mnmA	PGN_0366	COG0482J	tRNA-specific 2-thiouridylase MnmA	DEG10220066	PGN_0366	PGN_0366	Porphyromonas gingivalis ATCC 33277
argS	PGN_0365	COG0018J	arginyl-tRNA synthetase	DEG10220065	PGN_0365	PGN_0365	Porphyromonas gingivalis ATCC 33277
-	PGN_0360	COG0162J	tyrosyl-tRNA synthetase	DEG10220064	PGN_0360	PGN_0360	Porphyromonas gingivalis ATCC 33277
-	PGN_0359	COG0719O	ABC transporter permease protein	DEG10220063	PGN_0359		Porphyromonas gingivalis ATCC 33277
-	PGN_0358	COG0396O	ABC transporter ATP-binding protein	DEG10220062	PGN_0358		Porphyromonas gingivalis ATCC 33277
-	PGN_0357	COG0719O	cysteine desulfurase	DEG10220061	PGN_0357		Porphyromonas gingivalis ATCC 33277
infB	PGN_0355	COG0532J	translation initiation factor IF-2	DEG10220060	PGN_0355	PGN_0355	Porphyromonas gingivalis ATCC 33277
nusA	PGN_0354	COG0195K	transcription elongation factor NusA	DEG10220059	PGN_0354	PGN_0354	Porphyromonas gingivalis ATCC 33277
-	PGN_0353	COG0779S	hypothetical protein	DEG10220058	PGN_0353		Porphyromonas gingivalis ATCC 33277
-	PGN_0311	-	hypothetical protein	DEG10220057	PGN_0311		Porphyromonas gingivalis ATCC 33277
-	PGN_0310	COG1587H	uroporphyrinogen-III synthase	DEG10220056	PGN_0310		Porphyromonas gingivalis ATCC 33277
rnpA	PGN_0309	COG0594J	ribonuclease P	DEG10220055	PGN_0309	PGN_0309	Porphyromonas gingivalis ATCC 33277
-	PGN_0301	COG2825M	hypothetical protein	DEG10220054	PGN_0301		Porphyromonas gingivalis ATCC 33277
-	PGN_0300	COG2825M	hypothetical protein	DEG10220053	PGN_0300		Porphyromonas gingivalis ATCC 33277
-	PGN_0299	COG4775M	hypothetical protein	DEG10220052	PGN_0299		Porphyromonas gingivalis ATCC 33277
-	PGN_0298	COG0020I	undecaprenyl pyrophosphate synthase	DEG10220051	PGN_0298	PGN_0298	Porphyromonas gingivalis ATCC 33277
-	PGN_0297	-	hypothetical protein	DEG10220050	PGN_0297		Porphyromonas gingivalis ATCC 33277
ragA	PGN_0293	COG4771P	receptor antigen A	DEG10220049	PGN_0293		Porphyromonas gingivalis ATCC 33277
metG	PGN_0281	COG0143J	methionyl-tRNA synthetase	DEG10220048	PGN_0281	PGN_0281	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
rplY	PGN_0279	COG1825J	50S ribosomal protein L25	DEG10220047	PGN_0279	PGN_0279	Porphyromonas gingivalis ATCC 33277
-	PGN_0278	COG0193J	peptidyl-tRNA hydrolase	DEG10220046	PGN_0278	PGN_0278	Porphyromonas gingivalis ATCC 33277
-	PGN_0272	COG1209M	hypothetical protein	DEG10220045	PGN_0272		Porphyromonas gingivalis ATCC 33277
-	PGN_0267	COG0117H	riboflavin biosynthesis protein	DEG10220044	PGN_0267	PGN_0267	Porphyromonas gingivalis ATCC 33277
aspS	PGN_0266	COG0173J	aspartyl-tRNA synthetase	DEG10220043	PGN_0266	PGN_0266	Porphyromonas gingivalis ATCC 33277
-	PGN_0264	COG0552U	signal recognition particle-docking protein	DEG10220042	PGN_0264	PGN_0264	Porphyromonas gingivalis ATCC 33277
-	PGN_0261	COG2204T	sigma-54-dependent transcriptional regulator	DEG10220041	PGN_0261	PGN_0261	Porphyromonas gingivalis ATCC 33277
-	PGN_0260	-	hypothetical protein	DEG10220040	PGN_0260		Porphyromonas gingivalis ATCC 33277
secG	PGN_0258	COG1314U	preprotein translocase subunit SecG	DEG10220039	PGN_0258	PGN_0258	Porphyromonas gingivalis ATCC 33277
-	PGN_0256	COG0388R	hydrolase	DEG10220038	PGN_0256	PGN_0256	Porphyromonas gingivalis ATCC 33277
-	PGN_0255	COG1192D	ParA chromosome partitioning protein	DEG10220037	PGN_0255	PGN_0255	Porphyromonas gingivalis ATCC 33277
-	PGN_0254	COG1475K	ParB chromosome partitioning protein	DEG10220036	PGN_0254	PGN_0254	Porphyromonas gingivalis ATCC 33277
-	PGN_0253	-	hypothetical protein	DEG10220035	PGN_0253		Porphyromonas gingivalis ATCC 33277
-	PGN_0251	COG0331I	malonyl CoA-ACP transacylase	DEG10220034	PGN_0251	PGN_0251	Porphyromonas gingivalis ATCC 33277
-	PGN_0250	COG2195E	aminoacyl-histidine dipeptidase	DEG10220033	PGN_0250		Porphyromonas gingivalis ATCC 33277
-	PGN_0249	COG0392S	hypothetical protein	DEG10220032	PGN_0249		Porphyromonas gingivalis ATCC 33277
ksgA	PGN_0248	COG0030J	dimethyladenosine transferase	DEG10220031	PGN_0248	PGN_0248	Porphyromonas gingivalis ATCC 33277
-	PGN_0247	COG2239P	magnesium transporter	DEG10220030	PGN_0247		Porphyromonas gingivalis ATCC 33277
gpmA	PGN_0243	COG0588G	phosphoglyceromutase	DEG10220029	PGN_0243	PGN_0243	Porphyromonas gingivalis ATCC 33277
-	PGN_0242	COG0438M	glycosyl transferase family 1	DEG10220028	PGN_0242		Porphyromonas gingivalis ATCC 33277
-	PGN_0209	COG0423J	glycyl-tRNA synthetase	DEG10220027	PGN_0209	PGN_0209	Porphyromonas gingivalis ATCC 33277
-	PGN_0208	COG0545O	hypothetical protein	DEG10220026	PGN_0208		Porphyromonas gingivalis ATCC 33277
surE	PGN_0207	COG0496R	stationary phase survival protein SurE	DEG10220025	PGN_0207	PGN_0207	Porphyromonas gingivalis ATCC 33277
-	PGN_0206	COG0763M	lipid A disaccharide synthase	DEG10220024	PGN_0206	PGN_0206	Porphyromonas gingivalis ATCC 33277
-	PGN_0203	COG2166R	SufE Fe/S-cluster-related protein	DEG10220023	PGN_0203	PGN_0203	Porphyromonas gingivalis ATCC 33277
-	PGN_0202	COG2234R	leucine aminopeptidase precursor	DEG10220022	PGN_0202	PGN_0202	Porphyromonas gingivalis ATCC 33277
-	PGN_0198	COG3858R	hypothetical protein	DEG10220021	PGN_0198		Porphyromonas gingivalis ATCC 33277
-	PGN_0192	COG1807M	hypothetical protein	DEG10220020	PGN_0192		Porphyromonas gingivalis ATCC 33277
engA	PGN_0191	COG1160R	GTP-binding protein EngA	DEG10220019	PGN_0191	PGN_0191	Porphyromonas gingivalis ATCC 33277
era	PGN_0190	COG1159R	GTP-binding protein Era	DEG10220018	PGN_0190	PGN_0190	Porphyromonas gingivalis ATCC 33277
-	PGN_0189	COG0332I	3-oxoacyl-ACP synthase	DEG10220017	PGN_0189	PGN_0189	Porphyromonas gingivalis ATCC 33277
-	PGN_0173	COG0057G	glyceraldehyde 3-phosphate dehydrogenase type I	DEG10220016	PGN_0173	PGN_0173	Porphyromonas gingivalis ATCC 33277
-	PGN_0172	-	hypothetical protein	DEG10220015	PGN_0172		Porphyromonas gingivalis ATCC 33277
thiG	PGN_0158	COG2022H	thiazole synthase	DEG10220014	PGN_0158	PGN_0158	Porphyromonas gingivalis ATCC 33277
-	PGN_0149	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10220013	PGN_0149	PGN_0149	Porphyromonas gingivalis ATCC 33277
-	PGN_0143	COG1539H	dihydroneopterin aldolase	DEG10220012	PGN_0143	PGN_0143	Porphyromonas gingivalis ATCC 33277
-	PGN_0138	-	hypothetical protein	DEG10220011	PGN_0138		Porphyromonas gingivalis ATCC 33277
-	PGN_0137	COG0180J	tryptophanyl-tRNA synthetase	DEG10220010	PGN_0137	PGN_0137	Porphyromonas gingivalis ATCC 33277

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_0097	COG2884D	cell-division ATP-binding protein	DEG10220009	PGN_0097	PGN_0097	Porphyromonas gingivalis ATCC 33277
-	PGN_0096	COG0527E	aspartate kinase	DEG10220008	PGN_0096	PGN_0096	Porphyromonas gingivalis ATCC 33277
-	PGN_0043	COG0465O	transmembrane AAA-metalloprotease FtsH	DEG10220007	PGN_0043		Porphyromonas gingivalis ATCC 33277
-	PGN_0042	COG4589R	phosphatidate cytidylyltransferase	DEG10220006	PGN_0042	PGN_0042	Porphyromonas gingivalis ATCC 33277
-	PGN_0034	COG0587L	DNA polymerase III alpha subunit	DEG10220005	PGN_0034	PGN_0034	Porphyromonas gingivalis ATCC 33277
-	PGN_0033	COG3118O	thioredoxin	DEG10220004	PGN_0033	PGN_0033	Porphyromonas gingivalis ATCC 33277
ispF	PGN_0024	COG0245I	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	DEG10220003	PGN_0024	PGN_0024	Porphyromonas gingivalis ATCC 33277
-	PGN_0023	COG3637M	hypothetical protein	DEG10220002	PGN_0023		Porphyromonas gingivalis ATCC 33277
dnaA	PGN_0001	COG0593L	chromosome replication initiator DnaA	DEG10220001	PGN_0001	PGN_0001	Porphyromonas gingivalis ATCC 33277
-	PGN_2033	COG0513LK.	ATP-dependent RNA helicase			PGN_2033	
-	PGN_2003	COG0608L	single-stranded-DNA-specific exonuclease			PGN_2003	
-	PGN_1980	COG0493ER	NADPH-dependent glutamate synthase			PGN_1980	
-	PGN_1954	COG1381L	DNA repair protein RecO			PGN_1954	
-	PGN_1945	COG0681U	signal peptidase-related protein			PGN_1945	
-	PGN_1943	COG0142H	polyprenyl synthetase			PGN_1943	
rpmB	PGN_1891	COG0227J	50S ribosomal protein L28			PGN_1891	
rpmG	PGN_1890	COG0267J	50S ribosomal protein L33			PGN_1890	
rpmC	PGN_1860	COG0255J	50S ribosomal protein L29			PGN_1860	
rplQ	PGN_1840	COG0203J	50S ribosomal protein L17			PGN_1840	
-	PGN_1812	COG0855P	polyphosphate kinase			PGN_1812	
-	PGN_1772	COG0296G	1,4-alpha-glucan branching enzyme			PGN_1772	
-	PGN_1771	COG0749L	DNA polymerase I			PGN_1771	
-	PGN_1764	COG1390C	v-type ATPase subunit E			PGN_1764	
-	PGN_1762	COG1155C	V-type ATP synthase subunit A			PGN_1762	
-	PGN_1761	COG1156C	V-type ATP synthase subunit B			PGN_1761	
-	PGN_1760	COG1394C	V-type ATP synthase subunit D			PGN_1760	
-	PGN_1759	COG1269C	v-type ATPase subunit I			PGN_1759	
-	PGN_1758	-	v-type ATPase subunit K			PGN_1758	
eno	PGN_1743	COG0148G	phosphopyruvate hydratase			PGN_1743	
-	PGN_1738	COG1022I	long-chain-fatty-acid-CoA ligase			PGN_1738	
recQII	PGN_1737	COG0514L	ATP-dependent DNA helicase RecQ			PGN_1737	
rpsU	PGN_1580	-	30S ribosomal protein S21			PGN_1580	
-	PGN_1569	COG0664T	transcriptional regulator Crp/Fnr family			PGN_1569	
-	PGN_1567	COG1195L	DNA replication and repair protein RecF			PGN_1567	
recQI	PGN_1551	COG0514L	ATP-dependent DNA helicase RecQ			PGN_1551	
panC	PGN_1492	COG0414H	pantoate--beta-alanine ligase			PGN_1492	
-	PGN_1418	COG0674C	pyruvate-flavodoxin oxidoreductase			PGN_1418	

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG	Strain name
-	PGN_1412	COG0005F	purine nucleoside phosphorylase			PGN_1412	
-	PGN_1396	COG1328F	anaerobic ribonucleoside triphosphate reductase			PGN_1396	
-	PGN_1384	COG0204I	1-acyl-sn-glycerol-3-phosphate acetyltransferase			PGN_1384	
-	PGN_1300	COG0664T	transcriptional regulator			PGN_1300	
-	PGN_1245	COG1022I	long-chain-fatty-acid-CoA ligase			PGN_1245	
-	PGN_1226	COG0209F	ribonucleotide reductase			PGN_1226	
-	PGN_1158	COG2820F	purine nucleoside phosphorylase			PGN_1158	
-	PGN_1120	COG3288C	NADPH-NAD transhydrogenase			PGN_1120	
ruvC	PGN_1113	COG0817L	Holliday junction resolvase			PGN_1113	
rpsA	PGN_1088	COG0539J	30S ribosomal protein S1			PGN_1088	
recA	PGN_1057	COG0468L	recombinase A			PGN_1057	
-	PGN_1049	COG1785P	alkaline phosphatase			PGN_1049	
-	PGN_1042	COG1294C	cytochrome d ubiquinol oxidase subunit II			PGN_1042	
-	PGN_1041	COG1271C	cytochrome d ubiquinol oxidase subunit I			PGN_1041	
-	PGN_1015	COG2812L	DNA polymerase III delta prime subunit			PGN_1015	
-	PGN_1014	COG0480J	elongation factor G			PGN_1014	
-	PGN_0976	COG0152F	phosphoribosylaminoimidazole-succinocarboxamide synthase			PGN_0976	
-	PGN_0933	COG2865K	transcriptional regulator			PGN_0933	
-	PGN_0923	COG0358L	DNA primase			PGN_0923	
-	PGN_0896	COG2027M	D-alanyl-D-alanine carboxypeptidase			PGN_0896	
-	PGN_0891	COG2070R	dioxygenase			PGN_0891	
-	PGN_0869	COG0768M	penicillin-binding protein 2			PGN_0869	
-	PGN_0808	COG0142H	isoprenyl synthetase			PGN_0808	
-	PGN_0792	COG1185J	polynucleotide phosphorylase			PGN_0792	
-	PGN_0696	COG1778R	hydrolase			PGN_0696	
rpmH	PGN_0694	COG0230J	50S ribosomal protein L34			PGN_0694	
-	PGN_0692	COG0560E	phosphoserine phosphatase			PGN_0692	
-	PGN_0658	COG1217T	GTP-binding elongation factor family protein TypA/BipA			PGN_0658	
rplI	PGN_0641	COG0359J	50S ribosomal protein L9			PGN_0641	
rpsR	PGN_0640	COG0238J	30S ribosomal protein S18			PGN_0640	
rpmE2	PGN_0636	COG0254J	50S ribosomal protein L31			PGN_0636	
-	PGN_0631	COG0206D	cell division protein FtsZ			PGN_0631	
-	PGN_0616	COG0231J	elongation factor P			PGN_0616	
-	PGN_0582	COG0550L	DNA topoisomerase I			PGN_0582	
-	PGN_0498	COG0479C	succinate dehydrogenase/fumarate reductase iron-sulfur subunit			PGN_0498	
sdhA	PGN_0497	COG1053C	succinate dehydrogenase flavoprotein subunit			PGN_0497	
-	PGN_0496	-	cytochrome B subunit			PGN_0496	
-	PGN_0465	COG0317TK	GTP pyrophosphokinase			PGN_0465	
-	PGN_0434	COG1866C	phosphoenolpyruvate carboxykinase			PGN_0434	

Gene	Synonym	COG	Product	DEG	Exp EG	Predicted EG
-	PGN_0423	COG0782K	transcription elongation factor			PGN_0423
rpsT	PGN_0394	COG0268J	30S ribosomal protein S20			PGN_0394
aspA	PGN_0377	COG1027E	aspartate ammonia-lyase			PGN_0377
-	PGN_0350	COG0023J	translation initation factor SUI1			PGN_0350
-	PGN_0327	COG0847L	DNA polymerase III epsilon chain			PGN_0327
-	PGN_0319	COG1595K	RNA polymerase sigma-70 factor ECF subfamily			PGN_0319
-	PGN_0313	COG4108J	peptide chain release factor 3			PGN_0313
-	PGN_0284	COG1846K	transcriptional regulator			PGN_0284
-	PGN_0274	COG1595K	RNA polymerase sigma-70 factor ECF subfamily			PGN_0274
rpmF	PGN_0188	COG0333J	50S ribosomal protein L32			PGN_0188
rpsP	PGN_0167	COG0228J	30S ribosomal protein S16			PGN_0167
-	PGN_0159	COG0352H	thiamin-phosphate pyrophosphorylase			PGN_0159
-	PGN_0084	COG0550L	DNA topoisomerase I			PGN_0084
-	PGN_0044	COG0012J	GTP-dependent nucleic acid-binding protein EngD			PGN_0044
rplS	PGN_0035	COG0335J	50S ribosomal protein L19			PGN_0035
-	PGN_0026	COG0295F	cytidine deaminase			PGN_0026
-	PGN_0015	COG1846K	transcriptional regulator			PGN_0015

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
dnaA	COG0593L	chromosomal replication initiation protein	PGTDC60_0001	P. gingivalis TDC60	DEG10220001	PG0001	PG0001	P. gingivalis W83
-	COG1846K	MarR family transcriptional regulator	PGTDC60_0017	P. gingivalis TDC60	DEG10220002	PG0020	PG0020	P. gingivalis W83
ispF	COG0245I	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PGTDC60_0025	P. gingivalis TDC60	DEG10220003	PG0028	PG0028	P. gingivalis W83
trx	COG3118O	thioredoxin	PGTDC60_0034	P. gingivalis TDC60	DEG10220004	PG0034	PG0034	P. gingivalis W83
cdsA	COG0575I	phosphatidate cytidylyltransferase	PGTDC60_0043	P. gingivalis TDC60	DEG10220006	PG0046	PG0046	P. gingivalis W83
-	COG0465O	cell division protein FtsH	PGTDC60_0044	P. gingivalis TDC60			PG0047	P. gingivalis W83
pncB	COG1488H	nicotinate phosphoribosyltransferase	PGTDC60_0339	P. gingivalis TDC60	DEG10220441	PG0057	PG0057	P. gingivalis W83
nadD	COG1057H	nicotinic acid mononucleotide adenylyltransferase	PGTDC60_0340	P. gingivalis TDC60	DEG10220442	PG0058	PG0058	P. gingivalis W83
lpxA	COG1043M	UDP-N-acetylglucosamine acyltransferase	PGTDC60_0350	P. gingivalis TDC60	DEG10220443	PG0070	PG0070	P. gingivalis W83
-	COG0774M	bifunctional UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase/(3R)-hydroxymyristoyl-ACP dehydratase	PGTDC60_0351	P. gingivalis TDC60	DEG10220444	PG0071	PG0071	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
lpxD	COG1044M	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	PGTDC60_0352	P. gingivalis TDC60	DEG10220445	PG0072	PG0072	P. gingivalis W83
prfA	COG0216J	peptide chain release factor 1	PGTDC60_1068	P. gingivalis TDC60	DEG10220446	PG0074	PG0074	P. gingivalis W83
-	COG0150F	phosphoribosylformylglycinamidine cyclo-ligase	PGTDC60_0355	P. gingivalis TDC60	DEG10220447	PG0075	PG0075	P. gingivalis W83
pheT	COG0072J	phenylalanyl-tRNA synthetase subunit beta	PGTDC60_0377	P. gingivalis TDC60	DEG10220450	PG0099	PG0099	P. gingivalis W83
gpmA	COG0588G	phosphoglyceromutase	PGTDC60_0407	P. gingivalis TDC60	DEG10220029	PG0130	PG0130	P. gingivalis W83
fabD	COG0331I	malonyl CoA-ACP transacylase	PGTDC60_0415	P. gingivalis TDC60	DEG10220034	PG0138	PG0138	P. gingivalis W83
spo0J	COG1475K	spoOJ protein	PGTDC60_0418	P. gingivalis TDC60	DEG10220036	PG0141	PG0141	P. gingivalis W83
soj	COG1192D	SpoOJ regulator protein	PGTDC60_0419	P. gingivalis TDC60	DEG10220037	PG0142	PG0142	P. gingivalis W83
-	COG0388R	carbon-nitrogen family hydrolase	PGTDC60_0420	P. gingivalis TDC60	DEG10220038	PG0143	PG0143	P. gingivalis W83
-	COG2204T	sigma-54-dependent transcriptional regulator	PGTDC60_0425	P. gingivalis TDC60	DEG10220041	PG0148	PG0148	P. gingivalis W83
ftsY	COG0552U	signal recognition particle-docking protein FtsY	PGTDC60_0428	P. gingivalis TDC60	DEG10220042	PG0151	PG0151	P. gingivalis W83
aspS	COG0173J	aspartyl-tRNA synthetase	PGTDC60_0430	P. gingivalis TDC60	DEG10220043	PG0153	PG0153	P. gingivalis W83
pth	COG0193J	peptidyl-tRNA hydrolase	PGTDC60_0442	P. gingivalis TDC60	DEG10220046	PG0166	PG0166	P. gingivalis W83
rplY	COG1825J	50S ribosomal protein L25	PGTDC60_0443	P. gingivalis TDC60	DEG10220047	PG0167	PG0167	P. gingivalis W83
metG	COG0143J	methionyl-tRNA synthetase	PGTDC60_0445	P. gingivalis TDC60	DEG10220048	PG0170	PG0170	P. gingivalis W83
uppS	COG0020I	undecaprenyl pyrophosphate synthase	PGTDC60_0461	P. gingivalis TDC60	DEG10220051	PG0190	PG0190	P. gingivalis W83
rnpA	-	ribonuclease P	PGTDC60_0475	P. gingivalis TDC60	DEG10220055	PG0201	PG0201	P. gingivalis W83
nusA	COG0195K	transcription elongation factor NusA	PGTDC60_0534	P. gingivalis TDC60	DEG10220059	PG0254	PG0254	P. gingivalis W83
infB	COG0532J	translation initiation factor IF-2	PGTDC60_0535	P. gingivalis TDC60	DEG10220060	PG0255	PG0255	P. gingivalis W83
argS	COG0018J	arginyl-tRNA synthetase	PGTDC60_0547	P. gingivalis TDC60	DEG10220065	PG0267	PG0267	P. gingivalis W83
mnmA	COG0482J	tRNA-specific 2-thiouridylase MnmA	PGTDC60_0548	P. gingivalis TDC60	DEG10220066	PG0268	PG0268	P. gingivalis W83
ssb	COG0629L	ssDNA-binding protein	PGTDC60_0551	P. gingivalis TDC60	DEG10220067	PG0271	PG0271	P. gingivalis W83
-	COG2878C	ferredoxin	PGTDC60_1423	P. gingivalis TDC60	DEG10220360	PG0303	PG0303	P. gingivalis W83
-	COG4656C	RnfABCDGE type electron transport complex subunit C	PGTDC60_1424	P. gingivalis TDC60	DEG10220359	PG0304	PG0304	P. gingivalis W83
-	COG4658C	RnfABCDGE type electron transport complex subunit D	PGTDC60_1425	P. gingivalis TDC60	DEG10220358	PG0305	PG0305	P. gingivalis W83
-	COG4659C	RnfABCDGE type electron transport complex subunit G	PGTDC60_1426	P. gingivalis TDC60	DEG10220357	PG0306	PG0306	P. gingivalis W83
-	COG4660C	electron transport complex protein RsxE	PGTDC60_1427	P. gingivalis TDC60	DEG10220356	PG0307	PG0307	P. gingivalis W83
-	COG4657C	RnfABCDGE type electron transport complex subunit A	PGTDC60_1428	P. gingivalis TDC60	DEG10220355	PG0308	PG0308	P. gingivalis W83
rplU	COG0261J	50S ribosomal protein L21	PGTDC60_1434	P. gingivalis TDC60	DEG10220350	PG0314	PG0314	P. gingivalis W83
rpmA	COG0211J	50S ribosomal protein L27	PGTDC60_1435	P. gingivalis TDC60	DEG10220349	PG0315	PG0315	P. gingivalis W83
serS	COG0172J	seryl-tRNA synthetase	PGTDC60_1436	P. gingivalis TDC60	DEG10220348	PG0316	PG0316	P. gingivalis W83
rho	COG1158K	transcription termination factor Rho	PGTDC60_1451	P. gingivalis TDC60	DEG10220347	PG0332	PG0332	P. gingivalis W83
engB	COG0218R	ribosome biogenesis GTP-binding protein YsxC	PGTDC60_1462	P. gingivalis TDC60	DEG10220346	PG0346	PG0346	P. gingivalis W83
-	COG1853R	flavin reductase domain-containing protein	PGTDC60_1475	P. gingivalis TDC60	DEG10220345	PG0359	PG0359	P. gingivalis W83
-	COG0187L	DNA topoisomerase IV subunit B	PGTDC60_1483	P. gingivalis TDC60	DEG10220341	PG0368	PG0368	P. gingivalis W83
coaD	COG0669H	phosphopantetheine adenylyltransferase	PGTDC60_1484	P. gingivalis TDC60	DEG10220340	PG0369	PG0369	P. gingivalis W83
rplM	COG0102J	50S ribosomal protein L13	PGTDC60_1490	P. gingivalis TDC60	DEG10220339	PG0375	PG0375	P. gingivalis W83
rpsI	COG0103J	30S ribosomal protein S9	PGTDC60_1491	P. gingivalis TDC60	DEG10220338	PG0376	PG0376	P. gingivalis W83
rpsB	COG0052J	30S ribosomal protein S2	PGTDC60_1492	P. gingivalis TDC60	DEG10220337	PG0377	PG0377	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
tsf	COG0264J	elongation factor Ts	PGTDC60_1493	P. gingivalis TDC60	DEG10220336	PG0378	PG0378	P. gingivalis W83
rpsU	-	30S ribosomal protein S21	PGTDC60_1500	P. gingivalis TDC60		PG0385	PG0385	P. gingivalis W83
tuf	COG0050J	elongation factor Tu	PGTDC60_1502	P. gingivalis TDC60	DEG10220335	PG0387	PG0387	P. gingivalis W83
nusG	COG0250K	transcription antitermination protein NusG	PGTDC60_1504	P. gingivalis TDC60	DEG10220333	PG0389	PG0389	P. gingivalis W83
rplK	COG0080J	50S ribosomal protein L11	PGTDC60_1505	P. gingivalis TDC60	DEG10220332	PG0390	PG0390	P. gingivalis W83
rplA	COG0081J	50S ribosomal protein L1	PGTDC60_1506	P. gingivalis TDC60	DEG10220331	PG0391	PG0391	P. gingivalis W83
rplJ	COG0244J	50S ribosomal protein L10	PGTDC60_1507	P. gingivalis TDC60	DEG10220330	PG0392	PG0392	P. gingivalis W83
rplL	COG0222J	50S ribosomal protein L7/L12	PGTDC60_1508	P. gingivalis TDC60	DEG10220329	PG0393	PG0393	P. gingivalis W83
rpoC	COG0086K	DNA-directed RNA polymerase subunit beta'	PGTDC60_1510	P. gingivalis TDC60	DEG10220327	PG0395	PG0395	P. gingivalis W83
-	COG1418R	phosphodiesterase	PGTDC60_1516	P. gingivalis TDC60	DEG10220323	PG0401	PG0401	P. gingivalis W83
-	COG0760O	PpiC-type peptidyl-prolyl cis-trans isomerase	PGTDC60_1527	P. gingivalis TDC60	DEG10220319	PG0415	PG0415	P. gingivalis W83
-	COG1521K	pantothenate kinase	PGTDC60_1567	P. gingivalis TDC60	DEG10220316	PG0447	PG0447	P. gingivalis W83
folC	COG0285H	folylpolyglutamate synthase	PGTDC60_1580	P. gingivalis TDC60	DEG10220311	PG0463	PG0463	P. gingivalis W83
purA	COG0104F	adenylosuccinate synthetase	PGTDC60_1581	P. gingivalis TDC60	DEG10220310	PG0464	PG0464	P. gingivalis W83
fur	COG0735P	ferric uptake transcriptional regulator	PGTDC60_1582	P. gingivalis TDC60	DEG10220309	PG0465	PG0465	P. gingivalis W83
manA	COG1482G	mannose-6-phosphate isomerase	PGTDC60_1584	P. gingivalis TDC60	DEG10220308	PG0468	PG0468	P. gingivalis W83
panC	COG0414H	pantoate--beta-alanine ligase	PGTDC60_1594	P. gingivalis TDC60		PG0477	PG0477	P. gingivalis W83
-	COG0237H	kinase	PGTDC60_1599	P. gingivalis TDC60	DEG10220306	PG0483	PG0483	P. gingivalis W83
yajC	COG1862U	preprotein translocase subunit YajC	PGTDC60_1601	P. gingivalis TDC60	DEG10220304	PG0485	PG0485	P. gingivalis W83
ruvB	COG2255L	Holliday junction DNA helicase RuvB	PGTDC60_1603	P. gingivalis TDC60	DEG10220302	PG0488	PG0488	P. gingivalis W83
tgt	COG0343J	queuine tRNA-ribosyltransferase	PGTDC60_1617	P. gingivalis TDC60	DEG10220300	PG0500	PG0500	P. gingivalis W83
-	COG0795R	hypothetical protein	PGTDC60_1618	P. gingivalis TDC60	DEG10220299	PG0501	PG0501	P. gingivalis W83
gmk	COG0194F	guanylate kinase	PGTDC60_1631	P. gingivalis TDC60	DEG10220294	PG0512	PG0512	P. gingivalis W83
secA	COG0653U	preprotein translocase subunit SecA	PGTDC60_1633	P. gingivalis TDC60	DEG10220292	PG0514	PG0514	P. gingivalis W83
groEL	COG0459O	molecular chaperone GroEL	PGTDC60_1639	P. gingivalis TDC60	DEG10220290	PG0520	PG0520	P. gingivalis W83
groES	COG0234O	co-chaperonin GroES	PGTDC60_1640	P. gingivalis TDC60	DEG10220289	PG0521	PG0521	P. gingivalis W83
pyrG	COG0504F	CTP synthetase	PGTDC60_1644	P. gingivalis TDC60	DEG10220287	PG0525	PG0525	P. gingivalis W83
-	COG0706U	putative inner membrane protein translocase component YidC	PGTDC60_1645	P. gingivalis TDC60	DEG10220286	PG0526	PG0526	P. gingivalis W83
nadE	COG0171H	NAD synthetase	PGTDC60_1649	P. gingivalis TDC60	DEG10220285	PG0531	PG0531	P. gingivalis W83
asd	COG0136E	aspartate-semialdehyde dehydrogenase	PGTDC60_1695	P. gingivalis TDC60	DEG10220113	PG0571	PG0571	P. gingivalis W83
mraW	COG0275M	S-adenosyl-methyltransferase MraW	PGTDC60_1697	P. gingivalis TDC60	DEG10220114	PG0573	PG0573	P. gingivalis W83
-	COG0768M	penicillin-binding protein 2	PGTDC60_1699	P. gingivalis TDC60	DEG10220116	PG0575	PG0575	P. gingivalis W83
murE	COG0769M	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	PGTDC60_1700	P. gingivalis TDC60	DEG10220117	PG0576	PG0576	P. gingivalis W83
mraY	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	PGTDC60_1701	P. gingivalis TDC60	DEG10220118	PG0577	PG0577	P. gingivalis W83
murD	COG0771M	UDP-N-acetylmuramoylalanine--D-glutamate ligase	PGTDC60_1702	P. gingivalis TDC60	DEG10220119	PG0578	PG0578	P. gingivalis W83
murG	COG0707M	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	PGTDC60_1704	P. gingivalis TDC60	DEG10220121	PG0580	PG0580	P. gingivalis W83
murC	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	PGTDC60_1705	P. gingivalis TDC60	DEG10220122	PG0581	PG0581	P. gingivalis W83
ftsA	COG0849D	cell division protein FtsA	PGTDC60_1707	P. gingivalis TDC60	DEG10220124	PG0583	PG0583	P. gingivalis W83
ftsz	COG0206D	cell division protein FtsZ	PGTDC60_1708	P. gingivalis TDC60		PG0584	PG0584	P. gingivalis W83
guaA	COG0519F	GMP synthase	PGTDC60_1715	P. gingivalis TDC60	DEG10220125	PG0589	PG0589	P. gingivalis W83
rpsF	COG0360J	30S ribosomal protein S6	PGTDC60_1720	P. gingivalis TDC60	DEG10220127	PG0595	PG0595	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
rpsR	COG0238J	30S ribosomal protein S18	PGTDC60_1721	P. gingivalis TDC60			PG0596	P. gingivalis W83
ribBA	COG0108H	3,4-dihydroxy-2-butanone 4-phosphate synthase	PGTDC60_1724	P. gingivalis TDC60	DEG10220129	PG0599	PG0599	P. gingivalis W83
cmk	COG0283F	cytidylate kinase	PGTDC60_1729	P. gingivalis TDC60	DEG10220131	PG0603	PG0603	P. gingivalis W83
tpiA	COG0149G	triosephosphate isomerase	PGTDC60_1751	P. gingivalis TDC60	DEG10220136	PG0623	PG0623	P. gingivalis W83
folE	COG0302H	GTP cyclohydrolase I	PGTDC60_1753	P. gingivalis TDC60	DEG10220138	PG0625	PG0625	P. gingivalis W83
-	COG1137R	ABC transporter ATP-binding protein	PGTDC60_0947	P. gingivalis TDC60	DEG10220139	PG0628	PG0628	P. gingivalis W83
ppnK	COG0061G	inorganic polyphosphate/ATP-NAD kinase	PGTDC60_1758	P. gingivalis TDC60	DEG10220140	PG0629	PG0629	P. gingivalis W83
pdxJ	COG0854H	pyridoxine 5'-phosphate synthase	PGTDC60_1759	P. gingivalis TDC60	DEG10220141	PG0630	PG0630	P. gingivalis W83
lpxK	COG1663M	tetraacyldisaccharide 4'-kinase	PGTDC60_1767	P. gingivalis TDC60	DEG10220142	PG0638	PG0638	P. gingivalis W83
sppA	COG0616OU	signal peptide peptidase SppA, 67K type	PGTDC60_1768	P. gingivalis TDC60	DEG10220143	PG0639	PG0639	P. gingivalis W83
-	COG1778R	YrbI family phosphatase	PGTDC60_1785	P. gingivalis TDC60		PG0658	PG0658	P. gingivalis W83
LYS1	COG1748E	saccharopine dehydrogenase	PGTDC60_1802	P. gingivalis TDC60	DEG10220144	PG0677	PG0677	P. gingivalis W83
ddl	COG1181M	D-alanyl-alanine synthetase A	PGTDC60_1850	P. gingivalis TDC60	DEG10220150	PG0729	PG0729	P. gingivalis W83
ribE	COG0307H	riboflavin synthase subunit alpha	PGTDC60_1855	P. gingivalis TDC60	DEG10220153	PG0733	PG0733	P. gingivalis W83
-	COG0520E	class V aminotransferase	PGTDC60_1857	P. gingivalis TDC60	DEG10220155	PG0735	PG0735	P. gingivalis W83
topA	COG0550L	DNA topoisomerase I	PGTDC60_1872	P. gingivalis TDC60	DEG10220157	PG0754	PG0754	P. gingivalis W83
-	COG1960I	acyl-CoA dehydrogenase	PGTDC60_1890	P. gingivalis TDC60	DEG10220158	PG0775	PG0775	P. gingivalis W83
etfA-1	COG2025C	electron transfer flavoprotein subunit alpha	PGTDC60_1891	P. gingivalis TDC60	DEG10220159	PG0776	PG0776	P. gingivalis W83
etfB-1	COG2086C	electron transfer flavoprotein subunit beta	PGTDC60_1892	P. gingivalis TDC60	DEG10220160	PG0777	PG0777	P. gingivalis W83
obgE	COG0536R	GTPase ObgE	PGTDC60_1905	P. gingivalis TDC60	DEG10220166	PG0790	PG0790	P. gingivalis W83
adk	COG0563F	adenylate kinase	PGTDC60_1906	P. gingivalis TDC60	DEG10220167	PG0791	PG0791	P. gingivalis W83
hpt	COG0634F	hypoxanthine phosphoribosyltransferase	PGTDC60_1907	P. gingivalis TDC60	DEG10220168	PG0792	PG0792	P. gingivalis W83
fbp	COG3855G	fructose-1,6-bisphosphatase	PGTDC60_1909	P. gingivalis TDC60	DEG10220169	PG0793	PG0793	P. gingivalis W83
leuS	COG0495J	leucyl-tRNA synthetase	PGTDC60_1912	P. gingivalis TDC60	DEG10220171	PG0796	PG0796	P. gingivalis W83
nagB	COG0363G	glucosamine-6-phosphate deaminase	PGTDC60_1922	P. gingivalis TDC60	DEG10220174	PG0803	PG0803	P. gingivalis W83
-	COG0426C	flavodoxin	PGTDC60_1923	P. gingivalis TDC60	DEG10220175	PG0804	PG0804	P. gingivalis W83
-	COG1712R	Gfo/Idh/MocA family oxidoreductase	PGTDC60_1925	P. gingivalis TDC60	DEG10220177	PG0806	PG0806	P. gingivalis W83
ruvA	COG0632L	Holliday junction DNA helicase RuvA	PGTDC60_1928	P. gingivalis TDC60	DEG10220179	PG0811	PG0811	P. gingivalis W83
-	COG0358L	mobilizable transposon, excision protein	PGTDC60_1026	P. gingivalis TDC60			PG0841	P. gingivalis W83
-	COG1945S	hypothetical protein	PGTDC60_0831	P. gingivalis TDC60	DEG10220227	PG0903	PG0903	P. gingivalis W83
-	COG4591M	hypothetical protein	PGTDC60_0845	P. gingivalis TDC60	DEG10220224	PG0922	PG0922	P. gingivalis W83
rbfA	COG0858J	ribosome-binding factor A	PGTDC60_0846	P. gingivalis TDC60	DEG10220223	PG0923	PG0923	P. gingivalis W83
tmk	COG1435F	thymidine kinase	PGTDC60_0848	P. gingivalis TDC60	DEG10220221	PG0925	PG0925	P. gingivalis W83
-	COG2812L	DNA polymerase III, delta prime subunit	PGTDC60_0855	P. gingivalis TDC60			PG0932	P. gingivalis W83
ispE	COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	PGTDC60_0858	P. gingivalis TDC60	DEG10220218	PG0935	PG0935	P. gingivalis W83
-	COG0775F	AMP nucleosidase	PGTDC60_0870	P. gingivalis TDC60	DEG10220213	PG0948	PG0948	P. gingivalis W83
-	COG1466L	hypothetical protein	PGTDC60_0871	P. gingivalis TDC60	DEG10220212	PG0949	PG0949	P. gingivalis W83
purE	COG0041F	phosphoribosylaminoimidazole carboxylase catalytic subunit PurE	PGTDC60_0873	P. gingivalis TDC60	DEG10220210	PG0951	PG0951	P. gingivalis W83
ispG	COG0821I	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	PGTDC60_0874	P. gingivalis TDC60	DEG10220209	PG0952	PG0952	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
dut	COG0756F	deoxyuridine 5'-triphosphate nucleotidohydrolase	PGTDC60_0875	P. gingivalis TDC60	DEG10220208	PG0953	PG0953	P. gingivalis W83
-	COG4942D	M24/M37 family peptidase	PGTDC60_0878	P. gingivalis TDC60	DEG10220206	PG0956	PG0956	P. gingivalis W83
trmB	COG0220R	tRNA (guanine-N(7)-)-methyltransferase	PGTDC60_0882	P. gingivalis TDC60		PG0960	PG0960	P. gingivalis W83
proS	COG0442J	prolyl-tRNA synthetase	PGTDC60_0884	P. gingivalis TDC60	DEG10220203	PG0962	PG0962	P. gingivalis W83
-	COG0688I	phosphatidylserine decarboxylase	PGTDC60_0887	P. gingivalis TDC60	DEG10220201	PG0965	PG0965	P. gingivalis W83
rplT	COG0292J	50S ribosomal protein L20	PGTDC60_0906	P. gingivalis TDC60	DEG10220199	PG0989	PG0989	P. gingivalis W83
rpmI	COG0291J	50S ribosomal protein L35	PGTDC60_0907	P. gingivalis TDC60	DEG10220198	PG0990	PG0990	P. gingivalis W83
infC	COG0290J	translation initiation factor IF-3	PGTDC60_0908	P. gingivalis TDC60	DEG10220197	PG0991	PG0991	P. gingivalis W83
thrS	COG0441J	threonyl-tRNA synthetase	PGTDC60_0909	P. gingivalis TDC60	DEG10220196	PG0992	PG0992	P. gingivalis W83
-	COG0789K	transcriptional regulator	PGTDC60_0973	P. gingivalis TDC60	DEG10220266	PG1052	PG1052	P. gingivalis W83
ackA	COG0282C	acetate kinase	PGTDC60_1127	P. gingivalis TDC60	DEG10220242	PG1081	PG1081	P. gingivalis W83
pta	COG0280C	phosphotransacetylase	PGTDC60_1126	P. gingivalis TDC60	DEG10220243	PG1082	PG1082	P. gingivalis W83
pgm	COG1109G	phosphomannomutase	PGTDC60_1115	P. gingivalis TDC60	DEG10220246	PG1094	PG1094	P. gingivalis W83
rpoN	COG1508K	RNA polymerase sigma-54 factor	PGTDC60_1103	P. gingivalis TDC60	DEG10220248	PG1105	PG1105	P. gingivalis W83
murF	COG0770M	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	PGTDC60_1102	P. gingivalis TDC60	DEG10220249	PG1106	PG1106	P. gingivalis W83
panD	COG0853H	aspartate alpha-decarboxylase	PGTDC60_1101	P. gingivalis TDC60	DEG10220250	PG1114	PG1114	P. gingivalis W83
ffh	COG0541U	signal recognition particle protein	PGTDC60_1100	P. gingivalis TDC60	DEG10220251	PG1115	PG1115	P. gingivalis W83
purB	COG0015F	adenylosuccinate lyase	PGTDC60_1092	P. gingivalis TDC60	DEG10220255	PG1123	PG1123	P. gingivalis W83
uraA	COG2233F	uracil permease	PGTDC60_1089	P. gingivalis TDC60	DEG10220257	PG1126	PG1126	P. gingivalis W83
trxB	COG0492O	thioredoxin reductase	PGTDC60_1079	P. gingivalis TDC60	DEG10220259	PG1134	PG1134	P. gingivalis W83
-	COG0111HE	erythronate-4-phosphate dehydrogenase	PGTDC60_1193	P. gingivalis TDC60	DEG10220272	PG1220	PG1220	P. gingivalis W83
gdh	COG0334E	glutamate dehydrogenase	PGTDC60_1202	P. gingivalis TDC60	DEG10220273	PG1232	PG1232	P. gingivalis W83
-	COG1309K	TetR family transcriptional regulator	PGTDC60_1211	P. gingivalis TDC60	DEG10220275	PG1240	PG1240	P. gingivalis W83
lepA	COG0481M	GTP-binding protein LepA	PGTDC60_1212	P. gingivalis TDC60	DEG10220276	PG1241	PG1241	P. gingivalis W83
dnaB	COG0305L	replicative DNA helicase	PGTDC60_1213	P. gingivalis TDC60	DEG10220277	PG1242	PG1242	P. gingivalis W83
alaS	COG0013J	alanyl-tRNA synthetase	PGTDC60_1218	P. gingivalis TDC60	DEG10220278	PG1246	PG1246	P. gingivalis W83
-	COG4591M	hypothetical protein	PGTDC60_1224	P. gingivalis TDC60	DEG10220279	PG1252	PG1252	P. gingivalis W83
ligA	COG0272L	NAD-dependent DNA ligase	PGTDC60_1225	P. gingivalis TDC60	DEG10220280	PG1253	PG1253	P. gingivalis W83
recR	COG0353L	recombination protein RecR	PGTDC60_1227	P. gingivalis TDC60	DEG10220282	PG1255	PG1255	P. gingivalis W83
-	COG1530J	ribonuclease	PGTDC60_1228	P. gingivalis TDC60	DEG10220283	PG1256	PG1256	P. gingivalis W83
hup-2	COG0776L	DNA-binding protein HU	PGTDC60_1229	P. gingivalis TDC60	DEG10220284	PG1258	PG1258	P. gingivalis W83
serC	COG1932HE	phosphoserine aminotransferase	PGTDC60_2200	P. gingivalis TDC60	DEG10220112	PG1278	PG1278	P. gingivalis W83
-	COG0111HE	D-isomer specific 2-hydroxyacid dehydrogenase	PGTDC60_2199	P. gingivalis TDC60	DEG10220111	PG1279	PG1279	P. gingivalis W83
fcl	COG0451MG	GDP-fucose synthetase	PGTDC60_2191	P. gingivalis TDC60	DEG10220230	PG1289	PG1289	P. gingivalis W83
ruvC	COG0817L	Holliday junction resolvase	PGTDC60_2148	P. gingivalis TDC60			PG1324	P. gingivalis W83
murB	COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	PGTDC60_2130	P. gingivalis TDC60	DEG10220232	PG1342	PG1342	P. gingivalis W83
dxr	COG0743I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	PGTDC60_2104	P. gingivalis TDC60	DEG10220234	PG1364	PG1364	P. gingivalis W83
rimM	COG0806J	16S rRNA-processing protein RimM	PGTDC60_2103	P. gingivalis TDC60	DEG10220235	PG1365	PG1365	P. gingivalis W83
murA	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	PGTDC60_2102	P. gingivalis TDC60	DEG10220236	PG1366	PG1366	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
pgi	COG0166G	glucose-6-phosphate isomerase	PGTDC60_2100	P. gingivalis TDC60	DEG10220238	PG1368	PG1368	P. gingivalis W83
gpsA	COG0240C	glycerol-3-phosphate dehydrogenase	PGTDC60_2099	P. gingivalis TDC60	DEG10220239	PG1369	PG1369	P. gingivalis W83
lysS	COG1190J	lysyl-tRNA synthetase	PGTDC60_2098	P. gingivalis TDC60	DEG10220240	PG1370	PG1370	P. gingivalis W83
gyrA	COG0188L	DNA gyrase subunit A	PGTDC60_2077	P. gingivalis TDC60	DEG10220187	PG1386	PG1386	P. gingivalis W83
-	COG0772D	rod shape-determining protein RodA	PGTDC60_2072	P. gingivalis TDC60	DEG10220186	PG1392	PG1392	P. gingivalis W83
-	COG0768M	penicillin-binding protein 2	PGTDC60_2071	P. gingivalis TDC60			PG1393	P. gingivalis W83
-	COG1792M	rod shape-determining protein MreC	PGTDC60_2069	P. gingivalis TDC60	DEG10220184	PG1395	PG1395	P. gingivalis W83
mreB	COG1077D	rod shape-determining protein MreB	PGTDC60_2068	P. gingivalis TDC60	DEG10220183	PG1396	PG1396	P. gingivalis W83
purH	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	PGTDC60_2067	P. gingivalis TDC60	DEG10220182	PG1397	PG1397	P. gingivalis W83
dnaX	COG2812L	DNA polymerase III subunits gamma and tau	PGTDC60_2042	P. gingivalis TDC60	DEG10220190	PG1418	PG1418	P. gingivalis W83
ribH	COG0054H	6,7-dimethyl-8-ribityllumazine synthase	PGTDC60_2035	P. gingivalis TDC60	DEG10220191	PG1428	PG1428	P. gingivalis W83
ispD	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	PGTDC60_2029	P. gingivalis TDC60	DEG10220180	PG1434	PG1434	P. gingivalis W83
-	COG0451MG	NAD dependent protein	-	P. gingivalis TDC60	DEG10220105	PG1504	PG1504	P. gingivalis W83
-	COG2865K	hypothetical protein	-	P. gingivalis TDC60			PG1512	P. gingivalis W83
-	COG0406G	phosphoribosyltransferase /phosphoglycerate mutase	-	P. gingivalis TDC60			PG1513	P. gingivalis W83
-	COG2177D	cell division protein FtsX	PGTDC60_0762	P. gingivalis TDC60	DEG10220109	PG1536	PG1536	P. gingivalis W83
rfbD	COG1091M	dTDP-4-dehydrorhamnose reductase	PGTDC60_0737	P. gingivalis TDC60	DEG10220104	PG1561	PG1561	P. gingivalis W83
rfbC	COG1898M	dTDP-4-dehydrorhamnose 3,5-epimerase	PGTDC60_0736	P. gingivalis TDC60	DEG10220103	PG1562	PG1562	P. gingivalis W83
rfbA	COG1209M	glucose-1-phosphate thymidylyltransferase	PGTDC60_0735	P. gingivalis TDC60	DEG10220102	PG1563	PG1563	P. gingivalis W83
-	COG1519M	3-deoxy-D-manno-octulosonic-acid transferase	PGTDC60_0733	P. gingivalis TDC60	DEG10220101	PG1565	PG1565	P. gingivalis W83
gltX	COG0008J	glutamyl-tRNA synthetase	PGTDC60_0732	P. gingivalis TDC60	DEG10220100	PG1566	PG1566	P. gingivalis W83
folP	COG0294H	dihydropteroate synthase	PGTDC60_0710	P. gingivalis TDC60	DEG10220097	PG1589	PG1589	P. gingivalis W83
rpe	COG0036G	ribulose-phosphate 3-epimerase	PGTDC60_0706	P. gingivalis TDC60	DEG10220096	PG1595	PG1595	P. gingivalis W83
ileS	COG0060J	isoleucyl-tRNA synthetase	PGTDC60_0705	P. gingivalis TDC60	DEG10220095	PG1596	PG1596	P. gingivalis W83
-	COG1734T	DnaK suppressor protein	PGTDC60_0704	P. gingivalis TDC60	DEG10220094	PG1597	PG1597	P. gingivalis W83
-	COG0597MU	lipoprotein signal peptidase	PGTDC60_0703	P. gingivalis TDC60	DEG10220093	PG1598	PG1598	P. gingivalis W83
-	COG0340H	biotin--acetyl-CoA-carboxylase ligase	PGTDC60_0700	P. gingivalis TDC60	DEG10220092	PG1601	PG1601	P. gingivalis W83
-	COG0127F	putative deoxyribonucleoside-triphosphatase	PGTDC60_1046	P. gingivalis TDC60	DEG10220090	PG1603	PG1603	P. gingivalis W83
mmdC	COG4770I	methylmalonyl-CoA decarboxylase subunit gamma	PGTDC60_0690	P. gingivalis TDC60	DEG10220089	PG1609	PG1609	P. gingivalis W83
mmdA	COG4799I	methylmalonyl-CoA decarboxylase subunit alpha	PGTDC60_0687	P. gingivalis TDC60	DEG10220086	PG1612	PG1612	P. gingivalis W83
frdB	COG0479C	succinate dehydrogenase/fumarate reductase iron-sulfur subunit	PGTDC60_0685	P. gingivalis TDC60			PG1614	P. gingivalis W83
-	-	hypothetical protein	PGTDC60_0683	P. gingivalis TDC60			PG1616	P. gingivalis W83
-	COG0188L	DNA topoisomerase IV subunit A	PGTDC60_0657	P. gingivalis TDC60	DEG10220082	PG1622	PG1622	P. gingivalis W83
pgk	COG0126G	phosphoglycerate kinase	PGTDC60_0623	P. gingivalis TDC60	DEG10220080	PG1677	PG1677	P. gingivalis W83
-	COG1136V	ABC transporter ATP-binding protein	PGTDC60_0609	P. gingivalis TDC60	DEG10220079	PG1692	PG1692	P. gingivalis W83
gyrB	COG0187L	DNA gyrase subunit B	PGTDC60_0600	P. gingivalis TDC60	DEG10220076	PG1702	PG1702	P. gingivalis W83
pdxH	COG0259H	pyridoxamine-phosphate oxidase	PGTDC60_0590	P. gingivalis TDC60	DEG10220074	PG1714	PG1714	P. gingivalis W83
gcp	COG0533O	putative DNA-binding/iron metalloprotein/AP endonuclease	PGTDC60_0576	P. gingivalis TDC60	DEG10220072	PG1724	PG1724	P. gingivalis W83
kdsA	COG2877M	2-dehydro-3-deoxyphosphooctonate aldolase	PGTDC60_0559	P. gingivalis TDC60	DEG10220071	PG1743	PG1743	P. gingivalis W83
-	COG0698G	ribose 5-phosphate isomerase B	PGTDC60_1388	P. gingivalis TDC60	DEG10220363	PG1747	PG1747	P. gingivalis W83
tkt	COG0021G	transketolase	PGTDC60_1387	P. gingivalis TDC60	DEG10220364	PG1748	PG1748	P. gingivalis W83
fbaB	COG3588G	fructose-1,6-bisphosphate aldolase	PGTDC60_1381	P. gingivalis TDC60	DEG10220365	PG1755	PG1755	P. gingivalis W83
rpsO	COG0184J	30S ribosomal protein S15	PGTDC60_1378	P. gingivalis TDC60	DEG10220366	PG1758	PG1758	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
secDF	COG0342U	bifunctional preprotein translocase subunit SecD/SecF	PGTDC60_1374	P. gingivalis TDC60	DEG10220367	PG1762	PG1762	P. gingivalis W83
fabF	COG0304IQ	3-oxoacyl-ACP synthase	PGTDC60_1372	P. gingivalis TDC60	DEG10220368	PG1764	PG1764	P. gingivalis W83
acpP	COG0236IQ	acyl carrier protein	PGTDC60_1371	P. gingivalis TDC60	DEG10220369	PG1765	PG1765	P. gingivalis W83
pheS	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	PGTDC60_1365	P. gingivalis TDC60	DEG10220369	PG1771	PG1771	P. gingivalis W83
grpE	COG0576O	heat shock protein GrpE	PGTDC60_1361	P. gingivalis TDC60	DEG10220370	PG1775	PG1775	P. gingivalis W83
dnaJ	COG0484O	molecular chaperone DnaJ	PGTDC60_1360	P. gingivalis TDC60	DEG10220371	PG1776	PG1776	P. gingivalis W83
-	COG2908S	hypothetical protein	PGTDC60_1358	P. gingivalis TDC60	DEG10220373	PG1778	PG1778	P. gingivalis W83
glgB	COG0296G	1,4-alpha-glucan branching protein	PGTDC60_0101	P. gingivalis TDC60	DEG10220374	PG1793	PG1793	P. gingivalis W83
polA	COG0749L	DNA polymerase type I	PGTDC60_1489	P. gingivalis TDC60	DEG10220375	PG1794	PG1794	P. gingivalis W83
atpD	COG1394C	V-type ATP synthase subunit D	PGTDC60_0086	P. gingivalis TDC60		PG1805	PG1805	P. gingivalis W83
spoT	COG0317TK	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	PGTDC60_0083	P. gingivalis TDC60	DEG10220378	PG1808	PG1808	P. gingivalis W83
dnaG	COG0358L	DNA primase	PGTDC60_0077	P. gingivalis TDC60	DEG10220377	PG1814	PG1814	P. gingivalis W83
kdsB	COG1212M	3-deoxy-manno-octulosonate cytidylyltransferase	PGTDC60_0076	P. gingivalis TDC60	DEG10220376	PG1815	PG1815	P. gingivalis W83
-	COG2249R	quinone family NAD(P)H dehydrogenase	PGTDC60_0075	P. gingivalis TDC60	DEG10220375	PG1816	PG1816	P. gingivalis W83
-	COG0297G	glycogen synthase-like protein	PGTDC60_0061	P. gingivalis TDC60	DEG10220374	PG1834	PG1834	P. gingivalis W83
coaBC	COG0452H	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	PGTDC60_0114	P. gingivalis TDC60	DEG10220381	PG1851	PG1851	P. gingivalis W83
-	COG0847L	exonuclease	PGTDC60_0115	P. gingivalis TDC60	DEG10220382	PG1852	PG1852	P. gingivalis W83
dnaN	COG0592L	DNA polymerase III subunit beta	PGTDC60_0116	P. gingivalis TDC60	DEG10220383	PG1853	PG1853	P. gingivalis W83
-	COG2131F	cytidine/deoxycytidylate deaminase	PGTDC60_0121	P. gingivalis TDC60	DEG10220384	PG1856	PG1856	P. gingivalis W83
cysS	COG0215J	cysteinyl-tRNA synthetase	PGTDC60_0138	P. gingivalis TDC60	DEG10220386	PG1878	PG1878	P. gingivalis W83
metK	COG0192H	S-adenosylmethionine synthetase	PGTDC60_0165	P. gingivalis TDC60	DEG10220389	PG1896	PG1896	P. gingivalis W83
-	COG3201H	transporter	PGTDC60_0167	P. gingivalis TDC60	DEG10220390	PG1898	PG1898	P. gingivalis W83
frr	COG0233J	ribosome recycling factor	PGTDC60_0170	P. gingivalis TDC60	DEG10220391	PG1901	PG1901	P. gingivalis W83
pyrH	COG0528F	uridylate kinase	PGTDC60_0171	P. gingivalis TDC60	DEG10220392	PG1902	PG1902	P. gingivalis W83
rpoA	COG0202K	DNA-directed RNA polymerase subunit alpha	PGTDC60_0181	P. gingivalis TDC60	DEG10220394	PG1911	PG1911	P. gingivalis W83
rpsD	COG0522J	30S ribosomal protein S4	PGTDC60_0182	P. gingivalis TDC60	DEG10220395	PG1912	PG1912	P. gingivalis W83
rpsK	COG0100J	30S ribosomal protein S11	PGTDC60_0183	P. gingivalis TDC60	DEG10220396	PG1913	PG1913	P. gingivalis W83
rpsM	COG0099J	30S ribosomal protein S13	PGTDC60_0184	P. gingivalis TDC60	DEG10220397	PG1914	PG1914	P. gingivalis W83
rpmJ	COG0257J	50S ribosomal protein L36	PGTDC60_0185	P. gingivalis TDC60	DEG10220398	PG1915	PG1915	P. gingivalis W83
infA	COG0361J	translation initiation factor IF-1	PGTDC60_0186	P. gingivalis TDC60	DEG10220399	PG1916	PG1916	P. gingivalis W83
map	COG0024J	methionine aminopeptidase	PGTDC60_0187	P. gingivalis TDC60	DEG10220400	PG1917	PG1917	P. gingivalis W83
secY	COG0201U	preprotein translocase subunit SecY	PGTDC60_0188	P. gingivalis TDC60	DEG10220401	PG1918	PG1918	P. gingivalis W83
rplO	COG0200J	50S ribosomal protein L15	PGTDC60_0189	P. gingivalis TDC60	DEG10220402	PG1919	PG1919	P. gingivalis W83
rpmD	COG1841J	50S ribosomal protein L30	PGTDC60_0190	P. gingivalis TDC60	DEG10220403	PG1920	PG1920	P. gingivalis W83
rpsE	COG0098J	30S ribosomal protein S5	PGTDC60_0191	P. gingivalis TDC60	DEG10220404	PG1921	PG1921	P. gingivalis W83
rplR	COG0256J	50S ribosomal protein L18	PGTDC60_0192	P. gingivalis TDC60	DEG10220405	PG1922	PG1922	P. gingivalis W83
rplF	COG0097J	50S ribosomal protein L6	PGTDC60_0193	P. gingivalis TDC60	DEG10220406	PG1923	PG1923	P. gingivalis W83
rpsH	COG0096J	30S ribosomal protein S8	PGTDC60_0194	P. gingivalis TDC60	DEG10220407	PG1924	PG1924	P. gingivalis W83
rpsN	COG0199J	30S ribosomal protein S14	PGTDC60_0195	P. gingivalis TDC60	DEG10220408	PG1925	PG1925	P. gingivalis W83
rplE	COG0094J	50S ribosomal protein L5	PGTDC60_0196	P. gingivalis TDC60	DEG10220409	PG1926	PG1926	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
rplX	COG0198J	50S ribosomal protein L24	PGTDC60_0197	P. gingivalis TDC60	DEG10220410	PG1927	PG1927	P. gingivalis W83
rplN	COG0093J	50S ribosomal protein L14	PGTDC60_0198	P. gingivalis TDC60	DEG10220411	PG1928	PG1928	P. gingivalis W83
rpsQ	COG0186J	30S ribosomal protein S17	PGTDC60_0199	P. gingivalis TDC60	DEG10220412	PG1929	PG1929	P. gingivalis W83
rpmC	-	50S ribosomal protein L29	PGTDC60_0200	P. gingivalis TDC60			PG1930	P. gingivalis W83
rplP	COG0197J	50S ribosomal protein L16	PGTDC60_0201	P. gingivalis TDC60	DEG10220413	PG1931	PG1931	P. gingivalis W83
rpsC	COG0092J	30S ribosomal protein S3	PGTDC60_0202	P. gingivalis TDC60	DEG10220414	PG1932	PG1932	P. gingivalis W83
rplV	COG0091J	50S ribosomal protein L22	PGTDC60_0203	P. gingivalis TDC60	DEG10220415	PG1933	PG1933	P. gingivalis W83
rpsS	COG0185J	30S ribosomal protein S19	PGTDC60_0204	P. gingivalis TDC60	DEG10220416	PG1934	PG1934	P. gingivalis W83
rplB	COG0090J	50S ribosomal protein L2	PGTDC60_0205	P. gingivalis TDC60	DEG10220417	PG1935	PG1935	P. gingivalis W83
rplW	COG0089J	50S ribosomal protein L23	PGTDC60_0206	P. gingivalis TDC60	DEG10220418	PG1936	PG1936	P. gingivalis W83
rplD	COG0088J	50S ribosomal protein L4	PGTDC60_0207	P. gingivalis TDC60	DEG10220419	PG1937	PG1937	P. gingivalis W83
rplC	COG0087J	50S ribosomal protein L3	PGTDC60_0208	P. gingivalis TDC60	DEG10220420	PG1938	PG1938	P. gingivalis W83
rpsJ	COG0051J	30S ribosomal protein S10	PGTDC60_0209	P. gingivalis TDC60	DEG10220421	PG1939	PG1939	P. gingivalis W83
fusA	COG0480J	elongation factor G	PGTDC60_0210	P. gingivalis TDC60	DEG10220422	PG1940	PG1940	P. gingivalis W83
rpsG	COG0049J	30S ribosomal protein S7	PGTDC60_0211	P. gingivalis TDC60	DEG10220423	PG1941	PG1941	P. gingivalis W83
rpsL	COG0048J	30S ribosomal protein S12	PGTDC60_0212	P. gingivalis TDC60	DEG10220424	PG1942	PG1942	P. gingivalis W83
glnS	COG0008J	glutaminyl-tRNA synthetase	PGTDC60_0224	P. gingivalis TDC60	DEG10220425	PG1951	PG1951	P. gingivalis W83
-	COG0451MG	NAD dependent epimerase/reductase-like protein	PGTDC60_0227	P. gingivalis TDC60	DEG10220428	PG1954	PG1954	P. gingivalis W83
rpmB	COG0227J	50S ribosomal protein L28	PGTDC60_0232	P. gingivalis TDC60		PG1960	PG1960	P. gingivalis W83
-	COG0142H	polyprenyl synthetase	PGTDC60_0271	P. gingivalis TDC60		PG1998	PG1998	P. gingivalis W83
lepB	COG0681U	signal peptidase I	PGTDC60_0274	P. gingivalis TDC60	DEG10220432	PG2001	PG2001	P. gingivalis W83
dapB	COG0289E	dihydrodipicolinate reductase	PGTDC60_0275	P. gingivalis TDC60	DEG10220433	PG2002	PG2002	P. gingivalis W83
fmt	COG0223J	methionyl-tRNA formyltransferase	PGTDC60_0299	P. gingivalis TDC60	DEG10220436	PG2023	PG2023	P. gingivalis W83
dapA	COG0329EM	dihydrodipicolinate synthase	PGTDC60_0327	P. gingivalis TDC60	DEG10220439	PG2052	PG2052	P. gingivalis W83
thyA	COG0207F	thymidylate synthase	PGTDC60_2223	P. gingivalis TDC60	DEG10220458	PG2060	PG2060	P. gingivalis W83
folA	COG0262H	dihydrofolate reductase	PGTDC60_2222	P. gingivalis TDC60	DEG10220457	PG2061	PG2061	P. gingivalis W83
hisS	COG0124J	histidyl-tRNA synthetase	PGTDC60_2221	P. gingivalis TDC60	DEG10220456	PG2062	PG2062	P. gingivalis W83
pdxA	COG1995H	pyridoxal phosphate biosynthetic protein PdxA	PGTDC60_2217	P. gingivalis TDC60	DEG10220454	PG2067	PG2067	P. gingivalis W83
tagD	COG0615MI	glycerol-3-phosphate cytidylyltransferase	PGTDC60_2216	P. gingivalis TDC60	DEG10220453	PG2068	PG2068	P. gingivalis W83
trpS	COG0180J	tryptophanyl-tRNA synthetase	PGTDC60_1334	P. gingivalis TDC60	DEG10220010	PG2085	PG2085	P. gingivalis W83
folB	COG1539H	dihydroneopterin aldolase	PGTDC60_1328	P. gingivalis TDC60	DEG10220012	PG2091	PG2091	P. gingivalis W83
prsA	COG0462FE	ribose-phosphate pyrophosphokinase	PGTDC60_1322	P. gingivalis TDC60	DEG10220013	PG2097	PG2097	P. gingivalis W83
thiG	COG2022H	thiazole synthase	PGTDC60_1312	P. gingivalis TDC60	DEG10220014	PG2108	PG2108	P. gingivalis W83
rpsP	COG0228J	30S ribosomal protein S16	PGTDC60_1303	P. gingivalis TDC60			PG2117	P. gingivalis W83
gapA	COG0057G	glyceraldehyde 3-phosphate dehydrogenase, type I	PGTDC60_1297	P. gingivalis TDC60	DEG10220016	PG2124	PG2124	P. gingivalis W83
fabH	COG0332I	3-oxoacyl-ACP synthase	PGTDC60_0997	P. gingivalis TDC60	DEG10220017	PG2141	PG2141	P. gingivalis W83
era	COG1159R	GTP-binding protein Era	PGTDC60_1281	P. gingivalis TDC60	DEG10220018	PG2142	PG2142	P. gingivalis W83
engA	COG1160R	GTP-binding protein EngA	PGTDC60_1280	P. gingivalis TDC60	DEG10220019	PG2143	PG2143	P. gingivalis W83
-	-	glutamine cyclotransferase-like protein	PGTDC60_1267	P. gingivalis TDC60	DEG10220022	PG2157	PG2157	P. gingivalis W83
-	COG2166R	hypothetical protein	PGTDC60_1266	P. gingivalis TDC60	DEG10220023	PG2158	PG2158	P. gingivalis W83
surE	COG0496R	stationary phase survival protein SurE	PGTDC60_1260	P. gingivalis TDC60	DEG10220025	PG2163	PG2163	P. gingivalis W83
glyS	COG0423J	glycyl-tRNA synthetase	PGTDC60_1258	P. gingivalis TDC60	DEG10220027	PG2165	PG2165	P. gingivalis W83
lysC	COG0527E	aspartate kinase	PGTDC60_0050	P. gingivalis TDC60	DEG10220008	PG2189	PG2189	P. gingivalis W83
ftsE	COG2884D	cell-division ATP-binding protein	PGTDC60_0049	P. gingivalis TDC60	DEG10220009	PG2190	PG2190	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
def	COG0242J	peptide deformylase	PGTDC60_2229	P. gingivalis TDC60			PG2201	P. gingivalis W83
manC	COG0836M	mannose-1-phosphate guanylyltransferase	PGTDC60_2241	P. gingivalis TDC60	DEG10220459	PG2215	PG2215	P. gingivalis W83
dxs	COG1154HI	1-deoxy-D-xylulose-5-phosphate synthase	PGTDC60_2243	P. gingivalis TDC60	DEG10220460	PG2217	PG2217	P. gingivalis W83
-	COG0621J	MiaB-like tRNA modifying enzyme	PGTDC60_2248	P. gingivalis TDC60	DEG10220461	PG2221	PG2221	P. gingivalis W83
-	COG1560M	acyltransferase	PGTDC60_2249	P. gingivalis TDC60	DEG10220462	PG2222	PG2222	P. gingivalis W83
dnaE	COG0587L	DNA polymerase III subunit alpha	PGTDC60_0035	P. gingivalis TDC60			PG0035	P. gingivalis W83
lpxB	COG0763M	lipid A disaccharide synthase	PGTDC60_1261	P. gingivalis TDC60			PG2162	P. gingivalis W83
ksgA	COG0030J	dimethyladenosine transferase	PGTDC60_0412	P. gingivalis TDC60			PG0135	P. gingivalis W83
ribD	COG0117H	riboflavin biosynthesis protein RibD	PGTDC60_0431	P. gingivalis TDC60			PG0155	P. gingivalis W83
tyrS	COG0162J	tyrosyl-tRNA synthetase	PGTDC60_0542	P. gingivalis TDC60			PG0263	P. gingivalis W83
-	COG1674D	FtsK/SpoIIIE family protein	PGTDC60_0674	P. gingivalis TDC60			PG1636	P. gingivalis W83
-	COG0772D	cell division protein FtsW	PGTDC60_1703	P. gingivalis TDC60			PG0579	P. gingivalis W83
-	-	cell division protein FtsQ	PGTDC60_1706	P. gingivalis TDC60			PG0582	P. gingivalis W83
rpoD	COG0568K	RNA polymerase sigma-70 factor	PGTDC60_1719	P. gingivalis TDC60			PG0594	P. gingivalis W83
-	COG0795R	hypothetical protein	PGTDC60_1723	P. gingivalis TDC60			PG0598	P. gingivalis W83
ispH	COG0761IM	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	PGTDC60_1730	P. gingivalis TDC60			PG0604	P. gingivalis W83
-	COG5009M	penicillin-binding protein 1A	PGTDC60_1910	P. gingivalis TDC60			PG0794	P. gingivalis W83
-	COG0617J	poly(A) polymerase	PGTDC60_1918	P. gingivalis TDC60			pg0801	P. gingivalis W83
dnaK	COG0443O	molecular chaperone DnaK	PGTDC60_1180	P. gingivalis TDC60			PG1208	P. gingivalis W83
-	COG1595K	ECF subfamily RNA polymerase sigma factor	PGTDC60_0901	P. gingivalis TDC60			PG0985	P. gingivalis W83
ribF	COG0196H	riboflavin biosynthesis protein RibF	PGTDC60_0879	P. gingivalis TDC60			PG0957	P. gingivalis W83
gmd	COG1089M	GDP-mannose 4,6-dehydratase	PGTDC60_2192	P. gingivalis TDC60			PG1288	P. gingivalis W83
etfB-2	COG2086C	electron transfer flavoprotein subunit beta	PGTDC60_1131	P. gingivalis TDC60			PG1077	P. gingivalis W83
-	COG0787M	putative bifunctional UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase/alanine racemase	PGTDC60_1111	P. gingivalis TDC60			PG1097	P. gingivalis W83
asnC	COG0017J	asparaginyl-tRNA synthetase	PGTDC60_1094	P. gingivalis TDC60			PG1121	P. gingivalis W83
valS	COG0525J	valyl-tRNA synthetase	PGTDC60_1082	P. gingivalis TDC60			PG1132	P. gingivalis W83
-	COG1438K	transcriptional regulator	PGTDC60_0962	P. gingivalis TDC60			PG1040	P. gingivalis W83
fabG	COG1028IQR	3-oxoacyl-ACP reductase	PGTDC60_1210	P. gingivalis TDC60			PG1239	P. gingivalis W83
guaB	COG0516F	inosine 5-monophosphate dehydrogenase	PGTDC60_1642	P. gingivalis TDC60			PG0523	P. gingivalis W83
ogt	COG0350L	methylated-DNA--protein-cysteine S-methyltransferase	PGTDC60_1602	P. gingivalis TDC60			PG0486	P. gingivalis W83
-	-	hypothetical protein	PGTDC60_1572	P. gingivalis TDC60			PG0452	P. gingivalis W83
rpoB	COG0085K	DNA-directed RNA polymerase subunit beta	PGTDC60_1509	P. gingivalis TDC60			PG0394	P. gingivalis W83
-	COG1109G	phosphomannomutase	PGTDC60_0283	P. gingivalis TDC60			PG2010	P. gingivalis W83
-	COG0037D	hypothetical protein	PGTDC60_0322	P. gingivalis TDC60			PG2046	P. gingivalis W83
-	COG0513LKJ	DEAD/DEAH box helicase	PGTDC60_0364	P. gingivalis TDC60			PG0086	P. gingivalis W83
-	COG0295F	cytidine deaminase	PGTDC60_0027	P. gingivalis TDC60			PG0030	P. gingivalis W83
rplS	COG0335J	50S ribosomal protein L19	PGTDC60_0036	P. gingivalis TDC60			PG0037	P. gingivalis W83
-	COG0012J	GTP-dependent nucleic acid-binding protein EngD	PGTDC60_0045	P. gingivalis TDC60			PG0048	P. gingivalis W83
recJ	COG0608L	single-stranded-DNA-specific exonuclease RecJ	PGTDC60_0336	P. gingivalis TDC60			PG0054	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
-	COG1595K	ECF subfamily RNA polymerase sigma factor	PGTDC60_0438	P. gingivalis TDC60			PG0162	P. gingivalis W83
-	COG1846K	transcriptional regulator	PGTDC60_0448	P. gingivalis TDC60			PG0173	P. gingivalis W83
prfC	COG4108J	peptide chain release factor 3	PGTDC60_0479	P. gingivalis TDC60			PG0205	P. gingivalis W83
-	COG1595K	ECF subfamily RNA polymerase sigma factor	PGTDC60_0490	P. gingivalis TDC60			PG0214	P. gingivalis W83
-	COG0847L	exonuclease	PGTDC60_0502	P. gingivalis TDC60			PG0223	P. gingivalis W83
-	COG0023J	translation initation factor SUI1	PGTDC60_0526	P. gingivalis TDC60			PG0248	P. gingivalis W83
-	COG0664T	Crp/FNR family transcriptional regulator	PGTDC60_1511	P. gingivalis TDC60			PG0396	P. gingivalis W83
recF	COG1195L	recF protein	PGTDC60_1513	P. gingivalis TDC60			PG0398	P. gingivalis W83
recQ-1	COG0514L	ATP-dependent DNA helicase RecQ	PGTDC60_1528	P. gingivalis TDC60			PG0416	P. gingivalis W83
-	COG0674C	pyruvate ferredoxin/flavodoxin oxidoreductase	PGTDC60_1673	P. gingivalis TDC60			PG0548	P. gingivalis W83
-	COG0005F	purine nucleoside phosphorylase	PGTDC60_1684	P. gingivalis TDC60			PG0558	P. gingivalis W83
rpmE2	COG0254J	50S ribosomal protein L31	PGTDC60_1717	P. gingivalis TDC60			PG0592	P. gingivalis W83
rplI	COG0359J	50S ribosomal protein L9	PGTDC60_1722	P. gingivalis TDC60			PG0597	P. gingivalis W83
typA	COG1217T	GTP-binding protein TypA	PGTDC60_1743	P. gingivalis TDC60			PG0615	P. gingivalis W83
serB	COG0560E	phosphoserine phosphatase	PGTDC60_1781	P. gingivalis TDC60			PG0653	P. gingivalis W83
rpmH	COG0230J	50S ribosomal protein L34	PGTDC60_1783	P. gingivalis TDC60			PG0656	P. gingivalis W83
pnpA	COG1185J	polynucleotide phosphorylase	PGTDC60_1883	P. gingivalis TDC60			PG0766	P. gingivalis W83
-	COG0142H	polyprenyl synthetase	PGTDC60_1899	P. gingivalis TDC60			PG0784	P. gingivalis W83
recA	COG0468L	recombinase A	PGTDC60_0809	P. gingivalis TDC60			PG0881	P. gingivalis W83
-	COG1785P	alkaline phosphatase	PGTDC60_0817	P. gingivalis TDC60			PG0890	P. gingivalis W83
cydB	COG1294C	cytochrome d ubiquinol oxidase subunit II	PGTDC60_0827	P. gingivalis TDC60			PG0899	P. gingivalis W83
cydA	COG1271C	cytochrome d ubiquinol oxidase subunit I	PGTDC60_0828	P. gingivalis TDC60			PG0900	P. gingivalis W83
-	COG0480J	elongation factor G	PGTDC60_0856	P. gingivalis TDC60			PG0933	P. gingivalis W83
hemH	COG0152F	phosphoribosylaminoimidazole-succinocarboxamide synthase	PGTDC60_0896	P. gingivalis TDC60			PG0976	P. gingivalis W83
-	COG0664T	transcriptional regulator	PGTDC60_0974	P. gingivalis TDC60			PG1053	P. gingivalis W83
nrd	COG0209F	ribonucleotide reductase	PGTDC60_1086	P. gingivalis TDC60			PG1129	P. gingivalis W83
-	COG1022I	long-chain-fatty-acid--CoA ligase	PGTDC60_1067	P. gingivalis TDC60			PG1145	P. gingivalis W83
-	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	PGTDC60_1221	P. gingivalis TDC60			PG1249	P. gingivalis W83
-	COG1328F	anaerobic ribonucleoside triphosphate reductase	PGTDC60_1231	P. gingivalis TDC60			PG1260	P. gingivalis W83
efp-2	COG0231J	elongation factor P	-	P. gingivalis TDC60			PG1274	P. gingivalis W83
rpsA	COG0539J	30S ribosomal protein S1	PGTDC60_2180	P. gingivalis TDC60			PG1297	P. gingivalis W83
pntB	COG1282C	NAD(P) transhydrogenase subunit beta	PGTDC60_2140	P. gingivalis TDC60			PG1332	P. gingivalis W83
-	COG2820F	phosphorylase	PGTDC60_2097	P. gingivalis TDC60			PG1371	P. gingivalis W83
fabK	COG2070R	enoyl-ACP reductase	PGTDC60_2045	P. gingivalis TDC60			PG1416	P. gingivalis W83
dacB	COG2027M	D-alanyl-D-alanine carboxypeptidase	PGTDC60_2040	P. gingivalis TDC60			PG1422	P. gingivalis W83
topB-2	COG0550L	DNA topoisomerase III	PGTDC60_0994	P. gingivalis TDC60			PG1495	P. gingivalis W83
queA	COG0809J	S-adenosylmethionine--tRNA ribosyltransferase-isomerase	PGTDC60_0758	P. gingivalis TDC60			PG1540	P. gingivalis W83
folK	COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	PGTDC60_0757	P. gingivalis TDC60			PG1541	P. gingivalis W83
sdhA	COG1053C	succinate dehydrogenase flavoprotein subunit	PGTDC60_0684	P. gingivalis TDC60			PG1615	P. gingivalis W83

Gene	COG	Gene	Predicted EG	STRAIN	DEG code	Experimental EG	Predicted EG	STRAIN
pckA	COG1866C	phosphoenolpyruvate carboxykinase	PGTDC60_0624	P. gingivalis TDC60			PG1676	P. gingivalis W83
greA	COG0782K	transcription elongation factor GreA	PGTDC60_0612	P. gingivalis TDC60			PG1688	P. gingivalis W83
rpsT	COG0268J	30S ribosomal protein S20	PGTDC60_0577	P. gingivalis TDC60			PG1723	P. gingivalis W83
aspA	COG1027E	aspartate ammonia-lyase	PGTDC60_0561	P. gingivalis TDC60			PG1741	P. gingivalis W83
-	COG1390C	v-type ATPase subunit E	PGTDC60_0090	P. gingivalis TDC60			PG1801	P. gingivalis W83
atpA	COG1155C	V-type ATP synthase subunit A	PGTDC60_0088	P. gingivalis TDC60			PG1803	P. gingivalis W83
atpB	COG1156C	V-type ATP synthase subunit B	PGTDC60_0087	P. gingivalis TDC60			PG1804	P. gingivalis W83
atpI	COG1269C	v-type ATPase subunit I	PGTDC60_0085	P. gingivalis TDC60			PG1806	P. gingivalis W83
atpK	-	v-type ATPase subunit K	PGTDC60_0084	P. gingivalis TDC60			PG1807	P. gingivalis W83
eno	COG0148G	phosphopyruvate hydratase	PGTDC60_0069	P. gingivalis TDC60			PG1824	P. gingivalis W83
-	COG1022I	long-chain-fatty-acid--CoA ligase	PGTDC60_0064	P. gingivalis TDC60			PG1829	P. gingivalis W83
recQ-2	COG0514L	ATP-dependent DNA helicase RecQ	PGTDC60_0063	P. gingivalis TDC60			PG1831	P. gingivalis W83
ppk	COG0855P	polyphosphate kinase	PGTDC60_0144	P. gingivalis TDC60			PG1885	P. gingivalis W83
rplQ	COG0203J	50S ribosomal protein L17	PGTDC60_0180	P. gingivalis TDC60			PG1910	P. gingivalis W83
rpmG	COG0267J	50S ribosomal protein L33	PGTDC60_0231	P. gingivalis TDC60			PG1959	P. gingivalis W83
-	COG1381L	DNA repair protein RecO	PGTDC60_0282	P. gingivalis TDC60			PG2009	P. gingivalis W83
gltD	COG0493ER	glutamate synthase small subunit	PGTDC60_0311	P. gingivalis TDC60			PG2033	P. gingivalis W83
thiE	COG0352H	thiamine-phosphate pyrophosphorylase	PGTDC60_1311	P. gingivalis TDC60			PG2109	P. gingivalis W83
rpmF	COG0333J	50S ribosomal protein L32	PGTDC60_1283	P. gingivalis TDC60			PG2140	P. gingivalis W83

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
dnaJ	b0015	COG0484O, COG0484O	chaperone Hsp40, DnaK co-chaperone				b0015
lptD	b0054	COG1452M, COG1452M	LPS assembly OM complex LptDE, beta-barrel component	DEG10180011| DEG10190006	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0054
rluA	b0058	COG0564J,COG0564J	dual specificity 23S rRNA pseudouridine(746), tRNA pseudouridine(32) synthase, SAM-dependent	DEG10180012	Escherichia coli MG1655 I		b0058
rsmH	b0082	COG0275M, COG0275M	16S rRNA m(4)C1402 methyltransferase, SAM-dependent	DEG10180013	Escherichia coli MG1655 I		b0082
ftsL	b0083	COG3116D,COG3116D	membrane bound cell division protein at septum containing leucine zipper motif	DEG10180014| DEG10190007	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0083
ftsW	b0089	COG0772D,COG0772D	lipid II flippase; integral membrane protein involved in stabilizing FstZ ring during cell division	DEG10180018| DEG10190013	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0089
ftsQ	b0093	COG1589M, COG1589M	divisome assembly protein, membrane anchored protein involved in growth of wall at septum	DEG10180022| DEG10190016	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0093
ftsA	b0094	COG0849D,COG0849D	ATP-binding cell division protein involved in recruitment of FtsK to Z ring	DEG10180023| DEG10190017	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0094
ftsZ	b0095	COG0206D,COG0206D	GTP-binding tubulin-like cell division protein	DEG10180024| DEG10190018	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0095
lpxC	b0096	COG0774M, COG0774M	UDP-3-O-acyl N-acetylglucosamine deacetylase	DEG10190019		Escherichia coli MG1655 II	b0096
lpxD	b0179	COG1044M, COG1044M	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	DEG10190037		Escherichia coli MG1655 II	b0096
map	b0168	COG0024J,COG0024J	methionine aminopeptidase	DEG10180038| DEG10190027	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0168
tsf	b0170	COG0264J,COG0264J	translation elongation factor EF-Ts	DEG10180040| DEG10190029	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0170
frr	b0172	COG0233J,COG0233J	ribosome recycling factor	DEG10180042| DEG10190031	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0172
bamA	b0177	COG4775M, COG4775M	BamABCDE complex OM biogenesis outer membrane pore-forming assembly factor	DEG10180046| DEG10190036	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0177
lpxA	b0181	COG1043M, COG1043M	UDP-N-acetylglucosamine acetyltransferase	DEG10180048| DEG10190039	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0181
lpxB	b0182	COG0763M, COG0763M	tetraacyldisaccharide-1-P synthase	DEG10180049| DEG10190040	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0182
tilS	b0188	COG0037D,COG0037D	tRNA(Ile)-lysidine synthetase	DEG10180053| DEG10190043	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0188
lpxH	b0524	COG2908S,COG2908S	UDP-2,3-diacylglucosamine pyrophosphohydrolase	DEG10180097| DEG10190057	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0524
mrdB	b0634	COG0772D,COG0772D	cell wall shape-determining protein	DEG10180108| DEG10190061	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0634
lptE	b0641	COG2980M, COG2980M	LPS assembly OM complex LptDE, lipoprotein component	DEG10180112| DEG10190065	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0641
fldA	b0684	COG0716C,COG0716C	flavodoxin 1	DEG10190069		Escherichia coli MG1655 II	b0684
infA	b0884	COG0361J,COG0361J	translation initiation factor IF-1	DEG10160139| DEG10190071| DEG10320086| DEG10330142	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0884

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
ftsK	b0890	COG1674D,COG1674D	DNA translocase at septal ring sorting daughter chromsomes	DEG10190073		Escherichia coli MG1655 II	b0890
lolA	b0891	COG2834M, COG2834M	lipoprotein chaperone	DEG10190074		Escherichia coli MG1655 II	b0891
lpxK	b0915	COG1663M, COG1663M	lipid A 4'kinase	DEG10180149|DEG10190078	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0915
kdsB	b0918	COG1212M, COG1212M	3-deoxy-manno-octulosonate cytidylyltransferase	DEG10180150|DEG10190079	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0918
mukF	b0922	COG3006D,COG3006D	chromosome condensin MukBEF, kleisin-like subunit, binds calcium	DEG10180151|DEG10190080	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0922
mukE	b0923	COG3095D,COG3095D	chromosome condensin MukBEF, MukE localization factor	DEG10180152|DEG10190081	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0923
mukB	b0924	COG3096D,COG3096D	chromosome condensin MukBEF, ATPase and DNA-binding subunit	DEG10180153|DEG10190082	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b0924
acpP	b1094	COG0236IQ, COG0236IQ	acyl carrier protein (ACP)	DEG10160116|DEG10190090|DEG10320114|DEG10330118	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1094
minE	b1174	COG0851D,COG0851D	cell division topological specificity factor	DEG10190098		Escherichia coli MG1655 II	b1174
pth	b1204	COG0193J,COG0193J	peptidyl-tRNA hydrolase	DEG10180202|DEG10190100	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1204
lolB	b1209	COG3017M, COG3017M	lipoprotein localization factor	DEG10190103		Escherichia coli MG1655 II	b1209
prfA	b1211	COG0216J,COG0216J	peptide chain release factor RF-1	DEG10190105		Escherichia coli MG1655 II	b1211
prmC	b1212	COG2890J,COG2890J	N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2	DEG10180206|DEG10190106	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1212
kdsA	b1215	COG2877M, COG2877M	3-deoxy-D-manno-octulosonate 8-phosphate synthase	DEG10190107		Escherichia coli MG1655 II	b1215
topA	b1274	COG0550L,COG0550L	DNA topoisomerase I, omega subunit	DEG10180221|DEG10190108	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1274
yciH	b1282	COG0023J,COG0023J	initiation factor function partial mimic, SUI1 family	DEG10030700	Escherichia coli MG1655 I		b1282
mpaA	b1326	COG2866E,COG2866E	murein peptide amidase A	DEG10180229	Escherichia coli MG1655 I		b1326
smrA	b1340	COG2840S,COG2840S	DNA endonuclease	DEG10180231	Escherichia coli MG1655 I		b1340
sufA	b1684	COG0316S,COG0316S	Fe-S cluster assembly protein	DEG10180280	Escherichia coli MG1655 I		b1684
infC	b1718	COG0290J,COG0290J	translation initiation factor IF-3	DEG10030595|DEG10180288|DEG10190120	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1718
tsaB	b1807	COG1214O, COG1214O	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; binding partner and protease for TsaD	DEG10180306|DEG10190124	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b1807
yebG	b1848	COG3141S,COG3141S	DNA damage-inducible protein regulated by LexA	DEG10180310	Escherichia coli MG1655 I		b1848
yefM	b2017	COG2161D,COG2161D	antitoxin of the YoeB-YefM toxin-antitoxin system	DEG10190128		Escherichia coli MG1655 II	b2017
gyrA	b2231	COG0188L,COG0188L	DNA gyrase (type II topoisomerase), subunit A	DEG10180351|DEG10190132	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2231
zipA	b2412	COG3115D,COG3115D	FtsZ stabilizer	DEG10180368|DEG10190140	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2412
der	b2511	COG1160R,COG1160R	GTPase; multicopy suppressor of ftsJ	DEG10180380|DEG10190143	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2511
fdx	b2525	COG0633C,COG0633C	[2Fe-2S] ferredoxin	DEG10180384	Escherichia coli MG1655 I		b2525
hscA	b2526	COG0443O, COG0443O	DnaK-like molecular chaperone specific for IscU	DEG10180385	Escherichia coli MG1655 I		b2526
tadA	b2559	COG0590FJ, COG0590FJ	tRNA-specific adenosine deaminase	DEG10180393|DEG10190147	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2559
era	b2566	COG1159R,COG1159R	membrane-associated, 16S rRNA-binding GTPase	DEG10180396|DEG10190149	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2566
rnc	b2567	COG0571K,COG0571K	RNase III	DEG10180397|DEG10190150	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2567
rpoE	b2573	COG1595K,COG1595K	RNA polymerase sigma E factor	DEG10190152		Escherichia coli MG1655 II	b2573
trxC	b2582	COG3118O, COG3118O	thioredoxin 2	DEG10030730|DEG10180400	Escherichia coli MG1655 I		b2582
trmD	b2607	COG0336J,COG0336J	tRNA m(1)G37 methyltransferase, SAM-dependent	DEG10180404|DEG10190156	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2607

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
rimM	b2608	COG0806J,COG0806J	16S rRNA processing protein	DEG10180405	Escherichia coli MG1655 I		b2608
grpE	b2614	COG0576O, COG0576O	heat shock protein	DEG10180409|DEG10190159	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2614
ftsB	b2748	COG2919D,COG2919D	cell division protein	DEG10180425|DEG10190164	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2748
mazE	b2783	COG2336T,COG2336T	antitoxin of the ChpA-ChpR toxin-antitoxin system	DEG10190167		Escherichia coli MG1655 II	b2783
lgt	b2828	COG0682M, COG0682M	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase	DEG10180429|DEG10190168	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2828
yqgF	b2949	COG0816L,COG0816L	putative Holliday junction resolvase	DEG10180442|DEG10190172	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b2949
ftsP	b3017	COG2132Q, COG2132Q	septal ring component that protects the divisome from stress; multicopy suppressor of ftsI(Ts)	DEG10050248	Escherichia coli MG1655 I		b3017
parC	b3019	COG0188L,COG0188L	DNA topoisomerase IV, subunit A	DEG10180449	Escherichia coli MG1655 I		b3019
mqsA	b3021	COG2944K,COG2944K	antitoxin for MqsR toxin; transcriptional repressor	DEG10180450|DEG10190174	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3021
parE	b3030	COG0187L,COG0187L	DNA topoisomerase IV, subunit B	DEG10180452|DEG10190175	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3030
cca	b3056	COG0617J,COG0617J	fused tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase and phosphatase	DEG10180455|DEG10190177	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3056
tsaD	b3064	COG0533O, COG0533O	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; glycation binding protein	DEG10190178		Escherichia coli MG1655 II	b3064
rpsU	b3065	COG0828J,COG0828J	30S ribosomal subunit protein S21	DEG10160215|DEG10330218	Escherichia coli MG1655 I		b3065
rpoD	b3067	COG0568K,COG0568K	RNA polymerase, sigma 70 (sigma D) factor	DEG10180457	Escherichia coli MG1655 I		b3067
infB	b3168	COG0532J,COG0532J	translation initiation factor IF-2	DEG10180471|DEG10190182	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3168
rimP	b3170	COG0779S,COG0779S	ribosome maturation factor for 30S subunits	DEG10180472	Escherichia coli MG1655 I		b3170
obgE	b3183	COG0536R,COG0536R	GTPase involved in cell partioning and DNA repair	DEG10180473|DEG10190185	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3183
kdsC	b3198	COG1778R,COG1778R	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase				b3198
lptA	b3200	COG1934S,COG1934S	periplasmic LPS-binding protein	DEG10190192		Escherichia coli MG1655 II	b3200
mreD	b3249	COG2891M, COG2891M	cell wall structural complex MreBCD transmembrane component MreD	DEG10190196		Escherichia coli MG1655 II	b3249
mreC	b3250	COG1792M, COG1792M	cell wall structural complex MreBCD transmembrane component MreC	DEG10180485|DEG10190197	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3250
mreB	b3251	COG1077D,COG1077D	cell wall structural complex MreBCD, actin-like component MreB	DEG10160241|DEG10180486|DEG10190198|DEG10330244	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3251
tsaC	b3282	COG0009J,COG0009J	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein, threonine-dependent ADP-forming ATPase	DEG10190201		Escherichia coli MG1655 II	b3282
def	b3287	COG0242J,COG0242J	peptide deformylase	DEG10180488|DEG10190202	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3287
tufA	b3339	COG0050J,COG0050J	translation elongation factor EF-Tu 1	DEG10180508	Escherichia coli MG1655 I		b3339
fusA	b3340	COG0480J,COG0480J	protein chain elongation factor EF-G, GTP-binding	DEG10180509|DEG10190231	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3340
rpoH	b3461	COG0568K,COG0568K	RNA polymerase, sigma 32 (sigma H) factor	DEG10180521|DEG10190237	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3461
waaC	b3621	COG0859M, COG0859M	ADP-heptose:LPS heptosyl transferase I	DEG10180535	Escherichia coli MG1655 I		b3621
waaU	b3623	COG0859M, COG0859M	lipopolysaccharide core biosynthesis	DEG10190245		Escherichia coli MG1655 II	b3623
waaA	b3633	COG1519M, COG1519M	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	DEG10180536|DEG10190246	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3633
gyrB	b3699	COG0187L,COG0187L	DNA gyrase, subunit B	DEG10190253	Escherichia coli MG1655 I		b3699
rep	b3778	COG0210L,COG0210L	DNA helicase and single-stranded DNA-dependent ATPase	DEG10180549	Escherichia coli MG1655 I		b3778

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trxA	b3781	COG3118O, COG3118O	thioredoxin 1	DEG10110205	Escherichia coli MG1655 I		b3781
ubiB	b3835	COG0661R,COG0661R	regulator of octaprenylphenol hydroxylation, ubiquinone synthesis; regulator of 2'-N-acetyltransferase; putative ABC1 family protein kinase	DEG10180557|DEG10190266	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3835
yihA	b3865	COG0218R,COG0218R	cell division GTP-binding protein	DEG10180560|DEG10190269	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b3865
ftsN	b3933	COG3087D,COG3087D	essential cell division protein	DEG10190270		Escherichia coli MG1655 II	b3933
tufB	b3980	COG0050J,COG0050J	translation elongation factor EF-Tu 2	DEG10180568	Escherichia coli MG1655 I		b3980
rplK	b3983	COG0080J,COG0080J	50S ribosomal subunit protein L11	DEG10160262|DEG10320328|DEG10330265	Escherichia coli MG1655 I		b3983
lexA	b4043	COG1974KT, COG1974KT	transcriptional repressor of SOS regulon	DEG10190282		Escherichia coli MG1655 II	b4043
groS	b4142	COG0234O, COG0234O	Cpn10 chaperonin GroES, small subunit of GroESL	DEG10180583|DEG10190286	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b4142
tsaE	b4168	COG0802R,COG0802R	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein; ADP binding protein	DEG10180588|DEG10190289	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b4168
chpS	b4224	COG2336T,COG2336T	antitoxin of the ChpBS toxin-antitoxin system	DEG10180594|DEG10190291	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b4224
dnaC	b4361	COG1484L,COG1484L	DNA biosynthesis protein	DEG10180605|DEG10190296	Escherichia coli MG1655 I	Escherichia coli MG1655 II	b4361
lptF	b4261	COG0795R,COG0795R	lipopolysaccharide export ABC permease of the LptBFGC export complex	DEG10180601|DEG10190294	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsR	b4202	COG0238J,COG0238J	30S ribosomal subunit protein S18	DEG10160345|DEG10190290|DEG10330350		Escherichia coli MG1655 II	
psd	b4160	COG0688I,COG0688I	phosphatidylserine decarboxylase	DEG10190287		Escherichia coli MG1655 II	
alsK	b4084	COG1940KG, COG1940KG	D-allose kinase	DEG10190285		Escherichia coli MG1655 II	
ssb	b4059	COG0629L,COG0629L	single-stranded DNA-binding protein	DEG10190284		Escherichia coli MG1655 II	
plsB	b4041	COG2937I,COG2937I	glycerol-3-phosphate O-acyltransferase	DEG10190281		Escherichia coli MG1655 II	
ubiA	b4040	COG0382H,COG0382H	p-hydroxybenzoate octaprenyltransferase	DEG10190280		Escherichia coli MG1655 II	
rpoC	b3988	COG0086K,COG0086K	RNA polymerase, beta prime subunit	DEG10180572|DEG10190279	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpoB	b3987	COG0085K,COG0085K	RNA polymerase, beta subunit	DEG10180571|DEG10190278	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secE	b3981	COG0690U,COG0690U	preprotein translocase membrane subunit	DEG10190274		Escherichia coli MG1655 II	
birA	b3973	COG0340H,COG0340H	bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase/ DNA-binding transcriptional repressor, bio-5'-AMP-binding	DEG10180566|DEG10190273	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murB	b3972	COG0812M, COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding	DEG10190272		Escherichia coli MG1655 II	
ubiD	b3843	COG0043H,COG0043H	3-octaprenyl-4-hydroxybenzoate decarboxylase	DEG10190267		Escherichia coli MG1655 II	
yidC	b3705	COG0706U,COG0706U	membrane protein insertase	DEG10190258		Escherichia coli MG1655 II	

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rpmH	b3703	COG0230J,COG0230J	50S ribosomal subunit protein L34	DEG10160274|DEG10190256|DEG10320310|DEG10330278		Escherichia coli MG1655 II	
dnaN	b3701	COG0592L,COG0592L	DNA polymerase III, beta subunit	DEG10190254		Escherichia coli MG1655 II	
spoT	b3650	COG0317TK,COG0317TK	bifunctional (p)ppGpp synthetase II/ guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase	DEG10190252		Escherichia coli MG1655 II	
rpmB	b3637	COG0227J,COG0227J	50S ribosomal subunit protein L28	DEG10190248		Escherichia coli MG1655 II	
gpsA	b3608	COG0240C,COG0240C	glycerol-3-phosphate dehydrogenase (NAD+)	DEG10190244		Escherichia coli MG1655 II	
ftsX	b3462	COG2177D,COG2177D	inner membrane putative ABC superfamily transporter permease	DEG10190238		Escherichia coli MG1655 II	
rpsG	b3341	COG0049J,COG0049J	30S ribosomal subunit protein S7	DEG10190232		Escherichia coli MG1655 II	
rplV	b3315	COG0091J,COG0091J	50S ribosomal subunit protein L22	DEG10160305|DEG10190224|DEG10320284|DEG10330309		Escherichia coli MG1655 II	
rpsC	b3314	COG0092J,COG0092J	30S ribosomal subunit protein S3	DEG10160306|DEG10190223|DEG10320283|DEG10330310		Escherichia coli MG1655 II	
rplP	b3313	COG0197J,COG0197J	50S ribosomal subunit protein L16	DEG10190222		Escherichia coli MG1655 II	
rpmC	b3312	COG0255J,COG0255J	50S ribosomal subunit protein L29	DEG10190221		Escherichia coli MG1655 II	
rplE	b3308	COG0094J,COG0094J	50S ribosomal subunit protein L5	DEG10190217		Escherichia coli MG1655 II	
rpmD	b3302	COG1841J,COG1841J	50S ribosomal subunit protein L30	DEG10190211		Escherichia coli MG1655 II	
rpsK	b3297	COG0100J,COG0100J	30S ribosomal subunit protein S11	DEG10190207		Escherichia coli MG1655 II	
rpsD	b3296	COG0522J,COG0522J	30S ribosomal subunit protein S4	DEG10190206		Escherichia coli MG1655 II	
rpoA	b3295	COG0202K,COG0202K	RNA polymerase, alpha subunit	DEG10110177|DEG10160325|DEG10190205|DEG10320265|DEG10330329		Escherichia coli MG1655 II	
rplQ	b3294	COG0203J,COG0203J	50S ribosomal subunit protein L17	DEG10190204		Escherichia coli MG1655 II	
accC	b3256	COG0439I,COG0439I	acetyl-CoA carboxylase, biotin carboxylase subunit	DEG10190200		Escherichia coli MG1655 II	
accB	b3255	COG0511I,COG0511I	acetyl CoA carboxylase, BCCP subunit	DEG10190199		Escherichia coli MG1655 II	
rplM	b3231	COG0102J,COG0102J	50S ribosomal subunit protein L13	DEG10160237|DEG10180481|DEG10190194|DEG10320258|DEG10330240	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsI	b3230	COG0103J,COG0103J	30S ribosomal subunit protein S9	DEG10180480|DEG10190193	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
mlaB	b3191	COG3113R,COG3113R	ABC transporter maintaining OM lipid asymmetry, cytoplasmic STAS component	DEG10190190		Escherichia coli MG1655 II	
murA	b3189	COG0766M,COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	DEG10190189		Escherichia coli MG1655 II	
rplU	b3186	COG0261J,COG0261J	50S ribosomal subunit protein L21	DEG10190187		Escherichia coli MG1655 II	
rpmA	b3185	COG0211J,COG0211J	50S ribosomal subunit protein L27	DEG10190186		Escherichia coli MG1655 II	
eno	b2779	COG0148G,COG0148G	enolase	DEG10190165		Escherichia coli MG1655 II	
csrA	b2696	COG1551T,COG1551T	pleiotropic regulatory protein for carbon source metabolism	DEG10160187|DEG10190161|DEG10320223|DEG10330189		Escherichia coli MG1655 II	
ligA	b2411	COG0272L,COG0272L	DNA ligase, NAD(+)-dependent	DEG10180367|DEG10190139	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
gltX	b2400	COG0008J,COG0008J	glutamyl-tRNA synthetase	DEG10180366|DEG10190138	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
fabB	b2323	COG0304IQ,COG0304IQ	3-oxoacyl-[acyl-carrier-protein] synthase I	DEG10180363|DEG10190137	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
accD	b2316	COG0777I,COG0777I	acetyl-CoA carboxylase, beta (carboxyltransferase) subunit	DEG10190136		Escherichia coli MG1655 II	
folC	b2315	COG0285H,COG0285H	bifunctional folylpolyglutamate synthase/ dihydrofolate synthase	DEG10190135		Escherichia coli MG1655 II	

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nrdA	b2234	COG0209F,COG0209F	ribonucleoside-diphosphate reductase 1, alpha subunit	DEG10180353|DEG10190133	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
metG	b2114	COG0143J,COG0143J	methionyl-tRNA synthetase	DEG10180342|DEG10190129	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
pheS	b1714	COG0016J,COG0016J	phenylalanine tRNA synthetase, alpha subunit	DEG10190118		Escherichia coli MG1655 II	
pheT	b1713	COG0072J,COG0072J	phenylalanine tRNA synthetase, beta subunit	DEG10190117		Escherichia coli MG1655 II	
hemA	b1210	COG0373H,COG0373H	glutamyl tRNA reductase	DEG10190104		Escherichia coli MG1655 II	
purB	b1131	COG0015F,COG0015F	adenylosuccinate lyase	DEG10190096		Escherichia coli MG1655 II	
asnS	b0930	COG0017J,COG0017J	asparaginyl tRNA synthetase	DEG10180155|DEG10190083	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
msbA	b0914	COG1132V,COG1132V	fused lipid transporter subunits of ABC superfamily: membrane component/ATP-binding component	DEG10180148|DEG10190077	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsA	b0911	COG0539J,COG0539J	30S ribosomal subunit protein S1	DEG10190076		Escherichia coli MG1655 II	
cydC	b0886	COG4987CO,COG4987CO	fused glutathione, cysteine exporter subunits of ABC superfamily: membrane component/ATP-binding component	DEG10180143|DEG10190072	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
glnS	b0680	COG0008J,COG0008J	glutamyl-tRNA synthetase	DEG10180117|DEG10190068	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
leuS	b0642	COG0495J,COG0495J	leucyl-tRNA synthetase	DEG10180113|DEG10190066	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
nadD	b0639	COG1057H,COG1057H	nicotinic acid mononucleotide adenylyltransferase, NAD(P)-dependent	DEG10190063		Escherichia coli MG1655 II	
mrdA	b0635	COG0768M,COG0768M	transpeptidase involved in peptidoglycan synthesis (penicillin-binding protein 2)	DEG10180109|DEG10190062	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
folD	b0529	COG0190H,COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	DEG10190059		Escherichia coli MG1655 II	
dnaX	b0470	COG2812L,COG2812L	DNA polymerase III/DNA elongation factor III, tau and gamma subunits	DEG10180088|DEG10190054	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dxs	b0420	COG1154HI,COG1154HI	1-deoxyxylulose-5-phosphate synthase, thiamine triphosphate-binding, FAD-requiring	DEG10180080|DEG10190052	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murC	b0091	COG0773M,COG0773M	UDP-N-acetylmuramate:L-alanine ligase	DEG10180020|DEG10190015	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murG	b0090	COG0707M,COG0707M	N-acetylglucosaminyl transferase	DEG10180019|DEG10190014	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murD	b0088	COG0771M,COG0771M	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase	DEG10180017|DEG10190012	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
mraY	b0087	COG0472M,COG0472M	phospho-N-acetylmuramoyl-pentapeptide transferase	DEG10190011		Escherichia coli MG1655 II	
murF	b0086	COG0770M,COG0770M	UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase	DEG10190010		Escherichia coli MG1655 II	
valS	b4258	COG0525J,COG0525J	valyl-tRNA synthetase	DEG10180599|DEG10190293	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ppa	b4226	COG0221C,COG0221C	inorganic pyrophosphatase	DEG10180595|DEG10190292	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dnaB	b4052	COG0305L,COG0305L	replicative DNA helicase	DEG10180580|DEG10190283	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplL	b3986	COG0222J,COG0222J	50S ribosomal subunit protein L7/L12	DEG10180570|DEG10190277	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplJ	b3985	COG0244J,COG0244J	50S ribosomal subunit protein L10	DEG10180569|DEG10190276	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murI	b3967	COG0796M,COG0796M	glutamate racemase	DEG10180565|DEG10190271	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
hemG	b3850	COG4635CH,COG4635CH	protoporphyrin oxidase, flavoprotein	DEG10180558|DEG10190268	Escherichia coli MG1655 I	Escherichia coli MG1655 II	

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
hemC	b3805	COG0181H,COG0181H	hydroxymethylbilane synthase	DEG10180552|DEG10190264	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
hemD	b3804	COG1587H,COG1587H	uroporphyrinogen III synthase	DEG10180551|DEG10190263	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
glmU	b3730	COG1207M, COG1207M	fused N-acetyl glucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyl transferase	DEG10180546|DEG10190261	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
glmS	b3729	COG0449M, COG0449M	L-glutamine:D-fructose-6-phosphate aminotransferase	DEG10180545|DEG10190260	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dnaA	b3702	COG0593L,COG0593L	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator	DEG10180542|DEG10190255	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
gmk	b3648	COG0194F,COG0194F	guanylate kinase	DEG10180540|DEG10190251	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dut	b3640	COG0756F,COG0756F	deoxyuridinetriphosphatase	DEG10180539|DEG10190250	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dfp	b3639	COG0452H,COG0452H	fused 4'-phosphopantothenoylcysteine decarboxylase/phosphopantothenoylcysteine synthetase, FMN-binding	DEG10180538|DEG10190249	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
coaD	b3634	COG0669H,COG0669H	pantetheine-phosphate adenylyltransferase	DEG10180537|DEG10190247	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
glyQ	b3560	COG0752J,COG0752J	glycine tRNA synthetase, alpha subunit	DEG10180530|DEG10190243	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ftsY	b3464	COG0552U,COG0552U	Signal Recognition Particle (SRP) receptor	DEG10180523|DEG10190240	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ftsE	b3463	COG2884D,COG2884D	putative ABC superfamily transporter ATP-binding subunit	DEG10180522|DEG10190239	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
asd	b3433	COG0136E,COG0136E	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	DEG10180519|DEG10190236	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
trpS	b3384	COG0180J,COG0180J	tryptophanyl-tRNA synthetase	DEG10180516|DEG10190234	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsL	b3342	COG0048J,COG0048J	30S ribosomal subunit protein S12	DEG10160296|DEG10180510|DEG10190233|DEG10320293|DEG10330300	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsJ	b3321	COG0051J,COG0051J	30S ribosomal subunit protein S10	DEG10180507|DEG10190230	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplC	b3320	COG0087J,COG0087J	50S ribosomal subunit protein L3	DEG10180506|DEG10190229	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplD	b3319	COG0088J,COG0088J	50S ribosomal subunit protein L4	DEG10110188|DEG10160301|DEG10180505|DEG10190228|DEG10320288|DEG10330305	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplW	b3318	COG0089J,COG0089J	50S ribosomal subunit protein L23	DEG10180504|DEG10190227	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplB	b3317	COG0090J,COG0090J	50S ribosomal subunit protein L2	DEG10180503|DEG10190226	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsS	b3316	COG0185J,COG0185J	30S ribosomal subunit protein S19	DEG10180502|DEG10190225	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsQ	b3311	COG0186J,COG0186J	30S ribosomal subunit protein S17	DEG10180501|DEG10190220	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplN	b3310	COG0093J,COG0093J	50S ribosomal subunit protein L14	DEG10180500|DEG10190219	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplX	b3309	COG0198J,COG0198J	50S ribosomal subunit protein L24	DEG10180499|DEG10190218|DEG10320278	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsN	b3307	COG0199J,COG0199J	30S ribosomal subunit protein S14	DEG10180498|DEG10190216	Escherichia coli MG1655 I	Escherichia coli MG1655 II	

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
rpsH	b3306	COG0096J,COG0096J	30S ribosomal subunit protein S8	DEG10160314|DEG10180497|DEG10190215|DEG10320275|DEG10330318	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplF	b3305	COG0097J,COG0097J	50S ribosomal subunit protein L6	DEG10180496|DEG10190214	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplR	b3304	COG0256J,COG0256J	50S ribosomal subunit protein L18	DEG10180495|DEG10190213	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsE	b3303	COG0098J,COG0098J	30S ribosomal subunit protein S5	DEG10110183|DEG10160317|DEG10180494|DEG10190212|DEG10320272|DEG10330321	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplO	b3301	COG0200J,COG0200J	50S ribosomal subunit protein L15	DEG10180493|DEG10190210	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secY	b3300	COG0201U,COG0201U	preprotein translocase membrane subunit	DEG10180492|DEG10190209	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsM	b3298	COG0099J,COG0099J	30S ribosomal subunit protein S13	DEG10180491|DEG10190208	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
fmt	b3288	COG0223J,COG0223J	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	DEG10180489|DEG10190203	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispB	b3187	COG0142H,COG0142H	octaprenyl diphosphate synthase	DEG10180474|DEG10190188	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ribB	b3041	COG0108H,COG0108H	3,4-dihydroxy-2-butanone-4-phosphate synthase	DEG10180454|DEG10190176	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
plsC	b3018	COG0204I,COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase	DEG10180448|DEG10190173	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
metK	b2942	COG0192H,COG0192H	S-adenosylmethionine synthetase	DEG10180439|DEG10190171	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
pgk	b2926	COG0126G,COG0126G	phosphoglycerate kinase	DEG10180437|DEG10190170	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
fbaA	b2925	COG0191G,COG0191G	fructose-bisphosphate aldolase, class II	DEG10180436|DEG10190169	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
pyrG	b2780	COG0504F,COG0504F	CTP synthetase	DEG10180426|DEG10190166	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispD	b2747	COG1211I,COG1211I	4-diphosphocytidyl-2C-methyl-D-erythritol synthase	DEG10180424|DEG10190163	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispF	b2746	COG0245I,COG0245I	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	DEG10180423|DEG10190162	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
nadK	b2615	COG0061G,COG0061G	NAD kinase	DEG10180410|DEG10190160	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ffh	b2610	COG0541U,COG0541U	Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)	DEG10180407|DEG10190158	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsP	b2609	COG0228J,COG0228J	30S ribosomal subunit protein S16	DEG10180406|DEG10190157	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rplS	b2606	COG0335J,COG0335J	50S ribosomal subunit protein L19	DEG10180403|DEG10190155	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
lepB	b2568	COG0681U,COG0681U	leader peptidase (signal peptidase I)	DEG10180398|DEG10190151	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
acpS	b2563	COG0736I,COG0736I	holo-[acyl-carrier-protein] synthase 1	DEG10180394|DEG10190148	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
suhB	b2533	COG0483G,COG0483G	inositol monophosphatase	DEG10180389|DEG10190146	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispG	b2515	COG0821I,COG0821I	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	DEG10180382|DEG10190145	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
hisS	b2514	COG0124J,COG0124J	histidyl tRNA synthetase	DEG10180381|DEG10190144	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dapA	b2478	COG0329EM,COG0329EM	dihydrodipicolinate synthase	DEG10180377|DEG10190142	Escherichia coli MG1655 I	Escherichia coli MG1655 II	

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)
dapE	b2472	COG0624E,COG0624E	N-succinyl-diaminopimelate deacylase	DEG10180376|DEG10190141	Escherichia coli MG1655 I	Escherichia coli MG1655 II
nrdB	b2235	COG0208F,COG0208F	ribonucleoside-diphosphate reductase 1, beta subunit, ferritin-like protein	DEG10180354|DEG10190134	Escherichia coli MG1655 I	Escherichia coli MG1655 II
folE	b2153	COG0302H,COG0302H	GTP cyclohydrolase I	DEG10180344|DEG10190130	Escherichia coli MG1655 I	Escherichia coli MG1655 II
pgsA	b1912	COG0558I,COG0558I	phosphatidylglycerophosphate synthetase	DEG10180325|DEG10190127	Escherichia coli MG1655 I	Escherichia coli MG1655 II
argS	b1876	COG0018J,COG0018J	arginyl-tRNA synthetase	DEG10180318|DEG10190126	Escherichia coli MG1655 I	Escherichia coli MG1655 II
aspS	b1866	COG0173J,COG0173J	aspartyl-tRNA synthetase	DEG10180315|DEG10190125	Escherichia coli MG1655 I	Escherichia coli MG1655 II
gapA	b1779	COG0057G,COG0057G	glyceraldehyde-3-phosphate dehydrogenase A	DEG10180303|DEG10190123	Escherichia coli MG1655 I	Escherichia coli MG1655 II
nadE	b1740	COG0171H,COG0171H	NAD synthetase, NH3/glutamine-dependent	DEG10180294|DEG10190122	Escherichia coli MG1655 I	Escherichia coli MG1655 II
thrS	b1719	COG0441J,COG0441J	threonyl-tRNA synthetase	DEG10180289|DEG10190121	Escherichia coli MG1655 I	Escherichia coli MG1655 II
rplT	b1716	COG0292J,COG0292J	50S ribosomal subunit protein L20	DEG10160096|DEG10180287|DEG10190119|DEG10320130|DEG10330098	Escherichia coli MG1655 I	Escherichia coli MG1655 II
ribC	b1662	COG0307H,COG0307H	riboflavin synthase, alpha subunit	DEG10180277|DEG10190115	Escherichia coli MG1655 I	Escherichia coli MG1655 II
tyrS	b1637	COG0162J,COG0162J	tyrosyl-tRNA synthetase	DEG10180273|DEG10190114	Escherichia coli MG1655 I	Escherichia coli MG1655 II
fabI	b1288	COG0623I,COG0623I	enoyl-[acyl-carrier-protein] reductase, NADH-dependent	DEG10180225|DEG10190110	Escherichia coli MG1655 I	Escherichia coli MG1655 II
ribA	b1277	COG0807H,COG0807H	GTP cyclohydrolase II	DEG10180222|DEG10190109	Escherichia coli MG1655 I	Escherichia coli MG1655 II
ispE	b1208	COG1947I,COG1947I	4-diphosphocytidyl-2-C-methylerythritol kinase	DEG10180205|DEG10190102	Escherichia coli MG1655 I	Escherichia coli MG1655 II
prs	b1207	COG0462FE,COG0462FE	phosphoribosylpyrophosphate synthase	DEG10180204|DEG10190101	Escherichia coli MG1655 I	Escherichia coli MG1655 II
lolE	b1118	COG4591M,COG4591M	lipoprotein-releasing system transmembrane protein	DEG10180186|DEG10190095	Escherichia coli MG1655 I	Escherichia coli MG1655 II
lolC	b1116	COG4591M,COG4591M	lipoprotein-releasing system transmembrane protein	DEG10180184|DEG10190093	Escherichia coli MG1655 I	Escherichia coli MG1655 II
holB	b1099	COG0470L,COG0470L	DNA polymerase III, delta prime subunit	DEG10180182|DEG10190092	Escherichia coli MG1655 I	Escherichia coli MG1655 II
tmk	b1098	COG0125F,COG0125F	thymidylate kinase	DEG10180181|DEG10190091	Escherichia coli MG1655 I	Escherichia coli MG1655 II
fabG	b1093	COG1028IQR,COG1028IQR	3-oxoacyl-[acyl-carrier-protein] reductase	DEG10180180|DEG10190089	Escherichia coli MG1655 I	Escherichia coli MG1655 II
fabD	b1092	COG0331I,COG0331I	malonyl-CoA-[acyl-carrier-protein] transacylase	DEG10180179|DEG10190088	Escherichia coli MG1655 I	Escherichia coli MG1655 II
rne	b1084	COG1530J,COG1530J	fused ribonucleaseE: endoribonuclease/RNA-binding protein/RNA degradosome binding protein	DEG10180176|DEG10190086	Escherichia coli MG1655 I	Escherichia coli MG1655 II
murJ	b1069	COG0728R,COG0728R	putative peptidoglycan lipid II flippase	DEG10180175|DEG10190085	Escherichia coli MG1655 I	Escherichia coli MG1655 II
fabA	b0954	COG0764I,COG0764I	beta-hydroxydecanoyl thioester dehydrase	DEG10180156|DEG10190084	Escherichia coli MG1655 I	Escherichia coli MG1655 II
serS	b0893	COG0172J,COG0172J	seryl-tRNA synthetase, also charges selenocysteinyl-tRNA with serine	DEG10180145|DEG10190075	Escherichia coli MG1655 I	Escherichia coli MG1655 II
cydA	b0733	COG1271C,COG1271C	cytochrome d terminal oxidase, subunit I	DEG10180126|DEG10190070	Escherichia coli MG1655 I	Escherichia coli MG1655 II
holA	b0640	COG1466L,COG1466L	DNA polymerase III, delta subunit	DEG10180111|DEG10190064	Escherichia coli MG1655 I	Escherichia coli MG1655 II
cysS	b0526	COG0215J,COG0215J	cysteinyl-tRNA synthetase	DEG10180099|DEG10190058	Escherichia coli MG1655 I	Escherichia coli MG1655 II
hemH	b0475	COG0276H,COG0276H	ferrochelatase	DEG10180090|DEG10190056	Escherichia coli MG1655 I	Escherichia coli MG1655 II
adk	b0474	COG0563F,COG0563F	adenylate kinase	DEG10180089|DEG10190055	Escherichia coli MG1655 I	Escherichia coli MG1655 II
ispA	b0421	COG0142H,COG0142H	geranyltranstransferase	DEG10180081|DEG10190053	Escherichia coli MG1655 I	Escherichia coli MG1655 II

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
thiL	b0417	COG0611H,COG0611H	thiamine monophosphate kinase	DEG10180078|DEG10190051	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ribE	b0415	COG0054H,COG0054H	riboflavin synthase beta chain	DEG10180076|DEG10190050	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ribD	b0414	COG0117H,COG0117H	fused diaminohydroxyphosphoribosylaminopyrimidine deaminase and 5-amino-6-(5-phosphoribosylamino) uracil reductase	DEG10180075|DEG10190049	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secF	b0409	COG0341U,COG0341U	SecYEG protein translocase auxillary subunit	DEG10180074|DEG10190048	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secD	b0408	COG0342U,COG0342U	SecYEG protein translocase auxillary subunit	DEG10180073|DEG10190047	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
hemB	b0369	COG0113H,COG0113H	5-aminolevulinate dehydratase (porphobilinogen synthase)	DEG10180069|DEG10190046	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
proS	b0194	COG0442J,COG0442J	prolyl-tRNA synthetase	DEG10180054|DEG10190044	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
accA	b0185	COG0825I,COG0825I	acetyl-CoA carboxylase, carboxytransferase, alpha subunit	DEG10180052|DEG10190042	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dnaE	b0184	COG0587L,COG0587L	DNA polymerase III alpha subunit	DEG10180051|DEG10190041	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
fabZ	b0180	COG0764I,COG0764I	(3R)-hydroxymyristol acyl carrier protein dehydratase	DEG10180047|DEG10190038	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
cdsA	b0175	COG0575I,COG0575I	CDP-diglyceride synthase	DEG10180045|DEG10190034	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispU	b0174	COG0020I,COG0020I	undecaprenyl pyrophosphate synthase	DEG10180044|DEG10190033	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dxr	b0173	COG0743I,COG0743I	1-deoxy-D-xylulose 5-phosphate reductoisomerase	DEG10180043|DEG10190032	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
pyrH	b0171	COG0528F,COG0528F	uridylate kinase	DEG10180041|DEG10190030	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
rpsB	b0169	COG0052J,COG0052J	30S ribosomal subunit protein S2	DEG10180039|DEG10190028	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dapD	b0166	COG2171E,COG2171E	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	DEG10180036|DEG10190026	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
hemL	b0154	COG0001H,COG0001H	glutamate-1-semialdehyde aminotransferase (aminomutase)	DEG10180034|DEG10190024	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
folK	b0142	COG0801H,COG0801H	2-amino-4-hydroxy-6-hydroxymethyldihyropteridine pyrophosphokinase	DEG10180033|DEG10190023	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
can	b0126	COG0288P,COG0288P	carbonic anhydrase	DEG10180031|DEG10190022	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secA	b0098	COG0653U,COG0653U	preprotein translocase subunit, ATPase	DEG10180026|DEG10190021	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
secM	b0097	-	regulator of secA translation	DEG10180025|DEG10190020	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
murE	b0085	COG0769M,COG0769M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase	DEG10180016|DEG10190009	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ftsI	b0084	COG0768M,COG0768M	transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3)	DEG10180015|DEG10190008	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
folA	b0048	COG0262H,COG0262H	dihydrofolate reductase	DEG10180010|DEG10190005	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dapB	b0031	COG0289E,COG0289E	dihydrodipicolinate reductase	DEG10180009|DEG10190004	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ispH	b0029	COG0761IM,COG0761IM	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 4Fe-4S protein	DEG10180008|DEG10190003	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
lspA	b0027	COG0597MU,COG0597MU	prolipoprotein signal peptidase (signal peptidase II)	DEG10180007|DEG10190002	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
ribF	b0025	COG0196H,COG0196H	bifunctional riboflavin kinase/FAD synthetase	DEG10180005|DEG10190001	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
yagG	b0270	COG2211G,COG2211G	CP4-6 prophage; putative sugar transporter	DEG10180060|DEG10190045	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
cohE	b1145	COG1974KT,COG1974KT	e14 prophage; repressor protein phage e14	DEG10180194|DEG10190097	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
minD	b1175	COG2894D,COG2894D	membrane ATPase of the MinC-MinD-MinE system	DEG10180197|DEG10190099	Escherichia coli MG1655 I	Escherichia coli MG1655 II	
dicA	b1570	COG1396K,COG1396K	Qin prophage; putative regulator for DicB	DEG10180263|DEG10190112	Escherichia coli MG1655 I	Escherichia coli MG1655 II	

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
erpA	b0156	COG0316S,COG0316S	iron-sulfur cluster insertion protein	DEG10190025		Escherichia coli MG1655 II	
rseP	b0176	COG0750M, COG0750M	inner membrane zinc RIP metalloprotease; RpoE activator, by degrading RseA; cleaved signal peptide endoprotease	DEG10190035		Escherichia coli MG1655 II	
entD	b0583	COG2977Q, COG2977Q	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex	DEG10190060		Escherichia coli MG1655 II	
lnt	b0657	COG0815M, COG0815M	apolipoprotein N-acyltransferase	DEG10190067		Escherichia coli MG1655 II	
yejM	b2188	COG3083R,COG3083R	essential inner membrane DUF3413 domain-containing protein; lipid A production and membrane permeability factor	DEG10190131		Escherichia coli MG1655 II	
bamD	b2595	COG4105R,COG4105R	BamABCDE complex OM biogenesis lipoprotein	DEG10190154		Escherichia coli MG1655 II	
rsmI	b3146	COG0313R,COG0313R	16S rRNA C1402 2'-O-ribose methyltransferase, SAM-dependent	DEG10190180		Escherichia coli MG1655 II	
yhbV	b3159	COG0826O, COG0826O	U32 peptidase family protein	DEG10190181		Escherichia coli MG1655 II	
nusA	b3169	COG0195K,COG0195K	transcription termination/antitermination L factor	DEG10190183		Escherichia coli MG1655 II	
ftsH	b3178	COG0465O, COG0465O	protease, ATP-dependent zinc-metallo	DEG10190184		Escherichia coli MG1655 II	
lptC	b3199	COG3117S,COG3117S	lipopolysaccharide export, IM-tethered periplasmic protein of the LptBFGC export complex	DEG10190191		Escherichia coli MG1655 II	
degS	b3235	COG0265O, COG0265O	serine endoprotease, periplasmic	DEG10190195		Escherichia coli MG1655 II	
yhhQ	b3471	COG1738S,COG1738S	DUF165 family inner membrane protein	DEG10190241		Escherichia coli MG1655 II	
rnpA	b3704	COG0594J,COG0594J	protein C5 component of RNase P	DEG10190257		Escherichia coli MG1655 II	
tnaB	b3709	COG0814E,COG0814E	tryptophan transporter of low affinity	DEG10190259		Escherichia coli MG1655 II	
ubiJ	b3834	COG3165S,COG3165S	aerobic ubiquinone synthesis protein, SCP2 family protein	DEG10190265		Escherichia coli MG1655 II	
nusG	b3982	COG0250K,COG0250K	transcription termination factor	DEG10190275		Escherichia coli MG1655 II	
lptG	b4262	COG0795R,COG0795R	lipopolysaccharide export ABC permease of the LptBFGC export complex	DEG10180602| DEG10190295	Escherichia coli MG1655 I		
lplA	b4386	COG0095H,COG0095H	lipoate-protein ligase A	DEG10180609	Escherichia coli MG1655 I		
dnaT	b4362	COG5529R,COG5529R	DNA biosynthesis protein (primosomal protein I)	DEG10180606	Escherichia coli MG1655 I		
sgcB	b4565	COG3414G,COG3414G	putative enzyme IIB component of PTS	DEG10180604	Escherichia coli MG1655 I		
sgcA	b4302	COG1762GT, COG1762GT	putative phosphotransferase enzyme IIA component	DEG10180603	Escherichia coli MG1655 I		
holC	b4259	COG2927L,COG2927L	DNA polymerase III, chi subunit	DEG10180600	Escherichia coli MG1655 I		
priB	b4201	COG2965L,COG2965L	primosomal protein N	DEG10180592	Escherichia coli MG1655 I		
rpsF	b4200	COG0360J,COG0360J	30S ribosomal subunit protein S6	DEG10180591	Escherichia coli MG1655 I		
hfq	b4172	COG1923R,COG1923R	global sRNA chaperone; HF-I, host factor for RNA phage Q beta replication	DEG10180590	Escherichia coli MG1655 I		
epmA	b4155	COG2269J,COG2269J	Elongation Factor P Lys34 lysyltransferase	DEG10180586	Escherichia coli MG1655 I		
groL	b4143	COG0459O, COG0459O	Cpn60 chaperonin GroEL, large subunit of GroESL	DEG10180584	Escherichia coli MG1655 I		
tyrB	b4054	COG1448E,COG1448E	tyrosine aminotransferase, tyrosine-repressible, PLP-dependent	DEG10180581	Escherichia coli MG1655 I		
zraP	b4002	COG3678UNTP,COG3678UNTP	Zn-dependent periplasmic chaperone	DEG10180575	Escherichia coli MG1655 I		
hemE	b3997	COG0407H,COG0407H	uroporphyrinogen decarboxylase	DEG10180574	Escherichia coli MG1655 I		
coaA	b3974	COG1072H,COG1072H	pantothenate kinase	DEG10180567	Escherichia coli MG1655 I		

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
argC	b3958	COG0002E,COG0002E	N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding	DEG10180564	Escherichia coli MG1655 I		
priA	b3935	COG1198L,COG1198L	Primosome factor n' (replication factor Y)	DEG10180563	Escherichia coli MG1655 I		
rhaD	b3902	COG0235G,COG0235G	rhamnulose-1-phosphate aldolase	DEG10180561	Escherichia coli MG1655 I		
ubiE	b3833	COG2226H,COG2226H	bifunctional 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase/ S-adenosylmethionine:2-DMK methyltransferase	DEG10180556	Escherichia coli MG1655 I		
dapF	b3809	COG0253E,COG0253E	diaminopimelate epimerase	DEG10180553	Escherichia coli MG1655 I		
atpF	b3736	COG0711C,COG0711C	F0 sector of membrane-bound ATP synthase, subunit b	DEG10180548	Escherichia coli MG1655 I		
atpC	b3731	COG0355C,COG0355C	F1 sector of membrane-bound ATP synthase, epsilon subunit	DEG10180547	Escherichia coli MG1655 I		
secB	b3609	COG1952U,COG1952U	protein export chaperone	DEG10180534	Escherichia coli MG1655 I		
cysE	b3607	COG1045E,COG1045E	serine acetyltransferase	DEG10180533	Escherichia coli MG1655 I		
glyS	b3559	COG0751J,COG0751J	glycine tRNA synthetase, beta subunit	DEG10180529	Escherichia coli MG1655 I		
gor	b3500	COG1249C,COG1249C	glutathione oxidoreductase	DEG10180527	Escherichia coli MG1655 I		
aroK	b3390	COG0703E,COG0703E	shikimate kinase I	DEG10180518	Escherichia coli MG1655 I		
rpe	b3386	COG0036G,COG0036G	D-ribulose-5-phosphate 3-epimerase	DEG10180517	Escherichia coli MG1655 I		
tusD	b3345	COG1553P,COG1553P	sulfurtransferase for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis	DEG10180513	Escherichia coli MG1655 I		
tusC	b3344	COG2923P,COG2923P	mnm(5)-s(2)U34-tRNA synthesis 2-thiolation protein	DEG10180512	Escherichia coli MG1655 I		
tusB	b3343	COG2168P,COG2168P	mnm(5)-s(2)U34-tRNA synthesis 2-thiolation protein	DEG10180511	Escherichia coli MG1655 I		
ptsN	b3204	COG1762GT, COG1762GT	sugar-specific enzyme IIA component of PTS	DEG10180477	Escherichia coli MG1655 I		
rpoN	b3202	COG1508K,COG1508K	RNA polymerase, sigma 54 (sigma N) factor	DEG10180476	Escherichia coli MG1655 I		
lptB	b3201	COG1137R,COG1137R	lipopolysaccharide export ABC transporter ATP-binding protein of the LptBFGC export complex	DEG10180475	Escherichia coli MG1655 I		
rpsO	b3165	COG0184J,COG0184J	30S ribosomal subunit protein S15	DEG10180470	Escherichia coli MG1655 I		
pnp	b3164	COG1185J,COG1185J	polynucleotide phosphorylase/polyadenylase	DEG10180469	Escherichia coli MG1655 I		
agaV	b3133	COG3444G,COG3444G	N-acetylgalactosamine-specific enzyme IIB component of PTS	DEG10180464	Escherichia coli MG1655 I		
tdcG	b4471	COG1760E,COG1760E	L-serine dehydratase 3, anaerobic	DEG10180462	Escherichia coli MG1655 I		
dnaG	b3066	COG0358L,COG0358L	DNA primase	DEG10180456	Escherichia coli MG1655 I		
ansB	b2957	COG0252EJ, COG0252EJ	periplasmic L-asparaginase 2	DEG10180443	Escherichia coli MG1655 I		
gshB	b2947	COG0189HJ, COG0189HJ	glutathione synthetase	DEG10180440	Escherichia coli MG1655 I		
tktA	b2935	COG0021G,COG0021G	transketolase 1, thiamine triphosphate-binding	DEG10180438	Escherichia coli MG1655 I		
ubiH	b2907	COG0654HC, COG0654HC	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding	DEG10180433	Escherichia coli MG1655 I		
ygfM	b2880	COG1319C,COG1319C	putative oxidoreductase	DEG10180430	Escherichia coli MG1655 I		
thyA	b2827	COG0207F,COG0207F	thymidylate synthetase	DEG10180428	Escherichia coli MG1655 I		
alaS	b2697	COG0013J,COG0013J	alanyl-tRNA synthetase	DEG10180418	Escherichia coli MG1655 I		
pssA	b2585	COG1502I,COG1502I	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)	DEG10180401|DEG10190153	Escherichia coli MG1655 I		

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
pdxJ	b2564	COG0854H,COG0854H	pyridoxine 5'-phosphate synthase	DEG10180395	Escherichia coli MG1655 I		
glyA	b2551	COG0112E,COG0112E	serine hydroxymethyltransferase	DEG10180392	Escherichia coli MG1655 I		
iscS	b2530	COG1104E,COG1104E	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent	DEG10180388	Escherichia coli MG1655 I		
ndk	b2518	COG0105F,COG0105F	multifunctional nucleoside diphosphate kinase and apyrimidinic endonuclease and 3'-phosphodiesterase	DEG10180383	Escherichia coli MG1655 I		
cysW	b2423	COG4208P,COG4208P	sulfate/thiosulfate ABC transporter subunit	DEG10180369	Escherichia coli MG1655 I		
ubiX	b2311	COG0163H,COG0163H	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	DEG10180361	Escherichia coli MG1655 I		
ackA	b2296	COG0282C,COG0282C	acetate kinase A and propionate kinase 2	DEG10180359	Escherichia coli MG1655 I		
menE	b2260	COG0318IQ, COG0318IQ	O-succinylbenzoate-CoA ligase	DEG10180357	Escherichia coli MG1655 I		
ubiG	b2232	COG2227H,COG2227H	bifunctional 3-demethylubiquinone-9 3-methyltransferase/ 2-octaprenyl-6-hydroxy phenol methylase	DEG10180352	Escherichia coli MG1655 I		
rplY	b2185	COG1825J,COG1825J	50S ribosomal subunit protein L25	DEG10180349	Escherichia coli MG1655 I		
yejE	b2179	COG4239R,COG4239R	microcin C transporter YejABEF, permease subunit; ABC family	DEG10180348	Escherichia coli MG1655 I		
mglB	b2150	COG1879G,COG1879G	methyl-galactoside transporter subunit	DEG10180343	Escherichia coli MG1655 I		
gatD	b2091	COG1063ER, COG1063ER	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding	DEG10180338	Escherichia coli MG1655 I		
wcaN	b2042	COG1210M, COG1210M	putative regulatory subunit for GalU	DEG10180334	Escherichia coli MG1655 I		
dcm	b1961	COG0270L,COG0270L	DNA cytosine methyltransferase	DEG10180330	Escherichia coli MG1655 I		
araF	b1901	COG1879G,COG1879G	L-arabinose transporter subunit	DEG10180324	Escherichia coli MG1655 I		
araG	b1900	COG1129G,COG1129G	fused L-arabinose transporter subunits of ABC superfamily: ATP-binding components	DEG10180323	Escherichia coli MG1655 I		
motA	b1890	COG1291N, COG1291N	proton conductor component of flagella motor	DEG10180321	Escherichia coli MG1655 I		
cheW	b1887	COG0835NT, COG0835NT	purine-binding chemotaxis protein	DEG10180320	Escherichia coli MG1655 I		
cheR	b1884	COG1352NT, COG1352NT	chemotaxis regulator, protein-glutamate methyltransferase	DEG10180319	Escherichia coli MG1655 I		
ruvC	b1863	COG0817L,COG0817L	component of RuvABC resolvasome, endonuclease	DEG10180312	Escherichia coli MG1655 I		
zwf	b1852	COG0364G,COG0364G	glucose-6-phosphate 1-dehydrogenase	DEG10180311	Escherichia coli MG1655 I		
selD	b1764	COG0709E,COG0709E	selenophosphate synthase	DEG10180301	Escherichia coli MG1655 I		
astA	b1747	COG3138E,COG3138E	arginine succinyltransferase	DEG10180298	Escherichia coli MG1655 I		
astB	b1745	COG3724E,COG3724E	succinylarginine dihydrolase	DEG10180297	Escherichia coli MG1655 I		
chbB	b1738	COG1440G,COG1440G	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	DEG10180293	Escherichia coli MG1655 I		
chbA	b1736	COG1447G,COG1447G	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS	DEG10180292	Escherichia coli MG1655 I		
btuE	b1710	COG0386O, COG0386O	glutathione peroxidase	DEG10180286	Escherichia coli MG1655 I		
aroH	b1704	COG0722E,COG0722E	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible	DEG10180285	Escherichia coli MG1655 I		
rstB	b1609	COG0642T,COG0642T	sensory histidine kinase of RstAB two-component system, low Mg-responsive via PhoQP	DEG10180268	Escherichia coli MG1655 I		
mnaT	b1448	COG1247M, COG1247M	methionine N-acyltransferase; L-amino acid N-acyltransferase	DEG10180250	Escherichia coli MG1655 I		
trg	b1421	COG0840NT, COG0840NT	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor	DEG10180242	Escherichia coli MG1655 I		

Gene	Synonym	COG	Product	DEG Pxu	Experiment 1 (Baba)	Experiment 2 (Gerdes)	predicted EG
pyrF	b1281	COG0284F,COG0284F	orotidine-5'-phosphate decarboxylase	DEG10180224	Escherichia coli MG1655 I		
btuR	b1270	COG2109H,COG2109H	cob(I)yrinic acid a,c-diamide adenosyltransferase	DEG10180219	Escherichia coli MG1655 I		
yciA	b1253	COG1607I,COG1607I	acyl-CoA esterase	DEG10180216	Escherichia coli MG1655 I		
oppD	b1246	COG0444EP,COG0444EP	oligopeptide transporter subunit	DEG10180214	Escherichia coli MG1655 I		
oppC	b1245	COG1173EP,COG1173EP	oligopeptide transporter subunit	DEG10180213	Escherichia coli MG1655 I		
tdk	b1238	COG1435F,COG1435F	thymidine kinase/deoxyuridine kinase	DEG10180212	Escherichia coli MG1655 I		
galU	b1236	COG1210M,COG1210M	glucose-1-phosphate uridylyltransferase	DEG10180210	Escherichia coli MG1655 I		
purU	b1232	COG0788F,COG0788F	formyltetrahydrofolate hydrolase	DEG10180208	Escherichia coli MG1655 I		
dhaL	b1199	COG2376G,COG2376G	dihydroxyacetone kinase, C-terminal domain	DEG10180200	Escherichia coli MG1655 I		
mnmA	b1133	COG0482J,COG0482J	tRNA(Gln,Lys,Glu) U34 2-thiouridylase, first step in mnm(5)-s(2)U34-tRNA synthesis	DEG10180190	Escherichia coli MG1655 I		
potC	b1124	COG1177E,COG1177E	polyamine transporter subunit	DEG10180188	Escherichia coli MG1655 I		
potD	b1123	COG0687E,COG0687E	polyamine transporter subunit	DEG10180187	Escherichia coli MG1655 I		
lolD	b1117	COG1136V,COG1136V	outer membrane-specific lipoprotein transporter subunit	DEG10180185|DEG10190094	Escherichia coli MG1655 I		
fabH	b1091	COG0332I,COG0332I	3-oxoacyl-[acyl-carrier-protein] synthase III	DEG10180178	Escherichia coli MG1655 I		
ghrA	b1033	COG0111HE,COG0111HE	glyoxylate/hydroxypyruvate reductase A	DEG10180170	Escherichia coli MG1655 I		
rutB	b1011	COG1335Q,COG1335Q	ureidoacrylate amidohydrolase	DEG10180168	Escherichia coli MG1655 I		
rutC	b1010	COG0251J,COG0251J	putative aminoacrylate deaminase, reactive intermediate detoxification; weak enamine/imine deaminase activity	DEG10180167	Escherichia coli MG1655 I		
torD	b0998	COG3381R,COG3381R	TorA-maturation chaperone	DEG10180165	Escherichia coli MG1655 I		
torR	b0995	COG0745TK,COG0745TK	response regulator in two-component regulatory system with TorS	DEG10180164	Escherichia coli MG1655 I		
mgsA	b0963	COG1803G,COG1803G	methylglyoxal synthase	DEG10180157	Escherichia coli MG1655 I		
cmk	b0910	COG0283F,COG0283F	cytidylate kinase	DEG10180147	Escherichia coli MG1655 I		
cydD	b0887	COG4988CO,COG4988CO	fused glutathione, cysteine exporter subunits of ABC superfamily: membrane component/ATP-binding component	DEG10180144	Escherichia coli MG1655 I		
glnP	b0810	COG0765E,COG0765E	glutamine transporter subunit	DEG10180133	Escherichia coli MG1655 I		
cydB	b0734	COG1294C,COG1294C	cytochrome d terminal oxidase, subunit II	DEG10180127	Escherichia coli MG1655 I		
sucB	b0727	COG0508C,COG0508C	dihydrolipoyltranssuccinase	DEG10180125	Escherichia coli MG1655 I		
sucA	b0726	COG0567C,COG0567C	2-oxoglutarate decarboxylase, thiamine triphosphate-binding	DEG10180124	Escherichia coli MG1655 I		
gltK	b0653	COG0765E,COG0765E	glutamate, aspartate ABC transporter permease subunit	DEG10180115	Escherichia coli MG1655 I		
gltL	b0652	COG1126E,COG1126E	glutamate, aspartate ABC transporter ATP-binding subunit	DEG10180114	Escherichia coli MG1655 I		
fepB	b0592	COG4592P,COG4592P	iron-enterobactin transporter subunit	DEG10180106	Escherichia coli MG1655 I		
appY	b0564	COG2207K,COG2207K	global transcriptional activator; DLP12 prophage	DEG10180105	Escherichia coli MG1655 I		
ybcF	b0521	COG0549E,COG0549E	putative carbonate kinase	DEG10180096	Escherichia coli MG1655 I		
allA	b0505	COG3194F,COG3194F	ureidoglycolate lyase, releasing urea	DEG10180094	Escherichia coli MG1655 I		

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
rnpA	COG0594J	ribonuclease P	DEG10100614	Rv3923c		Mycobacterium tuberculosis H37Rv
Rv3921c	COG0706U	putative inner membrane protein translocase component YidC	DEG10100613	Rv3921c	Rv3921c	Mycobacterium tuberculosis H37Rv
parB	COG1192D	PROBABLE CHROMOSOME PARTITIONING PROTEIN PARA	DEG10100612	Rv3918c		Mycobacterium tuberculosis H37Rv
parA	COG1475K	PROBABLE CHROMOSOME PARTITIONING PROTEIN PARB	DEG10100611	Rv3917c		Mycobacterium tuberculosis H37Rv
cwlM	COG0860M, COG3409M	PROBABLE HYDROLASE	DEG10100610	Rv3915		Mycobacterium tuberculosis H37Rv
trxB2	COG0492O	PROBABLE THIOREDOXIN REDUCTASE TRXB2 (TRXR) (TR)	DEG10100609	Rv3913	Rv3913	Mycobacterium tuberculosis H37Rv
pcnA	COG0617J	PROBABLE POLY(A) POLYMERASE PCNA (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (NTP POLYMERASE) (RNA ADENYLATING ENZYME) (POLY(A) POLYMERASE)	DEG10100608	Rv3907c	Rv3907c	Mycobacterium tuberculosis H37Rv
gltB	COG0067E,COG0069E,COG0070E	PROBABLE FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE [NADPH] (LARGE SUBUNIT) GLTB (L-GLUTAMATE SYNTHASE) (L-GLUTAMATE SYNTHETASE) (NADH-GLUTAMATE SYNTHASE) (GLUTAMATE SYNTHASE (NADH))(NADPH-GOGAT)	DEG10100607	Rv3859c	Rv3859c	Mycobacterium tuberculosis H37Rv
gltD	COG0493ER	glutamate synthase subunit beta	DEG10100606	Rv3858c	Rv3858c	Mycobacterium tuberculosis H37Rv
serS	COG0172J	seryl-tRNA synthetase	DEG10100605	Rv3834c	Rv3834c	Mycobacterium tuberculosis H37Rv
glfT	COG1216R	BIFUNCTIONAL UDP-GALACTOFURANOSYL TRANSFERASE GLFT	DEG10100604	Rv3808c	Rv3808c	Mycobacterium tuberculosis H37Rv
Rv3806c	COG0382H	phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase	DEG10100603	Rv3806c	Rv3806c	Mycobacterium tuberculosis H37Rv
Rv3805c	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100602	Rv3805c		Mycobacterium tuberculosis H37Rv
Rv3802c	-	PROBABLE CONSERVED MEMBRANE PROTEIN	DEG10100601	Rv3802c		Mycobacterium tuberculosis H37Rv
fadD32	COG0318IQ	acyl-CoA synthetase	DEG10100600	Rv3801c	Rv3801c	Mycobacterium tuberculosis H37Rv
pks13	COG3319Q,COG3321Q	POLYKETIDE SYNTHASE PKS13	DEG10100599	Rv3800c	Rv3800c	Mycobacterium tuberculosis H37Rv
accD4	COG4799I	PROBABLE PROPIONYL-CoA CARBOXYLASE BETA CHAIN 4 ACCD4 (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE)	DEG10100598	Rv3799c		Mycobacterium tuberculosis H37Rv
embB	-	INTEGRAL MEMBRANE INDOLYLACETYLINOSITOL ARABINOSYLTRANSFERASE EMBB (ARABINOSYLINDOLYLACETYLINOSITOL SYNTHASE)	DEG10100597	Rv3795		Mycobacterium tuberculosis H37Rv
embC	-	INTEGRAL MEMBRANE INDOLYLACETYLINOSITOL ARABINOSYLTRANSFERASE EMBC (ARABINOSYLINDOLYLACETYLINOSITOL SYNTHASE)	DEG10100596	Rv3793		Mycobacterium tuberculosis H37Rv
Rv3792	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100595	Rv3792		Mycobacterium tuberculosis H37Rv
Rv3791	COG1028IQR	short chain dehydrogenase	DEG10100594	Rv3791		Mycobacterium tuberculosis H37Rv
Rv3790	COG0277C	PROBABLE OXIDOREDUCTASE	DEG10100593	Rv3790		Mycobacterium tuberculosis H37Rv
rfbE	COG1216R	POSSIBLE L-RHAMNOSYLTRANSFERASE	DEG10100592	Rv3782		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
rfbE	COG1134GM	PROBABLE O-ANTIGEN/LIPOPOLYSACCHARIDE TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER RFBE	DEG10100591	Rv3781		Mycobacterium tuberculosis H37Rv
Rv3778c	COG0520E	POSSIBLE AMINOTRANSFERASE	DEG10100590	Rv3778c		Mycobacterium tuberculosis H37Rv
Rv3752c	COG0590FJ	POSSIBLE CYTIDINE/DEOXYCYTIDYLATE DEAMINASE	DEG10100589	Rv3752c		Mycobacterium tuberculosis H37Rv
Rv3722c	COG1167KE	hypothetical protein	DEG10100588	Rv3722c		Mycobacterium tuberculosis H37Rv
dnaZX	COG2812L	DNA polymerase III subunits gamma and tau	DEG10100587	Rv3721c	Rv3721c	Mycobacterium tuberculosis H37Rv
cobQ2	COG3442R	POSSIBLE COBYRIC ACID SYNTHASE COBQ2	DEG10100586	Rv3713		Mycobacterium tuberculosis H37Rv
Rv3712	COG0769M	POSSIBLE LIGASE	DEG10100585	Rv3712		Mycobacterium tuberculosis H37Rv
leuA	COG0119E	2-isopropylmalate synthase	DEG10100584	Rv3710	Rv3710	Mycobacterium tuberculosis H37Rv
ask	COG0527E	aspartate kinase	DEG10100583	Rv3709c	Rv3709c	Mycobacterium tuberculosis H37Rv
asd	COG0136E	aspartate-semialdehyde dehydrogenase	DEG10100582	Rv3708c	Rv3708c	Mycobacterium tuberculosis H37Rv
Rv3679	COG0003P	PROBABLE ANION TRANSPORTER ATPASE	DEG10100581	Rv3679		Mycobacterium tuberculosis H37Rv
Rv3669	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100580	Rv3669		Mycobacterium tuberculosis H37Rv
dppA	COG4166E	PROBABLE PERIPLASMIC DIPEPTIDE-BINDING LIPOPROTEIN DPPA	DEG10100579	Rv3666c	Rv3666c	Mycobacterium tuberculosis H37Rv
Rv3660c	-	hypothetical protein	DEG10100578	Rv3660c		Mycobacterium tuberculosis H37Rv
Rv3658c	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100577	Rv3658c		Mycobacterium tuberculosis H37Rv
cspA	COG1278K	PROBABLE COLD SHOCK PROTEIN A CSPA	DEG10100576	Rv3648c		Mycobacterium tuberculosis H37Rv
topA	COG0550L,COG1754R	DNA topoisomerase I	DEG10100575	Rv3646c	Rv3646c	Mycobacterium tuberculosis H37Rv
Rv3635	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100574	Rv3635		Mycobacterium tuberculosis H37Rv
galE1	COG0451MG	UDP-GLUCOSE 4-EPIMERASE GALE1 (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) (URIDINE DIPHOSPHATE GALACTOSE 4-EPIMERASE) (URIDINE DIPHOSPHO-GALACTOSE 4-EPIMERASE)	DEG10100573	Rv3634c	Rv3634c	Mycobacterium tuberculosis H37Rv
Rv3627c	COG2027M	hypothetical protein	DEG10100572	Rv3627c	Rv3627c	Mycobacterium tuberculosis H37Rv
mesJ	COG0037D	POSSIBLE CELL CYCLE PROTEIN MESJ	DEG10100571	Rv3625c		Mycobacterium tuberculosis H37Rv
Rv3611	-	HYPOTHETICAL ARGININE AND PROLINE RICH PROTEIN	DEG10100570	Rv3611		Mycobacterium tuberculosis H37Rv
ftsH	COG0465O	MEMBRANE-BOUND PROTEASE FTSH (CELL DIVISION PROTEIN)	DEG10100569	Rv3610c		Mycobacterium tuberculosis H37Rv
folE	COG0302H	GTP cyclohydrolase I	DEG10100568	Rv3609c	Rv3609c	Mycobacterium tuberculosis H37Rv
folP1	COG0294H	DIHYDROPTEROATE SYNTHASE 1 FOLP (DHPS 1) (DIHYDROPTEROATE PYROPHOSPHORYLASE 1) (DIHYDROPTEROATE DIPHOSPHORYLASE 1)	DEG10100567	Rv3608c	Rv3608c	Mycobacterium tuberculosis H37Rv
folB	COG1539H	PROBABLE DIHYDRONEOPTERIN ALDOLASE FOLB (DHNA)	DEG10100566	Rv3607c	Rv3607c	Mycobacterium tuberculosis H37Rv
Rv3604c	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN RICH IN ALANINE AND ARGININE AND PROLINE	DEG10100565	Rv3604c		Mycobacterium tuberculosis H37Rv
panC	COG0414H	pantoate--beta-alanine ligase	DEG10100564	Rv3602c	Rv3602c	Mycobacterium tuberculosis H37Rv
lysS	COG1190J	lysyl-tRNA synthetase	DEG10100563	Rv3598c	Rv3598c	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
lsr2	-	PROBABLE IRON-REGULATED LSR2 PROTEIN PRECURSOR	DEG10100562	Rv3597c		Mycobacterium tuberculosis H37Rv
clpC1	COG0542O	PROBABLE ATP-DEPENDENT PROTEASE ATP-BINDING SUBUNIT CLPC1	DEG10100561	Rv3596c		Mycobacterium tuberculosis H37Rv
lpqF	COG2367V	PROBABLE CONSERVED LIPOPROTEIN LPQF	DEG10100560	Rv3593		Mycobacterium tuberculosis H37Rv
ispD	COG1211I	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	DEG10100559	Rv3582c	Rv3582c	Mycobacterium tuberculosis H37Rv
ispF	COG0245I	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	DEG10100558	Rv3581c	Rv3581c	Mycobacterium tuberculosis H37Rv
cysS	COG0215J	cysteinyl-tRNA synthetase	DEG10100557	Rv3580c	Rv3580c	Mycobacterium tuberculosis H37Rv
Rv3579c	COG0566J	POSSIBLE TRNA/RRNA METHYLTRANSFERASE	DEG10100556	Rv3579c		Mycobacterium tuberculosis H37Rv
fadE33	COG1960I	PROBABLE ACYL-CoA DEHYDROGENASE FADE33	DEG10100555	Rv3564	Rv3564	Mycobacterium tuberculosis H37Rv
Rv3559c	COG1028IQR	short chain dehydrogenase	DEG10100554	Rv3559c	Rv3559c	Mycobacterium tuberculosis H37Rv
ufaA2	COG2030I	PROBABLE DEHYDROGENASE	DEG10100553	Rv3538		Mycobacterium tuberculosis H37Rv
otsA	COG0380G	PROBABLE ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] OTSA (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE) (TREHALOSEPHOSPHATE-UDP GLUCOSYLTRANSFERASE) (TREHALOSE-6-PHOSPHATE SYNTHETASE) (TREHALOSE-PHOSP	DEG10100552	Rv3490	Rv3490	Mycobacterium tuberculosis H37Rv
rmlC	COG1898M	dTDP-4-DEHYDRORHAMNOSE 3,5-EPIMERASE RMLC (dTDP-4-KETO-6-DEOXYGLUCOSE 3,5-EPIMERASE) (dTDP-L-RHAMNOSE SYNTHETASE) (THYMIDINE DIPHOSPHO-4-KETO-RHAMNOSE 3,5-EPIMERASE)	DEG10100551	Rv3465	Rv3465	Mycobacterium tuberculosis H37Rv
rmlB	COG1088M	dTDP-GLUCOSE 4,6-DEHYDRATASE RMLB	DEG10100550	Rv3464	Rv3464	Mycobacterium tuberculosis H37Rv
infA	COG0361J	translation initiation factor IF-1	DEG10100549	Rv3462c	Rv3462c	Mycobacterium tuberculosis H37Rv
rpsK	COG0100J	30S ribosomal protein S11	DEG10100548	Rv3459c	Rv3459c	Mycobacterium tuberculosis H37Rv
rpsD	COG0522J	30S ribosomal protein S4	DEG10100547	Rv3458c	Rv3458c	Mycobacterium tuberculosis H37Rv
rpoA	COG0202K	DNA-directed RNA polymerase subunit alpha	DEG10100546	Rv3457c	Rv3457c	Mycobacterium tuberculosis H37Rv
truA	COG0101J	tRNA pseudouridine synthase A	DEG10100545	Rv3455c	Rv3455c	Mycobacterium tuberculosis H37Rv
rplM	COG0102J	50S ribosomal protein L13	DEG10100544	Rv3443c	Rv3443c	Mycobacterium tuberculosis H37Rv
mrsA	COG1109G	PROBABLE PHOSPHO-SUGAR MUTASE / MRSA PROTEIN HOMOLOG	DEG10100543	Rv3441c	Rv3441c	Mycobacterium tuberculosis H37Rv
glmS	COG0449M	D-fructose-6-phosphate amidotransferase	DEG10100542	Rv3436c	Rv3436c	Mycobacterium tuberculosis H37Rv
Rv3427c	COG1484L	POSSIBLE TRANSPOSASE	DEG10100541	Rv3427c		Mycobacterium tuberculosis H37Rv
alr	COG0787M	alanine racemase	DEG10100540	Rv3423c	Rv3423c	Mycobacterium tuberculosis H37Rv
Rv3422c	COG0802R	hypothetical protein	DEG10100539	Rv3422c		Mycobacterium tuberculosis H37Rv
groES	COG0234O	co-chaperonin GroES	DEG10100538	Rv3418c		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
groEL1	COG0459O	chaperonin GroEL	DEG10100537	Rv3417c	Rv3417c	Mycobacterium tuberculosis H37Rv
guaB2	COG0516F,COG0517R	inositol-5-monophosphate dehydrogenase	DEG10100536	Rv3411c	Rv3411c	Mycobacterium tuberculosis H37Rv
idsA1	COG0142H	PROBABLE MULTIFUNCTIONAL GERANYLGERANYL PYROPHOSPHATE SYNTHETASE IDSA1 (GGPP SYNTHETASE) (GGPPSASE) (GERANYLGERANYL DIPHOSPHATE SYNTHASE): DIMETHYLALLYLTRANSFERASE (PRENYLTRANSFERASE) (GERANYL-DIPHOSPHATE SYNTHASE) + GERANYLTRANSTRANSFERASE (FARNESYL	DEG10100535	Rv3398c	Rv3398c	Mycobacterium tuberculosis H37Rv
guaA	COG0518F,COG0519F	bifunctional GMP synthase/glutamine amidotransferase protein	DEG10100534	Rv3396c	Rv3396c	Mycobacterium tuberculosis H37Rv
otsB2	COG0637R,COG1877G	POSSIBLE TREHALOSE 6-PHOSPHATE PHOSPHATASE OTSB2 (TREHALOSE-PHOSPHATASE) (TPP)	DEG10100533	Rv3372	Rv3372	Mycobacterium tuberculosis H37Rv
folD	COG0190H	PROBABLE BIFUNCTIONAL PROTEIN FOLD: METHYLENETETRAHYDROFOLATE DEHYDROGENASE + METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE	DEG10100532	Rv3356c		Mycobacterium tuberculosis H37Rv
PPE54	-	PPE FAMILY PROTEIN	DEG10100531	Rv3343c	Rv3343c	Mycobacterium tuberculosis H37Rv
meta	COG2021E	homoserine O-acetyltransferase	DEG10100530	Rv3341	Rv3341	Mycobacterium tuberculosis H37Rv
trpS	COG0180J	tryptophanyl-tRNA synthetase	DEG10100529	Rv3336c	Rv3336c	Mycobacterium tuberculosis H37Rv
nagA	COG1820G	PROBABLE N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE NAGA (GLCNAC 6-P DEACETYLASE)	DEG10100528	Rv3332	Rv3332	Mycobacterium tuberculosis H37Rv
accA3	COG4770I	PROBABLE BIFUNCTIONAL PROTEIN ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE (ALPHA CHAIN) ACCA3: BIOTIN CARBOXYLASE + BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)	DEG10100527	Rv3285	Rv3285	Mycobacterium tuberculosis H37Rv
Rv3281	-	hypothetical protein	DEG10100526	Rv3281		Mycobacterium tuberculosis H37Rv
purE	COG0041F	phosphoribosylaminoimidazole carboxylase catalytic subunit	DEG10100525	Rv3275c	Rv3275c	Mycobacterium tuberculosis H37Rv
Rv3271c	-	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100524	Rv3271c		Mycobacterium tuberculosis H37Rv
Rv3267	COG1316K	CONSERVED HYPOTHETICAL PROTEIN (CPSA-RELATED PROTEIN)	DEG10100523	Rv3267		Mycobacterium tuberculosis H37Rv
wbbL1	COG1216R	PROBABLE dTDP-RHA:A-D-GlcNAc-DIPHOSPHORYL POLYPRENOL, A-3-L-RHAMNOSYL TRANSFERASE WBBL1 (ALPHA-L-RHAMNOSE-(1->3)-ALPHA-D-GlcNAc(1->P)-P-DECAPRENY L)	DEG10100522	Rv3265c		Mycobacterium tuberculosis H37Rv
manB	COG1208MJ	D-ALPHA-D-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE MANB (D-ALPHA-D-HEPTOSE-1-PHOSPHATE GUANYLYLTRANSFERASE)	DEG10100521	Rv3264c	Rv3264c	Mycobacterium tuberculosis H37Rv
pmmA	COG1109G	phosphomannomutase/phosphoglucomutase	DEG10100520	Rv3257c	Rv3257c	Mycobacterium tuberculosis H37Rv
manA	COG1482G	PROBABLE MANNOSE-6-PHOSPHATE ISOMERASE MANA (PHOSPHOMANNOSE ISOMERASE) (PHOSPHOMANNOISOMERASE) (PMI) (PHOSPHOHEXOISOMERASE) (PHOSPHOHEXOMUTASE)	DEG10100519	Rv3255c	Rv3255c	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
sahH	COG0499H	S-adenosyl-L-homocysteine hydrolase	DEG10100518	Rv3248c	Rv3248c	Mycobacterium tuberculosis H37Rv
mtrB	COG0642T	TWO COMPONENT SENSORY TRANSDUCTION HISTIDINE KINASE MTRB	DEG10100517	Rv3245c	Rv3245c	Mycobacterium tuberculosis H37Rv
lpqB	-	PROBABLE CONSERVED LIPOPROTEIN LPQB	DEG10100516	Rv3244c		Mycobacterium tuberculosis H37Rv
Rv3243c	-	hypothetical protein	DEG10100515	Rv3243c		Mycobacterium tuberculosis H37Rv
secA1	COG0653U	preprotein translocase subunit SecA	DEG10100514	Rv3240c	Rv3240c	Mycobacterium tuberculosis H37Rv
Rv3201c	COG0210L,COG2887L	PROBABLE ATP-DEPENDENT DNA HELICASE	DEG10100513	Rv3201c	Rv3201c	Mycobacterium tuberculosis H37Rv
uvrD2	COG0210L	PROBABLE ATP-DEPENDENT DNA HELICASE II UVRD2	DEG10100512	Rv3198c	Rv3198c	Mycobacterium tuberculosis H37Rv
Rv3177	COG0596R	POSSIBLE PEROXIDASE (NON-HAEM PEROXIDASE)	DEG10100511	Rv3177		Mycobacterium tuberculosis H37Rv
fadE23	COG1960I	PROBABLE ACYL-CoA DEHYDROGENASE FADE23	DEG10100510	Rv3140	Rv3140	Mycobacterium tuberculosis H37Rv
fadE24	COG1960I	PROBABLE ACYL-CoA DEHYDROGENASE FADE24	DEG10100509	Rv3139	Rv3139	Mycobacterium tuberculosis H37Rv
Rv3137	COG0483G	PROBABLE MONOPHOSPHATASE	DEG10100508	Rv3137	Rv3137	Mycobacterium tuberculosis H37Rv
PPE50	-	PPE FAMILY PROTEIN	DEG10100507	Rv3135	Rv3135	Mycobacterium tuberculosis H37Rv
devS	COG2203T,COG4585T	TWO COMPONENT SENSOR HISTIDINE KINASE DEVS	DEG10100506	Rv3132c	Rv3132c	Mycobacterium tuberculosis H37Rv
Rv3131	-	hypothetical protein	DEG10100505	Rv3131		Mycobacterium tuberculosis H37Rv
Rv3113	COG0546R	POSSIBLE PHOSPHATASE	DEG10100504	Rv3113		Mycobacterium tuberculosis H37Rv
moaD1	COG1977H	PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN D MOAD1 (MOLYBDOPTERIN CONVERTING FACTOR SMALL SUBUNIT) (MOLYBDOPTERIN [MPT] CONVERTING FACTOR, SUBUNIT 1)	DEG10100503	Rv3112	Rv3112	Mycobacterium tuberculosis H37Rv
moaC	COG0315H	molybdenum cofactor biosynthesis protein C	DEG10100502	Rv3111	Rv3111	Mycobacterium tuberculosis H37Rv
moaA1	COG2896H	PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A MOAA1	DEG10100501	Rv3109	Rv3109	Mycobacterium tuberculosis H37Rv
prfB	COG1186J	peptide chain release factor 2	DEG10100500	Rv3105c	Rv3105c	Mycobacterium tuberculosis H37Rv
ftsX	COG2177D	PUTATIVE CELL DIVISION PROTEIN FTSX (SEPTATION COMPONENT-TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER)	DEG10100499	Rv3101c	Rv3101c	Mycobacterium tuberculosis H37Rv
nrdE	COG0209F	ribonucleotide-diphosphate reductase subunit alpha	DEG10100498	Rv3051c	Rv3051c	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
nrdf	COG0208F	ribonucleotide-diphosphate reductase subunit beta	DEG10100497	Rv3048c	Rv3048c	Mycobacterium tuberculosis H37Rv
ctaD	COG0843C	PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE I CTAD (CYTOCHROME AA3 SUBUNIT 1)	DEG10100496	Rv3043c	Rv3043c	Mycobacterium tuberculosis H37Rv
serB2	COG0560E,COG3830T	phosphoserine phosphatase	DEG10100495	Rv3042c	Rv3042c	Mycobacterium tuberculosis H37Rv
Rv3032	COG0438M	POSSIBLE TRANSFERASE	DEG10100494	Rv3032	Rv3032	Mycobacterium tuberculosis H37Rv
Rv3031	COG1543S	hypothetical protein	DEG10100493	Rv3031	Rv3031	Mycobacterium tuberculosis H37Rv
Rv3030	COG0500QR	hypothetical protein	DEG10100492	Rv3030		Mycobacterium tuberculosis H37Rv
fixA	COG2086C	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN (BETA-SUBUNIT) FIXA (BETA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS)	DEG10100491	Rv3029c		Mycobacterium tuberculosis H37Rv
iscS	COG1104E	PROBABLE CYSTEINE DESULFURASE ISCS (NIFS PROTEIN HOMOLOG) (NITROGENASE METALLOCLUSTERS BIOSYNTHESIS PROTEIN NIFS)	DEG10100490	Rv3025c	Rv3025c	Mycobacterium tuberculosis H37Rv
PPE46	-	PPE FAMILY PROTEIN	DEG10100489	Rv3018c	Rv3018c	Mycobacterium tuberculosis H37Rv
ligA	COG0272L	NAD-dependent DNA ligase LigA	DEG10100488	Rv3014c	Rv3014c	Mycobacterium tuberculosis H37Rv
gatA	COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A	DEG10100487	Rv3011c	Rv3011c	Mycobacterium tuberculosis H37Rv
gatB	COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	DEG10100486	Rv3009c	Rv3009c	Mycobacterium tuberculosis H37Rv
ilvB1	COG0028EH	acetolactate synthase 1 catalytic subunit	DEG10100485	Rv3003c	Rv3003c	Mycobacterium tuberculosis H37Rv
ilvn	COG0440E	subunit	DEG10100484	Rv3002c	Rv3002c	Mycobacterium tuberculosis H37Rv
ilvC	COG0059EH	ketol-acid reductoisomerase	DEG10100483	Rv3001c	Rv3001c	Mycobacterium tuberculosis H37Rv
lppY	-	PROBABLE CONSERVED LIPOPROTEIN LPPY	DEG10100482	Rv2999		Mycobacterium tuberculosis H37Rv
serA1	COG0111HE	PROBABLE D-3-PHOSPHOGLYCERATE DEHYDROGENASE SERA1 (PGDH)	DEG10100481	Rv2996c	Rv2996c	Mycobacterium tuberculosis H37Rv
leuB	COG0473CE	3-isopropylmalate dehydrogenase	DEG10100480	Rv2995c	Rv2995c	Mycobacterium tuberculosis H37Rv
glts	COG0008J	glutamyl-tRNA synthetase	DEG10100479	Rv2992c	Rv2992c	Mycobacterium tuberculosis H37Rv
leuD	COG0066E	isopropylmalate isomerase small subunit	DEG10100478	Rv2987c	Rv2987c	Mycobacterium tuberculosis H37Rv
hupB	COG0776L	PROBABLE DNA-BINDING PROTEIN HU HOMOLOG HUPB (HISTONE-LIKE PROTEIN) (HLP) (21-KDA LAMININ-2-BINDING PROTEIN)	DEG10100477	Rv2986c		Mycobacterium tuberculosis H37Rv
ddlA	COG1181M	D-alanyl-alanine synthetase A	DEG10100476	Rv2981c	Rv2981c	Mycobacterium tuberculosis H37Rv
thiL	COG0611H	thiamine monophosphate kinase	DEG10100475	Rv2977c	Rv2977c	Mycobacterium tuberculosis H37Rv
Rv2971	COG0656R	PROBABLE OXIDOREDUCTASE	DEG10100474	Rv2971		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
Rv2969c	COG1651O	POSSIBLE CONSERVED MEMBRANE OR SECRETED PROTEIN	DEG10100473	Rv2969c		Mycobacterium tuberculosis H37Rv
Rv2968c	COG4243S	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100472	Rv2968c		Mycobacterium tuberculosis H37Rv
pca	COG1038C	pyruvate carboxylase	DEG10100471	Rv2967c	Rv2967c	Mycobacterium tuberculosis H37Rv
Rv2927c	COG3599D	hypothetical protein	DEG10100470	Rv2927c		Mycobacterium tuberculosis H37Rv
Rv2926c	COG1399R	hypothetical protein	DEG10100469	Rv2926c		Mycobacterium tuberculosis H37Rv
rnc	COG0571K	ribonuclease III	DEG10100468	Rv2925c		Mycobacterium tuberculosis H37Rv
ffh	COG0541U	PROBABLE SIGNAL RECOGNITION PARTICLE PROTEIN FFH (FIFTY-FOUR HOMOLOG) (SRP PROTEIN)	DEG10100467	Rv2916c	Rv2916c	Mycobacterium tuberculosis H37Rv
Rv2908c	COG1837R	hypothetical protein	DEG10100466	Rv2908c		Mycobacterium tuberculosis H37Rv
rimM	COG0806J	16S rRNA-processing protein	DEG10100465	Rv2907c	Rv2907c	Mycobacterium tuberculosis H37Rv
trmD	COG0336J	tRNA (guanine-N(1)-)-methyltransferase	DEG10100464	Rv2906c	Rv2906c	Mycobacterium tuberculosis H37Rv
rplS	COG0335J	50S ribosomal protein L19	DEG10100463	Rv2904c	Rv2904c	Mycobacterium tuberculosis H37Rv
lepB	COG0681U	PROBABLE SIGNAL PEPTIDASE I LEPB (SPASE I) (LEADER PEPTIDASE I).	DEG10100462	Rv2903c	Rv2903c	Mycobacterium tuberculosis H37Rv
Rv2897c	COG0606O	hypothetical protein	DEG10100461	Rv2897c		Mycobacterium tuberculosis H37Rv
rpsB	COG0052J	30S ribosomal protein S2	DEG10100460	Rv2890c	Rv2890c	Mycobacterium tuberculosis H37Rv
tsf	COG0264J	elongation factor Ts	DEG10100459	Rv2889c	Rv2889c	Mycobacterium tuberculosis H37Rv
pyrH	COG0528F	uridylate kinase	DEG10100458	Rv2883c	Rv2883c	Mycobacterium tuberculosis H37Rv
frr	COG0233J	ribosome recycling factor	DEG10100457	Rv2882c	Rv2882c	Mycobacterium tuberculosis H37Rv
cdsA	COG0575I	PROBABLE INTEGRAL MEMBRANE PHOSPHATIDATE CYTIDYLYLTRANSFERASE CDSA	DEG10100456	Rv2881c	Rv2881c	Mycobacterium tuberculosis H37Rv
Rv2869c	COG0750M	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100455	Rv2869c		Mycobacterium tuberculosis H37Rv
nicT	COG3376P	POSSIBLE NICKEL-TRANSPORT INTEGRAL MEMBRANE PROTEIN NICT	DEG10100454	Rv2856		Mycobacterium tuberculosis H37Rv
mtr	COG1249C	mycothione/glutathione reductase	DEG10100453	Rv2855	Rv2855	Mycobacterium tuberculosis H37Rv
efpA	COG0477GEPR	POSSIBLE INTEGRAL MEMBRANE EFFLUX PROTEIN EFPA	DEG10100452	Rv2846c		Mycobacterium tuberculosis H37Rv
proS	COG0442J	prolyl-tRNA synthetase	DEG10100451	Rv2845c	Rv2845c	Mycobacterium tuberculosis H37Rv
nusA	COG0195K	transcription elongation factor NusA	DEG10100450	Rv2841c	Rv2841c	Mycobacterium tuberculosis H37Rv
infB	COG0532J	translation initiation factor IF-2	DEG10100449	Rv2839c	Rv2839c	Mycobacterium tuberculosis H37Rv
Rv2837c	COG0618R	hypothetical protein	DEG10100448	Rv2837c		Mycobacterium tuberculosis H37Rv
ugpB	COG1653G	PROBABLE Sn-GLYCEROL-3-PHOSPHATE-BINDING LIPOPROTEIN UGPB	DEG10100447	Rv2833c	Rv2833c	Mycobacterium tuberculosis H37Rv
ugpC	COG3839G	PROBABLE Sn-GLYCEROL-3-PHOSPHATE TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER UGPC	DEG10100446	Rv2832c	Rv2832c	Mycobacterium tuberculosis H37Rv
Rv2830c	COG4118D	hypothetical protein	DEG10100445	Rv2830c		Mycobacterium tuberculosis H37Rv
Rv2828c	COG4293S	hypothetical protein	DEG10100444	Rv2828c		Mycobacterium tuberculosis H37Rv
Rv2827c	COG0172J	hypothetical protein	DEG10100443	Rv2827c		Mycobacterium tuberculosis H37Rv
Rv2817c	COG1518L	hypothetical protein	DEG10100442	Rv2817c		Mycobacterium tuberculosis H37Rv
Rv2813	COG3267U	hypothetical protein	DEG10100441	Rv2813		Mycobacterium tuberculosis H37Rv
Rv2812	COG2801L	PROBABLE TRANSPOSASE	DEG10100440	Rv2812		Mycobacterium tuberculosis H37Rv

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ribF	COG0196H	bifunctional riboflavin kinase/FMN adenylyltransferase	DEG10100439	Rv2786c	Rv2786c	Mycobacterium tuberculosis H37Rv
thyX	COG1351F	FAD-dependent thymidylate synthase	DEG10100438	Rv2754c	Rv2754c	Mycobacterium tuberculosis H37Rv
dapA	COG0329EM	dihydrodipicolinate synthase	DEG10100437	Rv2753c	Rv2753c	Mycobacterium tuberculosis H37Rv
ftsK	COG1674D	POSSIBLE CELL DIVISION TRANSMEMBRANE PROTEIN FTSK	DEG10100436	Rv2748c		Mycobacterium tuberculosis H37Rv
Rv2747	COG1246E	N-acetylglutamate synthase	DEG10100435	Rv2747	Rv2747	Mycobacterium tuberculosis H37Rv
pgsA3	COG0558I	PROBABLE PGP SYNTHASE PGSA3 (CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE) (PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE)	DEG10100434	Rv2746c	Rv2746c	Mycobacterium tuberculosis H37Rv
Rv2739c	COG1819GC	POSSIBLE ALANINE RICH TRANSFERASE	DEG10100433	Rv2739c		Mycobacterium tuberculosis H37Rv
miaA	COG0324J	tRNA delta(2)-isopentenylpyrophosphate transferase	DEG10100432	Rv2727c	Rv2727c	Mycobacterium tuberculosis H37Rv
dapF	COG0253E	diaminopimelate epimerase	DEG10100431	Rv2726c	Rv2726c	Mycobacterium tuberculosis H37Rv
sigB	COG0568K	RNA polymerase sigma factor SigB	DEG10100430	Rv2710	Rv2710	Mycobacterium tuberculosis H37Rv
sigA	COG0568K	RNA polymerase sigma factor RpoD	DEG10100429	Rv2703	Rv2703	Mycobacterium tuberculosis H37Rv
ppgK	COG1940KG	POLYPHOSPHATE GLUCOKINASE PPGK (POLYPHOSPHATE-GLUCOSE PHOSPHOTRANSFERASE)	DEG10100428	Rv2702	Rv2702	Mycobacterium tuberculosis H37Rv
Rv2700	-	POSSIBLE CONSERVED SECRETED ALANINE RICH PROTEIN	DEG10100427	Rv2700		Mycobacterium tuberculosis H37Rv
Rv2698	-	PROBABLE CONSERVED ALANINE RICH TRANSMEMBRANE PROTEIN	DEG10100426	Rv2698		Mycobacterium tuberculosis H37Rv
dut	COG0756F	deoxyuridine 5'-triphosphate nucleotidohydrolase	DEG10100425	Rv2697c	Rv2697c	Mycobacterium tuberculosis H37Rv
dxs1	COG1154HI	1-deoxy-D-xylulose-5-phosphate synthase	DEG10100424	Rv2682c	Rv2682c	Mycobacterium tuberculosis H37Rv
Rv2673	-	POSSIBLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100423	Rv2673		Mycobacterium tuberculosis H37Rv
TB31.7	COG0589T	hypothetical protein	DEG10100422	Rv2623		Mycobacterium tuberculosis H37Rv
thrS	COG0441J	threonyl-tRNA synthetase	DEG10100421	Rv2614c	Rv2614c	Mycobacterium tuberculosis H37Rv
Rv2613c	COG0537FG	hypothetical protein	DEG10100420	Rv2613c		Mycobacterium tuberculosis H37Rv
pgsA1	COG0558I	PROBABLE PI SYNTHASE PGSA1 (PHOSPHATIDYLINOSITOL SYNTHASE) (CDP-DIACYLGLYCEROL--INOSITOL3-PHOSPHATIDYLTRANSFERASE)	DEG10100419	Rv2612c	Rv2612c	Mycobacterium tuberculosis H37Rv
Rv2611c	COG1560M	lipid A biosynthesis lauroyl acyltransferase	DEG10100418	Rv2611c		Mycobacterium tuberculosis H37Rv
ppiB	COG0652O	PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PPIB (CYCLOPHILIN) (PPIASE) (ROTAMASE) (PEPTIDYLPROLYL ISOMERASE)	DEG10100417	Rv2582		Mycobacterium tuberculosis H37Rv
hisS	COG0124J	histidyl-tRNA synthetase	DEG10100416	Rv2580c	Rv2580c	Mycobacterium tuberculosis H37Rv
alaS	COG0013J	alanyl-tRNA synthetase	DEG10100415	Rv2555c	Rv2555c	Mycobacterium tuberculosis H37Rv

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Rv2554c	COG0816L	Holliday junction resolvase-like protein	DEG10100414	Rv2554c	Rv2554c	Mycobacterium tuberculosis H37Rv
aroE	COG0169E	shikimate 5-dehydrogenase	DEG10100413	Rv2552c	Rv2552c	Mycobacterium tuberculosis H37Rv
aroF	COG0082E	chorismate synthase	DEG10100412	Rv2540c	Rv2540c	Mycobacterium tuberculosis H37Rv
aroK	COG0703E	shikimate kinase	DEG10100411	Rv2539c	Rv2539c	Mycobacterium tuberculosis H37Rv
aroB	COG0337E	3-dehydroquinate synthase	DEG10100410	Rv2538c	Rv2538c	Mycobacterium tuberculosis H37Rv
aroD	COG0757E	3-dehydroquinate dehydratase	DEG10100409	Rv2537c	Rv2537c	Mycobacterium tuberculosis H37Rv
efp	COG0231J	elongation factor P	DEG10100408	Rv2534c	Rv2534c	Mycobacterium tuberculosis H37Rv
nusB	COG0781K	transcription antitermination protein NusB	DEG10100407	Rv2533c	Rv2533c	Mycobacterium tuberculosis H37Rv
fas	COG0304IQ,COG0331I,COG2030I,COG4981I,COG	PROBABLE FATTY ACID SYNTHASE FAS (FATTY ACID SYNTHETASE)	DEG10100406	Rv2524c	Rv2524c	Mycobacterium tuberculosis H37Rv
Rv2516c	-	hypothetical protein	DEG10100405	Rv2516c		Mycobacterium tuberculosis H37Rv
Rv2515c	COG1396K,COG2856E	hypothetical protein	DEG10100404	Rv2515c		Mycobacterium tuberculosis H37Rv
orn	COG1949A	oligoribonuclease	DEG10100403	Rv2511		Mycobacterium tuberculosis H37Rv
Rv2510c	COG0433R	hypothetical protein	DEG10100402	Rv2510c		Mycobacterium tuberculosis H37Rv
Rv2507	-	POSSIBLE CONSERVED PROLINE RICH MEMBRANE PROTEIN	DEG10100401	Rv2507		Mycobacterium tuberculosis H37Rv
fadE19	COG1960I	POSSIBLE ACYL-CoA DEHYDROGENASE FADE19 (MMGC)	DEG10100400	Rv2500c		Mycobacterium tuberculosis H37Rv
Rv2477c	COG0488R	putative ABC transporter ATP-binding protein	DEG10100399	Rv2477c		Mycobacterium tuberculosis H37Rv
clpP2	COG0740OU	ATP-dependent Clp protease proteolytic subunit	DEG10100398	Rv2460c		Mycobacterium tuberculosis H37Rv
clpX	COG1219O	ATP-dependent protease ATP-binding subunit	DEG10100397	Rv2457c		Mycobacterium tuberculosis H37Rv
valS	COG0525J	valyl-tRNA synthetase	DEG10100396	Rv2448c	Rv2448c	Mycobacterium tuberculosis H37Rv
folC	COG0285H	PROBABLE FOLYLPOLYGLUTAMATE SYNTHASE PROTEIN FOLC (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS)	DEG10100395	Rv2447c	Rv2447c	Mycobacterium tuberculosis H37Rv
rne	COG1530J	POSSIBLE RIBONUCLEASE E RNE	DEG10100394	Rv2444c	Rv2444c	Mycobacterium tuberculosis H37Rv
rplU	COG0261J	50S ribosomal protein L21	DEG10100393	Rv2442c	Rv2442c	Mycobacterium tuberculosis H37Rv
rpmA	COG0211J	50S ribosomal protein L27	DEG10100392	Rv2441c	Rv2441c	Mycobacterium tuberculosis H37Rv
obg	COG0536R	GTPase ObgE	DEG10100391	Rv2440c		Mycobacterium tuberculosis H37Rv
proB	COG0263E	gamma-glutamyl kinase	DEG10100390	Rv2439c	Rv2439c	Mycobacterium tuberculosis H37Rv
nadE	COG0171H,COG0388R	NAD synthetase	DEG10100389	Rv2438c	Rv2438c	Mycobacterium tuberculosis H37Rv
Rv2437	COG2020O	hypothetical protein	DEG10100388	Rv2437		Mycobacterium tuberculosis H37Rv
nadD	COG1057H	nicotinic acid mononucleotide adenylyltransferase	DEG10100387	Rv2421c	Rv2421c	Mycobacterium tuberculosis H37Rv
Rv2418c	-	hypothetical protein	DEG10100386	Rv2418c		Mycobacterium tuberculosis H37Rv
rpsT	COG0268J	30S ribosomal protein S20	DEG10100385	Rv2412	Rv2412	Mycobacterium tuberculosis H37Rv
subI	COG1613P	PROBABLE SULFATE-BINDING LIPOPROTEIN SUBI	DEG10100384	Rv2400c	Rv2400c	Mycobacterium tuberculosis H37Rv

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cysT	COG0555O	PROBABLE SULFATE-TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER CYST	DEG10100383	Rv2399c	Rv2399c	Mycobacterium tuberculosis H37Rv
cysW	COG4208P	PROBABLE SULFATE-TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER CYSW	DEG10100382	Rv2398c	Rv2398c	Mycobacterium tuberculosis H37Rv
cysA/cysA	COG1118P	PROBABLE SULFATE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER CYSA1	DEG10100381	Rv2397c	Rv2397c	Mycobacterium tuberculosis H37Rv
cysH	COG0175EH	phosphoadenosine phosphosulfate reductase	DEG10100380	Rv2392	Rv2392	Mycobacterium tuberculosis H37Rv
nirA	COG0155P	PROBABLE FERREDOXIN-DEPENDENT NITRITE REDUCTASE NIRA	DEG10100379	Rv2391	Rv2391	Mycobacterium tuberculosis H37Rv
mbtI	COG0147EH	salicylate synthase MbtI	DEG10100378	Rv2386c	Rv2386c	Mycobacterium tuberculosis H37Rv
mbtC	COG3321Q	POLYKETIDE SYNTHETASE MBTC (POLYKETIDE SYNTHASE)	DEG10100377	Rv2382c	Rv2382c	Mycobacterium tuberculosis H37Rv
mbtG	COG3486Q	LYSINE-N-OXYGENASE MBTG (L-LYSINE 6-MONOOXYGENASE) (LYSINE N6-HYDROXYLASE)	DEG10100376	Rv2378c		Mycobacterium tuberculosis H37Rv
dnaJ2	COG0484O	PROBABLE CHAPERONE PROTEIN DNAJ2	DEG10100375	Rv2373c		Mycobacterium tuberculosis H37Rv
Rv2365c	-	hypothetical protein	DEG10100374	Rv2365c		Mycobacterium tuberculosis H37Rv
era	COG1159R	GTP-binding protein Era	DEG10100373	Rv2364c		Mycobacterium tuberculosis H37Rv
Rv2361c	COG0020I	LONG (C50) CHAIN Z-ISOPRENYL DIPHOSPHATE SYNTHASE (Z-DECAPRENYL DIPHOSPHATE SYNTHASE)	DEG10100372	Rv2361c	Rv2361c	Mycobacterium tuberculosis H37Rv
glyS	COG0423J	glycyl-tRNA synthetase	DEG10100371	Rv2357c	Rv2357c	Mycobacterium tuberculosis H37Rv
dnaG	COG0358L	DNA primase	DEG10100370	Rv2343c	Rv2343c	Mycobacterium tuberculosis H37Rv
moeW	COG0476H	hypothetical protein	DEG10100369	Rv2338c		Mycobacterium tuberculosis H37Rv
Rv2325c	COG0619P	hypothetical protein	DEG10100368	Rv2325c	Rv2325c	Mycobacterium tuberculosis H37Rv
Rv2319c	COG0589T	hypothetical protein	DEG10100367	Rv2319c		Mycobacterium tuberculosis H37Rv
Rv2283	-	hypothetical protein	DEG10100366	Rv2283		Mycobacterium tuberculosis H37Rv
cyp128	COG2124Q	PROBABLE CYTOCHROME P450 128 CYP128	DEG10100365	Rv2268c		Mycobacterium tuberculosis H37Rv
Rv2260	COG0491R	hypothetical protein	DEG10100364	Rv2260		Mycobacterium tuberculosis H37Rv
Rv2251	COG0277C	POSSIBLE FLAVOPROTEIN	DEG10100363	Rv2251		Mycobacterium tuberculosis H37Rv
accD6	COG4799I	ACETYL/PROPIONYL-CoA CARBOXYLASE (BETA SUBUNIT) ACCD6	DEG10100362	Rv2247	Rv2247	Mycobacterium tuberculosis H37Rv
kasB	COG0304IQ	3-oxoacyl-(acyl carrier protein) synthase II	DEG10100361	Rv2246	Rv2246	Mycobacterium tuberculosis H37Rv
kasA	COG0304IQ	3-oxoacyl-(acyl carrier protein) synthase II	DEG10100360	Rv2245	Rv2245	Mycobacterium tuberculosis H37Rv
acpm	COG0236IQ	acyl carrier protein	DEG10100359	Rv2244	Rv2244	Mycobacterium tuberculosis H37Rv
Rv2242	COG2508TQ	hypothetical protein	DEG10100358	Rv2242		Mycobacterium tuberculosis H37Rv
Rv2235	COG3346S	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100357	Rv2235		Mycobacterium tuberculosis H37Rv
cobC	COG0079E	hypothetical protein	DEG10100356	Rv2231c		Mycobacterium tuberculosis H37Rv
Rv2229c	COG1579R	hypothetical protein	DEG10100355	Rv2229c		Mycobacterium tuberculosis H37Rv
panB	COG0413H	3-methyl-2-oxobutanoate hydroxymethyltransferase	DEG10100354	Rv2225	Rv2225	Mycobacterium tuberculosis H37Rv
glnE	COG1391OT	GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE GLNE (Glutamine-synthetase adenylyltransferase)	DEG10100353	Rv2221c		Mycobacterium tuberculosis H37Rv

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glnA1	COG0174E	GLUTAMINE SYNTHETASE GLNA1 (GLUTAMINE SYNTHASE) (GS-I)	DEG10100352	Rv2220	Rv2220	Mycobacterium tuberculosis H37Rv
Rv2219	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100351	Rv2219		Mycobacterium tuberculosis H37Rv
lipA	COG0320H	lipoyl synthase	DEG10100350	Rv2218	Rv2218	Mycobacterium tuberculosis H37Rv
lipB	COG0321H	lipoyltransferase	DEG10100349	Rv2217	Rv2217	Mycobacterium tuberculosis H37Rv
dlaT	COG0508C	dihydrolipoamide acetyltransferase	DEG10100348	Rv2215	Rv2215	Mycobacterium tuberculosis H37Rv
gcvT	COG0404E	glycine cleavage system aminomethyltransferase T	DEG10100347	Rv2211c	Rv2211c	Mycobacterium tuberculosis H37Rv
ilvE	COG0115EH	branched-chain amino acid aminotransferase	DEG10100346	Rv2210c	Rv2210c	Mycobacterium tuberculosis H37Rv
asnB	COG0367E	Probable asparagine synthetase AsnB	DEG10100345	Rv2201	Rv2201	Mycobacterium tuberculosis H37Rv
ctaC	COG1622C	PROBABLE TRANSMEMBRANE CYTOCHROME C OXIDASE (SUBUNIT II) CTAC	DEG10100344	Rv2200c	Rv2200c	Mycobacterium tuberculosis H37Rv
qcrB	COG1290C	Probable Ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit)	DEG10100343	Rv2196	Rv2196	Mycobacterium tuberculosis H37Rv
qcrA	COG0723C	Probable Rieske iron-sulfur protein QcrA	DEG10100342	Rv2195	Rv2195	Mycobacterium tuberculosis H37Rv
qcrC	COG2010C	Probable Ubiquinol-cytochrome C reductase QcrC(cytochrome C subunit)	DEG10100341	Rv2194	Rv2194	Mycobacterium tuberculosis H37Rv
ctaE	COG1845C	PROBABLE CYTOCHROME C OXIDASE (SUBUNIT III) CTAE	DEG10100340	Rv2193	Rv2193	Mycobacterium tuberculosis H37Rv
trpD	COG0547E	anthranilate phosphoribosyltransferase	DEG10100339	Rv2192c	Rv2192c	Mycobacterium tuberculosis H37Rv
Rv2188c	COG0438M	hypothetical protein	DEG10100338	Rv2188c		Mycobacterium tuberculosis H37Rv
Rv2182c	COG0204I	1-acylglycerol-3-phosphate O-acyltransferase	DEG10100337	Rv2182c	Rv2182c	Mycobacterium tuberculosis H37Rv
Rv2179c	-	hypothetical protein	DEG10100336	Rv2179c		Mycobacterium tuberculosis H37Rv
aroG	COG3200E	Probable 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase, phenylalanine-repressible)	DEG10100335	Rv2178c	Rv2178c	Mycobacterium tuberculosis H37Rv
Rv2174	-	Possible conserved integral membrane protein	DEG10100334	Rv2174		Mycobacterium tuberculosis H37Rv
Rv2166c	COG2001S	hypothetical protein	DEG10100333	Rv2166c		Mycobacterium tuberculosis H37Rv
mraW	COG0275M	S-adenosyl-methyltransferase MraW	DEG10100332	Rv2165c	Rv2165c	Mycobacterium tuberculosis H37Rv
Rv2164c	-	PROBABLE CONSERVED PROLINE RICH MEMBRANE PROTEIN	DEG10100331	Rv2164c		Mycobacterium tuberculosis H37Rv
pbpB	COG0768M	Probable penicillin-binding membrane protein pbpB	DEG10100330	Rv2163c	Rv2163c	Mycobacterium tuberculosis H37Rv
murF	COG0770M	Probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate- D-alanyl-D-alanyl ligase MurF	DEG10100329	Rv2157c	Rv2157c	Mycobacterium tuberculosis H37Rv
murX	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	DEG10100328	Rv2156c	Rv2156c	Mycobacterium tuberculosis H37Rv
murD	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	DEG10100327	Rv2155c	Rv2155c	Mycobacterium tuberculosis H37Rv
ftsW	COG0772D	FtsW-like protein FtsW	DEG10100326	Rv2154c	Rv2154c	Mycobacterium tuberculosis H37Rv
murG	COG0707M	N-acetylglucosaminyl transferase	DEG10100325	Rv2153c	Rv2153c	Mycobacterium tuberculosis H37Rv
murC	COG0773M	UDP-N-acetylmuramate--L-alanine ligase	DEG10100324	Rv2152c	Rv2152c	Mycobacterium tuberculosis H37Rv

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ftsQ	COG1589M	POSSIBLE CELL DIVISION PROTEIN FTSQ	DEG10100323	Rv2151c		Mycobacterium tuberculosis H37Rv
ftsZ	COG0206D	cell division protein FtsZ	DEG10100322	Rv2150c	Rv2150c	Mycobacterium tuberculosis H37Rv
wag31	COG3599D	CONSERVED HYPOTHETICAL PROTEIN WAG31	DEG10100321	Rv2145c		Mycobacterium tuberculosis H37Rv
lppL	-	Probable conserved lipoprotein LppL	DEG10100320	Rv2138		Mycobacterium tuberculosis H37Rv
cysS2/cys	COG0215J	cysteinyl-tRNA synthetase	DEG10100319	Rv2130c	Rv2130c	Mycobacterium tuberculosis H37Rv
hisE	COG0140E	phosphoribosyl-ATP pyrophosphatase	DEG10100318	Rv2122c	Rv2122c	Mycobacterium tuberculosis H37Rv
hisG	COG0040E	ATP phosphoribosyltransferase	DEG10100317	Rv2121c	Rv2121c	Mycobacterium tuberculosis H37Rv
Rv2111c	-	hypothetical protein	DEG10100316	Rv2111c		Mycobacterium tuberculosis H37Rv
prcB	COG0638O	proteasome (beta subunit) PrcB	DEG10100315	Rv2110c		Mycobacterium tuberculosis H37Rv
prcA	COG0638O	proteasome (alpha subunit) PrcA	DEG10100314	Rv2109c		Mycobacterium tuberculosis H37Rv
tatC	COG0805U	Probable Sec-independent protein translocase transmembrane protein tatC	DEG10100313	Rv2093c	Rv2093c	Mycobacterium tuberculosis H37Rv
Rv2050	-	hypothetical protein	DEG10100312	Rv2050		Mycobacterium tuberculosis H37Rv
Rv2041c	COG1653G	Probable sugar-binding lipoprotein	DEG10100311	Rv2041c		Mycobacterium tuberculosis H37Rv
Rv2026c	COG0589T	hypothetical protein	DEG10100310	Rv2026c		Mycobacterium tuberculosis H37Rv
Rv2013	COG3547L	POSSIBLE TRANSPOSASE	DEG10100309	Rv2013		Mycobacterium tuberculosis H37Rv
mce3R	COG1309K	PROBABLE TRANSCRIPTIONAL REPRESSOR (PROBABLY TETR-FAMILY) MCE3R	DEG10100308	Rv1963c		Mycobacterium tuberculosis H37Rv
ureC	COG0804E	urease subunit alpha	DEG10100307	Rv1850	Rv1850	Mycobacterium tuberculosis H37Rv
gcvB	COG0403E,COG1003E	glycine dehydrogenase	DEG10100306	Rv1832	Rv1832	Mycobacterium tuberculosis H37Rv
Rv1828	COG0789K	hypothetical protein	DEG10100305	Rv1828		Mycobacterium tuberculosis H37Rv
PPE24	-	PPE FAMILY PROTEIN	DEG10100304	Rv1753c	Rv1753c	Mycobacterium tuberculosis H37Rv
Rv1738	-	hypothetical protein	DEG10100303	Rv1738		Mycobacterium tuberculosis H37Rv
Rv1730c	COG1680V	POSSIBLE PENICILLIN-BINDING PROTEIN	DEG10100302	Rv1730c		Mycobacterium tuberculosis H37Rv
fadB3	COG1250I	PROBABLE 3-HYDROXYBUTYRYL-CoA DEHYDROGENASE FADB3 (BETA-HYDROXYBUTYRYL-CoA DEHYDROGENASE) (BHBD)	DEG10100301	Rv1715		Mycobacterium tuberculosis H37Rv
Rv1714	COG1028IQR	Probable oxidoreductase	DEG10100300	Rv1714		Mycobacterium tuberculosis H37Rv
engA	COG1160R	GTP-binding protein EngA	DEG10100299	Rv1713		Mycobacterium tuberculosis H37Rv
cmk	COG0283F	cytidylate kinase	DEG10100298	Rv1712	Rv1712	Mycobacterium tuberculosis H37Rv
Rv1711	COG1187J	hypothetical protein	DEG10100297	Rv1711		Mycobacterium tuberculosis H37Rv
Rv1708	COG1192D	PUTATIVE INITIATION INHIBITOR PROTEIN	DEG10100296	Rv1708		Mycobacterium tuberculosis H37Rv
xerD	COG4974L	site-specific tyrosine recombinase XerD	DEG10100295	Rv1701		Mycobacterium tuberculosis H37Rv
pyrG	COG0504F	CTP synthetase	DEG10100294	Rv1699	Rv1699	Mycobacterium tuberculosis H37Rv
Rv1697	COG4825S	hypothetical protein	DEG10100293	Rv1697		Mycobacterium tuberculosis H37Rv
ppnK	COG0061G	inorganic polyphosphate/ATP-NAD kinase	DEG10100292	Rv1695	Rv1695	Mycobacterium tuberculosis H37Rv
tyrS	COG0162J	tyrosyl-tRNA synthetase	DEG10100291	Rv1689	Rv1689	Mycobacterium tuberculosis H37Rv
Rv1683	COG0318IQ, COG3243I	acyl-CoA synthetase	DEG10100290	Rv1683	Rv1683	Mycobacterium tuberculosis H37Rv
pks17	COG3321Q	Probable polyketide synthase pks17	DEG10100289	Rv1663		Mycobacterium tuberculosis H37Rv
pks8	COG3321Q	Probable polyketide synthase pks8	DEG10100288	Rv1662		Mycobacterium tuberculosis H37Rv
pks7	COG3321Q	Probable polyketide synthase pks7	DEG10100287	Rv1661		Mycobacterium tuberculosis H37Rv
argH	COG0165E	argininosuccinate lyase	DEG10100286	Rv1659	Rv1659	Mycobacterium tuberculosis H37Rv
argG	COG0137E	argininosuccinate synthase	DEG10100285	Rv1658	Rv1658	Mycobacterium tuberculosis H37Rv
argF	COG0078E	ornithine carbamoyltransferase	DEG10100284	Rv1656	Rv1656	Mycobacterium tuberculosis H37Rv
argD	COG4992E	acetylornithine aminotransferase	DEG10100283	Rv1655	Rv1655	Mycobacterium tuberculosis H37Rv
argB	COG0548E	acetylglutamate kinase	DEG10100282	Rv1654	Rv1654	Mycobacterium tuberculosis H37Rv

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argJ	COG1364E	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	DEG10100281	Rv1653	Rv1653	Mycobacterium tuberculosis H37Rv
argC	COG0002E	N-acetyl-gamma-glutamyl-phosphate reductase	DEG10100280	Rv1652	Rv1652	Mycobacterium tuberculosis H37Rv
pheT	COG0072J,COG0073R	phenylalanyl-tRNA synthetase subunit beta	DEG10100279	Rv1650	Rv1650	Mycobacterium tuberculosis H37Rv
pheS	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	DEG10100278	Rv1649	Rv1649	Mycobacterium tuberculosis H37Rv
infC	COG0290J	translation initiation factor IF-3	DEG10100277	Rv1641	Rv1641	Mycobacterium tuberculosis H37Rv
coaE	COG0237H,COG2320S	dephospho-CoA kinase/unknown domain fusion protein	DEG10100276	Rv1631	Rv1631	Mycobacterium tuberculosis H37Rv
rpsA	COG0539J	30S ribosomal protein S1	DEG10100275	Rv1630	Rv1630	Mycobacterium tuberculosis H37Rv
polA	COG0258L,COG0749L	DNA polymerase I	DEG10100274	Rv1629	Rv1629	Mycobacterium tuberculosis H37Rv
Rv1626	COG3707T	Probable two-component system transcriptional regulator	DEG10100273	Rv1626		Mycobacterium tuberculosis H37Rv
cydB	COG1294C	Probable integral membrane cytochrome D ubiquinol oxidase (subunit II) cydB (Cytochrome BD-I oxidase subunit II)	DEG10100272	Rv1622c	Rv1622c	Mycobacterium tuberculosis H37Rv
pykA	COG0469G	pyruvate kinase	DEG10100271	Rv1617	Rv1617	Mycobacterium tuberculosis H37Rv
lgt	COG0682M	prolipoprotein diacylglyceryl transferase	DEG10100270	Rv1614	Rv1614	Mycobacterium tuberculosis H37Rv
trpA	COG0159E	tryptophan synthase subunit alpha	DEG10100269	Rv1613	Rv1613	Mycobacterium tuberculosis H37Rv
trpB	COG0133E	tryptophan synthase subunit beta	DEG10100268	Rv1612	Rv1612	Mycobacterium tuberculosis H37Rv
trpC	COG0134E	indole-3-glycerol-phosphate synthase	DEG10100267	Rv1611	Rv1611	Mycobacterium tuberculosis H37Rv
Rv1610	-	POSSIBLE CONSERVED MEMBRANE PROTEIN	DEG10100266	Rv1610		Mycobacterium tuberculosis H37Rv
trpE	COG0147EH	anthranilate synthase component I	DEG10100265	Rv1609	Rv1609	Mycobacterium tuberculosis H37Rv
hisI	COG0139E	phosphoribosyl-AMP cyclohydrolase	DEG10100264	Rv1606	Rv1606	Mycobacterium tuberculosis H37Rv
hisF	COG0107E	imidazole glycerol phosphate synthase subunit HisF	DEG10100263	Rv1605	Rv1605	Mycobacterium tuberculosis H37Rv
hisA	COG0106E	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylidene amino] imidazole-4-carboxamide isomerase	DEG10100262	Rv1603	Rv1603	Mycobacterium tuberculosis H37Rv
hisH	COG0118E	imidazole glycerol phosphate synthase subunit HisH	DEG10100261	Rv1602	Rv1602	Mycobacterium tuberculosis H37Rv
hisB	COG0131E	imidazoleglycerol-phosphate dehydratase	DEG10100260	Rv1601	Rv1601	Mycobacterium tuberculosis H37Rv
hisC1	COG0079E	histidinol-phosphate aminotransferase	DEG10100259	Rv1600	Rv1600	Mycobacterium tuberculosis H37Rv
hisD	COG0141E	histidinol dehydrogenase	DEG10100258	Rv1599	Rv1599	Mycobacterium tuberculosis H37Rv
nadB	COG0029H	L-aspartate oxidase	DEG10100257	Rv1595	Rv1595	Mycobacterium tuberculosis H37Rv
nadA	COG0379H	quinolinate synthetase	DEG10100256	Rv1594	Rv1594	Mycobacterium tuberculosis H37Rv
dnaE1	COG0587L	DNA polymerase III subunit alpha	DEG10100255	Rv1547	Rv1547	Mycobacterium tuberculosis H37Rv
lspA	COG0597MU	lipoprotein signal peptidase	DEG10100254	Rv1539	Rv1539	Mycobacterium tuberculosis H37Rv
Rv1490	-	PROBABLE MEMBRANE PROTEIN	DEG10100253	Rv1490		Mycobacterium tuberculosis H37Rv
hemz	COG0276H	ferrochelatase	DEG10100252	Rv1485	Rv1485	Mycobacterium tuberculosis H37Rv
Rv1480	COG1721R	hypothetical protein	DEG10100251	Rv1480		Mycobacterium tuberculosis H37Rv
moxR1	COG0714R	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR1	DEG10100250	Rv1479		Mycobacterium tuberculosis H37Rv
Rv1477	COG0791M	HYPOTHETICAL INVASION PROTEIN	DEG10100249	Rv1477		Mycobacterium tuberculosis H37Rv
Rv1476	-	POSSIBLE MEMBRANE PROTEIN	DEG10100248	Rv1476		Mycobacterium tuberculosis H37Rv
acn	COG1048C	aconitate hydratase	DEG10100247	Rv1475c	Rv1475c	Mycobacterium tuberculosis H37Rv
Rv1466	COG2151R	hypothetical protein	DEG10100246	Rv1466		Mycobacterium tuberculosis H37Rv
Rv1465	COG0822C	POSSIBLE NITROGEN FIXATION RELATED PROTEIN	DEG10100245	Rv1465		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
csd	COG0520E	PROBABLE CYSTEINE DESULFURASE CSD	DEG10100244	Rv1464	Rv1464	Mycobacterium tuberculosis H37Rv
Rv1463	COG0396O	PROBABLE CONSERVED ATP-BINDING PROTEIN ABC TRANSPORTER	DEG10100243	Rv1463		Mycobacterium tuberculosis H37Rv
Rv1462	COG0719O	hypothetical protein	DEG10100242	Rv1462		Mycobacterium tuberculosis H37Rv
Rv1461	COG0719O,COG1372L	hypothetical protein	DEG10100241	Rv1461		Mycobacterium tuberculosis H37Rv
Rv1459c	-	POSSIBLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100240	Rv1459c		Mycobacterium tuberculosis H37Rv
Rv1457c	COG0842V	PROBABLE UNIDENTIFIED ANTIBIOTIC-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER	DEG10100239	Rv1457c		Mycobacterium tuberculosis H37Rv
Rv1456c	COG1612O	PROBABLE UNIDENTIFIED ANTIBIOTIC-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER	DEG10100238	Rv1456c	Rv1456c	Mycobacterium tuberculosis H37Rv
tkt	COG0021G	transketolase	DEG10100237	Rv1449c	Rv1449c	Mycobacterium tuberculosis H37Rv
tal	COG0176G	transaldolase	DEG10100236	Rv1448c	Rv1448c	Mycobacterium tuberculosis H37Rv
opcA	COG3429G	PUTATIVE OXPP CYCLE PROTEIN OPCA	DEG10100235	Rv1446c		Mycobacterium tuberculosis H37Rv
tpi	COG0149G	triosephosphate isomerase	DEG10100234	Rv1438	Rv1438	Mycobacterium tuberculosis H37Rv
pgk	COG0126G	phosphoglycerate kinase	DEG10100233	Rv1437	Rv1437	Mycobacterium tuberculosis H37Rv
gap	COG0057G	glyceraldehyde-3-phosphate dehydrogenase	DEG10100232	Rv1436	Rv1436	Mycobacterium tuberculosis H37Rv
uvrC	COG0322L	excinuclease ABC subunit C	DEG10100231	Rv1420	Rv1420	Mycobacterium tuberculosis H37Rv
ribH	COG0054H	riboflavin synthase subunit beta	DEG10100230	Rv1416	Rv1416	Mycobacterium tuberculosis H37Rv
ribA2	COG0108H,COG0807H	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein	DEG10100229	Rv1415	Rv1415	Mycobacterium tuberculosis H37Rv
ribG	COG0117H,COG1985H	PROBABLE BIFUNCTIONAL riboflavin biosynthesis protein RIBG	DEG10100228	Rv1409	Rv1409	Mycobacterium tuberculosis H37Rv
fmt	COG0223J	methionyl-tRNA formyltransferase	DEG10100227	Rv1406	Rv1406	Mycobacterium tuberculosis H37Rv
metK	COG0192H	S-adenosylmethionine synthetase	DEG10100226	Rv1392	Rv1392	Mycobacterium tuberculosis H37Rv
dfp	COG0452H	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase	DEG10100225	Rv1391	Rv1391	Mycobacterium tuberculosis H37Rv
rpoZ	COG1758K	DNA-directed RNA polymerase subunit omega	DEG10100224	Rv1390	Rv1390	Mycobacterium tuberculosis H37Rv
gmk	COG0194F	guanylate kinase	DEG10100223	Rv1389	Rv1389	Mycobacterium tuberculosis H37Rv
mIHF	-	PUTATIVE INTEGRATION HOST FACTOR MIHF	DEG10100222	Rv1388		Mycobacterium tuberculosis H37Rv
carA	COG0505EF	carbamoyl phosphate synthase small subunit	DEG10100221	Rv1383	Rv1383	Mycobacterium tuberculosis H37Rv
Rv1382	-	PROBABLE EXPORT OR MEMBRANE PROTEIN	DEG10100220	Rv1382		Mycobacterium tuberculosis H37Rv
pyrC	COG0044F	dihydroorotase	DEG10100219	Rv1381	Rv1381	Mycobacterium tuberculosis H37Rv
pyrB	COG0540F	aspartate carbamoyltransferase catalytic subunit	DEG10100218	Rv1380	Rv1380	Mycobacterium tuberculosis H37Rv
fabG2	COG1028IQR	3-ketoacyl-(acyl-carrier-protein) reductase	DEG10100217	Rv1350	Rv1350	Mycobacterium tuberculosis H37Rv
Rv1349	COG1132V	PROBABLE DRUGS-TRANSPORT TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER	DEG10100216	Rv1349	Rv1349	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
Rv1348	COG1132V,COG2375P	PROBABLE DRUGS-TRANSPORT TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER	DEG10100215	Rv1348	Rv1348	Mycobacterium tuberculosis H37Rv
Rv1347c	COG1670J	hypothetical protein	DEG10100214	Rv1347c		Mycobacterium tuberculosis H37Rv
pks14	-	hypothetical protein	DEG10100213	Rv1342c		Mycobacterium tuberculosis H37Rv
Rv1339	COG1234R	hypothetical protein	DEG10100212	Rv1339		Mycobacterium tuberculosis H37Rv
glgE	COG0366G	PROBABLE GLUCANASE GLGE	DEG10100211	Rv1327c	Rv1327c	Mycobacterium tuberculosis H37Rv
glgB	COG0296G	glycogen branching enzyme	DEG10100210	Rv1326c	Rv1326c	Mycobacterium tuberculosis H37Rv
murA	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	DEG10100209	Rv1315	Rv1315	Mycobacterium tuberculosis H37Rv
atpC	COG0355C	F0F1 ATP synthase subunit epsilon	DEG10100208	Rv1311	Rv1311	Mycobacterium tuberculosis H37Rv
atpD	COG0055C	F0F1 ATP synthase subunit beta	DEG10100207	Rv1310	Rv1310	Mycobacterium tuberculosis H37Rv
atpG	COG0224C	F0F1 ATP synthase subunit gamma	DEG10100206	Rv1309	Rv1309	Mycobacterium tuberculosis H37Rv
atpA	COG0056C	F0F1 ATP synthase subunit alpha	DEG10100205	Rv1308	Rv1308	Mycobacterium tuberculosis H37Rv
atpH	COG0711C,COG0712C	PROBABLE ATP SYNTHASE DELTA CHAIN ATPH	DEG10100204	Rv1307	Rv1307	Mycobacterium tuberculosis H37Rv
atpF	COG0711C	F0F1 ATP synthase subunit B	DEG10100203	Rv1306	Rv1306	Mycobacterium tuberculosis H37Rv
atpE	COG0636C	F0F1 ATP synthase subunit C	DEG10100202	Rv1305	Rv1305	Mycobacterium tuberculosis H37Rv
Rv1303	-	hypothetical protein	DEG10100201	Rv1303		Mycobacterium tuberculosis H37Rv
Rv1301	COG0009J	hypothetical protein	DEG10100200	Rv1301		Mycobacterium tuberculosis H37Rv
hemK	COG2890J	PROBABLE HEMK PROTEIN HOMOLOG HEMK	DEG10100199	Rv1300		Mycobacterium tuberculosis H37Rv
prfA	COG0216J	peptide chain release factor 1	DEG10100198	Rv1299	Rv1299	Mycobacterium tuberculosis H37Rv
rpmE	COG0254J	50S ribosomal protein L31	DEG10100197	Rv1298	Rv1298	Mycobacterium tuberculosis H37Rv
rho	COG1158K	transcription termination factor Rho	DEG10100196	Rv1297	Rv1297	Mycobacterium tuberculosis H37Rv
thrB	COG0083E	homoserine kinase	DEG10100195	Rv1296	Rv1296	Mycobacterium tuberculosis H37Rv
thrC	COG0498E	threonine synthase	DEG10100194	Rv1295	Rv1295	Mycobacterium tuberculosis H37Rv
thrA	COG0460E	homoserine dehydrogenase	DEG10100193	Rv1294	Rv1294	Mycobacterium tuberculosis H37Rv
lysA	COG0019E	PROBABLE DIAMINOPIMELATE DECARBOXYLASE LYSA (DAP DECARBOXYLASE)	DEG10100192	Rv1293	Rv1293	Mycobacterium tuberculosis H37Rv
argS	COG0018J	arginyl-tRNA synthetase	DEG10100191	Rv1292	Rv1292	Mycobacterium tuberculosis H37Rv
cysN	COG0529P,COG2895P	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	DEG10100190	Rv1286	Rv1286	Mycobacterium tuberculosis H37Rv
cysD	COG0175EH	sulfate adenylyltransferase subunit 2	DEG10100189	Rv1285	Rv1285	Mycobacterium tuberculosis H37Rv
Rv1284	COG0288P	hypothetical protein	DEG10100188	Rv1284		Mycobacterium tuberculosis H37Rv
Rv1278	COG0419L,COG4717S	hypothetical protein	DEG10100187	Rv1278		Mycobacterium tuberculosis H37Rv
lprB	-	POSSIBLE LIPOPROTEIN LPRB	DEG10100186	Rv1274		Mycobacterium tuberculosis H37Rv
Rv1254	COG1835I	PROBABLE ACYLTRANSFERASE	DEG10100185	Rv1254		Mycobacterium tuberculosis H37Rv
sucA/kgd	COG0508C,COG0567C	alpha-ketoglutarate decarboxylase	DEG10100184	Rv1248c	Rv1248c	Mycobacterium tuberculosis H37Rv
Rv1232c	COG2239P	hypothetical protein	DEG10100183	Rv1232c		Mycobacterium tuberculosis H37Rv
mrp	COG0489D	PROBABLE MRP-RELATED PROTEIN MRP	DEG10100182	Rv1229c		Mycobacterium tuberculosis H37Rv
htrA	COG0265O	PROBABLE SERINE PROTEASE HTRA (DEGP PROTEIN)	DEG10100181	Rv1223		Mycobacterium tuberculosis H37Rv
Rv1215c	COG2936R	hypothetical protein	DEG10100180	Rv1215c		Mycobacterium tuberculosis H37Rv
Rv1208	COG0463M	hypothetical protein	DEG10100179	Rv1208		Mycobacterium tuberculosis H37Rv
dapE	COG0624E	dipeptidase	DEG10100178	Rv1202	Rv1202	Mycobacterium tuberculosis H37Rv
Rv1201c	COG2171E	PROBABLE TRANSFERASE	DEG10100177	Rv1201c	Rv1201c	Mycobacterium tuberculosis H37Rv
Rv1194c	COG2508TQ	hypothetical protein	DEG10100176	Rv1194c		Mycobacterium tuberculosis H37Rv
fadD36	COG0318IQ	acyl-CoA synthetase	DEG10100175	Rv1193	Rv1193	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
Rv1188	COG0506E	PROBABLE PROLINE DEHYDROGENASE	DEG10100174	Rv1188	Rv1188	Mycobacterium tuberculosis H37Rv
rocA	COG1012C	PROBABLE PYRROLINE-5-CARBOXYLATE DEHYDROGENASE ROCA	DEG10100173	Rv1187	Rv1187	Mycobacterium tuberculosis H37Rv
Rv1186c	COG2508TQ	hypothetical protein	DEG10100172	Rv1186c		Mycobacterium tuberculosis H37Rv
papA3	COG1020Q	PROBABLE CONSERVED POLYKETIDE SYNTHASE ASSOCIATED PROTEIN PAPA3	DEG10100171	Rv1182		Mycobacterium tuberculosis H37Rv
fdxC	COG1146C	PROBABLE FERREDOXIN FDXC	DEG10100170	Rv1177		Mycobacterium tuberculosis H37Rv
PE/PE11	-	PE FAMILY PROTEIN	DEG10100169	Rv1169c	Rv1169c	Mycobacterium tuberculosis H37Rv
lpqW	COG0747E	PROBABLE CONSERVED LIPOPROTEIN LPQW	DEG10100168	Rv1166		Mycobacterium tuberculosis H37Rv
metE	COG0620E	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	DEG10100167	Rv1133c	Rv1133c	Mycobacterium tuberculosis H37Rv
Rv1128c	-	hypothetical protein	DEG10100166	Rv1128c		Mycobacterium tuberculosis H37Rv
Rv1126c	-	hypothetical protein	DEG10100165	Rv1126c		Mycobacterium tuberculosis H37Rv
gnd2	COG1023G	6-phosphogluconate dehydrogenase-like protein	DEG10100164	Rv1122	Rv1122	Mycobacterium tuberculosis H37Rv
fum	COG0114C	fumarate hydratase	DEG10100163	Rv1098c	Rv1098c	Mycobacterium tuberculosis H37Rv
desA2	-	POSSIBLE ACYL-[ACYL-CARRIER PROTEIN] DESATURASE DESA2 (ACYL-[ACP] DESATURASE) (STEAROYL-ACP DESATURASE)	DEG10100162	Rv1094	Rv1094	Mycobacterium tuberculosis H37Rv
coaA	COG1072H	pantothenate kinase	DEG10100161	Rv1092c	Rv1092c	Mycobacterium tuberculosis H37Rv
kdpE	COG0745TK	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN KDPE	DEG10100160	Rv1027c	Rv1027c	Mycobacterium tuberculosis H37Rv
Rv1026	COG0248FP	hypothetical protein	DEG10100159	Rv1026	Rv1026	Mycobacterium tuberculosis H37Rv
Rv1025	COG1507S	hypothetical protein	DEG10100158	Rv1025		Mycobacterium tuberculosis H37Rv
Rv1024	COG2919D	POSSIBLE CONSERVED MEMBRANE PROTEIN	DEG10100157	Rv1024		Mycobacterium tuberculosis H37Rv
eno	COG0148G	phosphopyruvate hydratase	DEG10100156	Rv1023	Rv1023	Mycobacterium tuberculosis H37Rv
glmU	COG1207M	Probable UDP-N-acetylglucosamine pyrophosphorylase glmU	DEG10100155	Rv1018c	Rv1018c	Mycobacterium tuberculosis H37Rv
prsA	COG0462FE	ribose-phosphate pyrophosphokinase	DEG10100154	Rv1017c	Rv1017c	Mycobacterium tuberculosis H37Rv
pth	COG0193J	peptidyl-tRNA hydrolase	DEG10100153	Rv1014c	Rv1014c	Mycobacterium tuberculosis H37Rv
ispE	COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	DEG10100152	Rv1011	Rv1011	Mycobacterium tuberculosis H37Rv
metS	COG0143J	methionyl-tRNA synthetase	DEG10100151	Rv1007c	Rv1007c	Mycobacterium tuberculosis H37Rv
pabB	COG0147EH	para-aminobenzoate synthase component I	DEG10100150	Rv1005c	Rv1005c	Mycobacterium tuberculosis H37Rv
Rv1002c	COG1928O	hypothetical protein	DEG10100149	Rv1002c		Mycobacterium tuberculosis H37Rv
galU	COG1210M	PROBABLE UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE GALU (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE)	DEG10100148	Rv0993	Rv0993	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
mprB	COG0642T	PROBABLE TWO COMPONENT SENSOR KINASE MPRB	DEG10100147	Rv0982	Rv0982	Mycobacterium tuberculosis H37Rv
accA2	COG0439I,COG0511I,COG4770I	PROBABLE ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN (ALPHA SUBUNIT) ACCA2: BIOTIN CARBOXYLASE + BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)	DEG10100146	Rv0973c	Rv0973c	Mycobacterium tuberculosis H37Rv
purH	COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	DEG10100145	Rv0957	Rv0957	Mycobacterium tuberculosis H37Rv
Rv0955	-	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100144	Rv0955		Mycobacterium tuberculosis H37Rv
sucD	COG0074C	succinyl-CoA synthetase subunit alpha	DEG10100143	Rv0952	Rv0952	Mycobacterium tuberculosis H37Rv
sucC	COG0045C	succinyl-CoA synthetase subunit beta	DEG10100142	Rv0951	Rv0951	Mycobacterium tuberculosis H37Rv
uvrD1	COG0210L	PROBABLE ATP-DEPENDENT DNA HELICASE II UVRD1	DEG10100141	Rv0949	Rv0949	Mycobacterium tuberculosis H37Rv
pgi	COG0166G	glucose-6-phosphate isomerase	DEG10100140	Rv0946c	Rv0946c	Mycobacterium tuberculosis H37Rv
Rv0900	-	POSSIBLE MEMBRANE PROTEIN	DEG10100139	Rv0900		Mycobacterium tuberculosis H37Rv
Rv0894	COG3903R	POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN (POSSIBLY LUXR-FAMILY)	DEG10100138	Rv0894		Mycobacterium tuberculosis H37Rv
serC	COG1932HE	phosphoserine aminotransferase	DEG10100137	Rv0884c	Rv0884c	Mycobacterium tuberculosis H37Rv
Rv0883c	-	hypothetical protein	DEG10100136	Rv0883c		Mycobacterium tuberculosis H37Rv
Rv0875c	-	POSSIBLE CONSERVED EXPORTED PROTEIN	DEG10100135	Rv0875c		Mycobacterium tuberculosis H37Rv
desA1	-	PROBABLE ACYL-[ACYL-CARRIER PROTEIN] DESATURASE DESA1 (ACYL-[ACP] DESATURASE) (STEAROYL-ACP DESATURASE) (PROTEIN DES)	DEG10100134	Rv0824c	Rv0824c	Mycobacterium tuberculosis H37Rv
Rv0817c	-	PROBABLE CONSERVED EXPORTED PROTEIN	DEG10100133	Rv0817c		Mycobacterium tuberculosis H37Rv
Rv0811c	COG0354R	hypothetical protein	DEG10100132	Rv0811c		Mycobacterium tuberculosis H37Rv
purF	COG0034F	amidophosphoribosyltransferase	DEG10100131	Rv0808	Rv0808	Mycobacterium tuberculosis H37Rv
purL	COG0046F	phosphoribosylformylglycinamidine synthase II	DEG10100130	Rv0803	Rv0803	Mycobacterium tuberculosis H37Rv
cfp29	COG1659S	29 KDa ANTIGEN CFP29	DEG10100129	Rv0798c		Mycobacterium tuberculosis H37Rv
purQ	COG0047F	phosphoribosylformylglycinamidine synthase subunit I	DEG10100128	Rv0788	Rv0788	Mycobacterium tuberculosis H37Rv
ptrBa	COG1770E	PROBABLE PROTEASE II PTRBA [FIRST PART] (OLIGOPEPTIDASE B)	DEG10100127	Rv0781		Mycobacterium tuberculosis H37Rv
purC	COG0152F	phosphoribosylaminoimidazole-succinocarboxamide synthase	DEG10100126	Rv0780	Rv0780	Mycobacterium tuberculosis H37Rv
purD	COG0151F	phosphoribosylamine--glycine ligase	DEG10100125	Rv0772	Rv0772	Mycobacterium tuberculosis H37Rv
PPE12	-	PPE FAMILY PROTEIN	DEG10100124	Rv0755c	Rv0755c	Mycobacterium tuberculosis H37Rv
Rv0744c	-	POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN	DEG10100123	Rv0744c		Mycobacterium tuberculosis H37Rv
Rv0736	COG5662K	PROBABLE CONSERVED MEMBRANE PROTEIN	DEG10100122	Rv0736		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
secY	COG0201U	preprotein translocase subunit SecY	DEG10100121	Rv0732	Rv0732	Mycobacterium tuberculosis H37Rv
rpmD	COG1841J	50S ribosomal protein L30	DEG10100120	Rv0722	Rv0722	Mycobacterium tuberculosis H37Rv
rpsE	COG0098J	30S ribosomal protein S5	DEG10100119	Rv0721	Rv0721	Mycobacterium tuberculosis H37Rv
rplR	COG0256J	50S ribosomal protein L18	DEG10100118	Rv0720	Rv0720	Mycobacterium tuberculosis H37Rv
rplF	COG0097J	50S ribosomal protein L6	DEG10100117	Rv0719	Rv0719	Mycobacterium tuberculosis H37Rv
rpsH	COG0096J	30S ribosomal protein S8	DEG10100116	Rv0718	Rv0718	Mycobacterium tuberculosis H37Rv
rplE	COG0094J	50S ribosomal protein L5	DEG10100115	Rv0716	Rv0716	Mycobacterium tuberculosis H37Rv
rplX	COG0198J	50S ribosomal protein L24	DEG10100114	Rv0715	Rv0715	Mycobacterium tuberculosis H37Rv
rplN	COG0093J	50S ribosomal protein L14	DEG10100113	Rv0714	Rv0714	Mycobacterium tuberculosis H37Rv
rpsQ	COG0186J	30S ribosomal protein S17	DEG10100112	Rv0710	Rv0710	Mycobacterium tuberculosis H37Rv
rpmC	COG0255J	50S ribosomal protein L29	DEG10100111	Rv0709	Rv0709	Mycobacterium tuberculosis H37Rv
rplP	COG0197J	50S ribosomal protein L16	DEG10100110	Rv0708	Rv0708	Mycobacterium tuberculosis H37Rv
rpsC	COG0092J	30S ribosomal protein S3	DEG10100109	Rv0707	Rv0707	Mycobacterium tuberculosis H37Rv
rplV	COG0091J	50S ribosomal protein L22	DEG10100108	Rv0706	Rv0706	Mycobacterium tuberculosis H37Rv
rpsS	COG0185J	30S ribosomal protein S19	DEG10100107	Rv0705	Rv0705	Mycobacterium tuberculosis H37Rv
rplB	COG0090J	50S ribosomal protein L2	DEG10100106	Rv0704	Rv0704	Mycobacterium tuberculosis H37Rv
rplW	COG0089J	50S ribosomal protein L23	DEG10100105	Rv0703	Rv0703	Mycobacterium tuberculosis H37Rv
rplD	COG0088J	50S ribosomal protein L4	DEG10100104	Rv0702	Rv0702	Mycobacterium tuberculosis H37Rv
rplC	COG0087J	50S ribosomal protein L3	DEG10100103	Rv0701	Rv0701	Mycobacterium tuberculosis H37Rv
rpsJ	COG0051J	30S ribosomal protein S10	DEG10100102	Rv0700	Rv0700	Mycobacterium tuberculosis H37Rv
Rv0697	COG2303E	PROBABLE DEHYDROGENASE	DEG10100101	Rv0697		Mycobacterium tuberculosis H37Rv
tuf	COG0050J	elongation factor Tu	DEG10100100	Rv0685	Rv0685	Mycobacterium tuberculosis H37Rv
fusA1	COG0480J	elongation factor G	DEG10100099	Rv0684	Rv0684	Mycobacterium tuberculosis H37Rv
rpsG	COG0049J	30S ribosomal protein S7	DEG10100098	Rv0683	Rv0683	Mycobacterium tuberculosis H37Rv
rpsL	COG0048J	30S ribosomal protein S12	DEG10100097	Rv0682	Rv0682	Mycobacterium tuberculosis H37Rv
echA5	COG1024I	enoyl-CoA hydratase	DEG10100096	Rv0675	Rv0675	Mycobacterium tuberculosis H37Rv
Rv0674	COG3327K	hypothetical protein	DEG10100095	Rv0674		Mycobacterium tuberculosis H37Rv
rpoC	COG0086K	DNA-directed RNA polymerase subunit beta'	DEG10100094	Rv0668	Rv0668	Mycobacterium tuberculosis H37Rv
rpoB	COG0085K	DNA-directed RNA polymerase subunit beta	DEG10100093	Rv0667	Rv0667	Mycobacterium tuberculosis H37Rv
Rv0666	-	POSSIBLE MEMBRANE PROTEIN	DEG10100092	Rv0666		Mycobacterium tuberculosis H37Rv
rplL	COG0222J	50S ribosomal protein L7/L12	DEG10100091	Rv0652	Rv0652	Mycobacterium tuberculosis H37Rv
rplJ	COG0244J	50S ribosomal protein L10	DEG10100090	Rv0651	Rv0651	Mycobacterium tuberculosis H37Rv
rplK	COG0080J	50S ribosomal protein L11	DEG10100089	Rv0640	Rv0640	Mycobacterium tuberculosis H37Rv
secE	COG0690U	preprotein translocase subunit SecE	DEG10100088	Rv0638	Rv0638	Mycobacterium tuberculosis H37Rv
Rv0636	COG2030I	hypothetical protein	DEG10100087	Rv0636		Mycobacterium tuberculosis H37Rv
Rv0635	-	hypothetical protein	DEG10100086	Rv0635		Mycobacterium tuberculosis H37Rv
Rv0628c	COG4398S	hypothetical protein	DEG10100085	Rv0628c		Mycobacterium tuberculosis H37Rv
Rv0627	COG1487R	hypothetical protein	DEG10100084	Rv0627		Mycobacterium tuberculosis H37Rv
Rv0607	-	hypothetical protein	DEG10100083	Rv0607		Mycobacterium tuberculosis H37Rv
yrbE2B	COG0767Q	CONSERVED HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN YRBE2B	DEG10100082	Rv0588	Rv0588	Mycobacterium tuberculosis H37Rv
grcC1	COG0142H	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC1 (POLYPRENYL PYROPHOSPHATE SYNTHETASE)	DEG10100081	Rv0562	Rv0562	Mycobacterium tuberculosis H37Rv
ubiE	COG2226H	ubiquinone/menaquinone biosynthesis methyltransferase	DEG10100080	Rv0558	Rv0558	Mycobacterium tuberculosis H37Rv
pimB	COG0438M	MANNOSYLTRANSFERASE PIMB	DEG10100079	Rv0557		Mycobacterium tuberculosis H37Rv
Rv0556	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100078	Rv0556		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
menD	COG1165H	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase	DEG10100077	Rv0555	Rv0555	Mycobacterium tuberculosis H37Rv
menC	COG4948MR	O-succinylbenzoate synthase	DEG10100076	Rv0553	Rv0553	Mycobacterium tuberculosis H37Rv
menE	COG0318IQ	O-succinylbenzoic acid--CoA ligase	DEG10100075	Rv0542c	Rv0542c	Mycobacterium tuberculosis H37Rv
Rv0541c	-	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100074	Rv0541c		Mycobacterium tuberculosis H37Rv
Rv0540	COG3222S	hypothetical protein	DEG10100073	Rv0540		Mycobacterium tuberculosis H37Rv
ccsA	COG0755O	POSSIBLE CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCSA	DEG10100072	Rv0529		Mycobacterium tuberculosis H37Rv
Rv0528	COG1333O	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100071	Rv0528		Mycobacterium tuberculosis H37Rv
ccdA	COG0785O	POSSIBLE CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA	DEG10100070	Rv0527		Mycobacterium tuberculosis H37Rv
Rv0526	COG0526OC	POSSIBLE THIOREDOXIN PROTEIN (THIOL-DISULFIDE INTERCHANGE PROTEIN)	DEG10100069	Rv0526		Mycobacterium tuberculosis H37Rv
Rv0525	COG0406G	hypothetical protein	DEG10100068	Rv0525		Mycobacterium tuberculosis H37Rv
hemL	COG0001H	glutamate-1-semialdehyde aminotransferase	DEG10100067	Rv0524	Rv0524	Mycobacterium tuberculosis H37Rv
hemD	COG0007H,COG1587H	PROBABLE UROPORPHYRIN-III C-METHYLTRANSFERASE HEMD (UROPORPHYRINOGEN III METHYLASE) (UROGEN III METHYLASE) (SUMT) (UROGEN III METHYLASE) (UROM)	DEG10100066	Rv0511	Rv0511	Mycobacterium tuberculosis H37Rv
hemC	COG0181H	porphobilinogen deaminase	DEG10100065	Rv0510	Rv0510	Mycobacterium tuberculosis H37Rv
hemA	COG0373H	glutamyl-tRNA reductase	DEG10100064	Rv0509	Rv0509	Mycobacterium tuberculosis H37Rv
proC	COG0345E	pyrroline-5-carboxylate reductase	DEG10100063	Rv0500	Rv0500	Mycobacterium tuberculosis H37Rv
Rv0479c	-	PROBABLE CONSERVED MEMBRANE PROTEIN	DEG10100062	Rv0479c		Mycobacterium tuberculosis H37Rv
lpdc	COG1249C	dihydrolipoamide dehydrogenase	DEG10100061	Rv0462	Rv0462	Mycobacterium tuberculosis H37Rv
mmpL4	COG2409R	PROBABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL4	DEG10100060	Rv0450c		Mycobacterium tuberculosis H37Rv
groEL2	COG0459O	chaperonin GroEL	DEG10100059	Rv0440	Rv0440	Mycobacterium tuberculosis H37Rv
Rv0430	-	hypothetical protein	DEG10100058	Rv0430		Mycobacterium tuberculosis H37Rv
def	COG0242J	peptide deformylase	DEG10100057	Rv0429c	Rv0429c	Mycobacterium tuberculosis H37Rv
ctpH	COG0474P	POSSIBLE METAL CATION TRANSPORTING P-TYPE ATPASE CTPH	DEG10100056	Rv0425c		Mycobacterium tuberculosis H37Rv
thiC	COG0422H	thiamine biosynthesis protein ThiC	DEG10100055	Rv0423c	Rv0423c	Mycobacterium tuberculosis H37Rv
thiD	COG0351H	phosphomethylpyrimidine kinase	DEG10100054	Rv0422c	Rv0422c	Mycobacterium tuberculosis H37Rv
thiG	COG2022H	thiazole synthase	DEG10100053	Rv0417	Rv0417	Mycobacterium tuberculosis H37Rv
thiS	COG2104H	sulfur carrier protein ThiS	DEG10100052	Rv0416	Rv0416	Mycobacterium tuberculosis H37Rv
thiO	COG0665E	POSSIBLE THIAMINE BIOSYNTHESIS OXIDOREDUCTASE THIO	DEG10100051	Rv0415	Rv0415	Mycobacterium tuberculosis H37Rv
Rv0412c	-	POSSIBLE CONSERVED MEMBRANE PROTEIN	DEG10100050	Rv0412c		Mycobacterium tuberculosis H37Rv
glnH	COG0834ET	PROBABLE GLUTAMINE-BINDING LIPOPROTEIN GLNH (GLNBP)	DEG10100049	Rv0411c		Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
pknG	COG0515RTKL	SERINE/THREONINE-PROTEIN KINASE PKNG (PROTEIN KINASE G) (STPK G)	DEG10100048	Rv0410c		Mycobacterium tuberculosis H37Rv
fadD30	COG0318IQ	acyl-CoA synthetase	DEG10100047	Rv0404	Rv0404	Mycobacterium tuberculosis H37Rv
fadE7	COG1960I	ACYL-CoA DEHYDROGENASE FADE7	DEG10100046	Rv0400c	Rv0400c	Mycobacterium tuberculosis H37Rv
lpqK	COG1680V	POSSIBLE CONSERVED LIPOPROTEIN LPQK	DEG10100045	Rv0399c		Mycobacterium tuberculosis H37Rv
clpB	COG0542O	PROBABLE ENDOPEPTIDASE ATP BINDING PROTEIN (CHAIN B) CLPB (CLPB PROTEIN) (HEAT SHOCK PROTEIN F84.1)	DEG10100044	Rv0384c		Mycobacterium tuberculosis H37Rv
Rv0383c	-	POSSIBLE CONSERVED SECRETED PROTEIN	DEG10100043	Rv0383c		Mycobacterium tuberculosis H37Rv
Rv0372c	COG1975O	hypothetical protein	DEG10100042	Rv0372c		Mycobacterium tuberculosis H37Rv
purA	COG0104F	adenylosuccinate synthetase	DEG10100041	Rv0357c	Rv0357c	Mycobacterium tuberculosis H37Rv
dnaJ1	COG0484O	PROBABLE CHAPERONE PROTEIN DNAJ1	DEG10100040	Rv0352		Mycobacterium tuberculosis H37Rv
grpE	COG0576O	PROBABLE GRPE PROTEIN (HSP-70 COFACTOR)	DEG10100039	Rv0351		Mycobacterium tuberculosis H37Rv
dnaK	COG0443O	molecular chaperone DnaK	DEG10100038	Rv0350	Rv0350	Mycobacterium tuberculosis H37Rv
Rv0347	-	PROBABLE CONSERVED MEMBRANE PROTEIN	DEG10100037	Rv0347		Mycobacterium tuberculosis H37Rv
Rv0338c	COG0247C	PROBABLE IRON-SULFUR-BINDING REDUCTASE	DEG10100036	Rv0338c		Mycobacterium tuberculosis H37Rv
aspC	COG0436E	aminotransferase AlaT	DEG10100035	Rv0337c	Rv0337c	Mycobacterium tuberculosis H37Rv
PE6	-	PE FAMILY PROTEIN	DEG10100034	Rv0335c	Rv0335c	Mycobacterium tuberculosis H37Rv
rmlA	COG1209M	ALPHA-D-GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE RMLA (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE)	DEG10100033	Rv0334	Rv0334	Mycobacterium tuberculosis H37Rv
Rv0312	COG0443O	CONSERVED HYPOTHETICAL PROLINE AND THREONINE RICH PROTEIN	DEG10100032	Rv0312		Mycobacterium tuberculosis H37Rv
Rv0311	-	hypothetical protein	DEG10100031	Rv0311		Mycobacterium tuberculosis H37Rv
Rv0292	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100030	Rv0292		Mycobacterium tuberculosis H37Rv
mycP3	COG1404O	PROBABLE MEMBRANE-ANCHORED MYCOSIN MYCP3 (SERINE PROTEASE) (SUBTILISIN-LIKE PROTEASE) (SUBTILASE-LIKE) (MYCOSIN-3)	DEG10100029	Rv0291		Mycobacterium tuberculosis H37Rv
Rv0290	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100028	Rv0290		Mycobacterium tuberculosis H37Rv
Rv0289	-	hypothetical protein	DEG10100027	Rv0289		Mycobacterium tuberculosis H37Rv
PPE4	-	PPE FAMILY PROTEIN	DEG10100026	Rv0286	Rv0286	Mycobacterium tuberculosis H37Rv
PE5	-	PE FAMILY PROTEIN	DEG10100025	Rv0285	Rv0285	Mycobacterium tuberculosis H37Rv

Gene	COG	Product	DEG code	Experiment EG	Predicted EG	STRAIN
Rv0284	COG1674D	POSSIBLE CONSERVED MEMBRANE PROTEIN	DEG10100024	Rv0284		Mycobacterium tuberculosis H37Rv
Rv0283	-	POSSIBLE CONSERVED MEMBRANE PROTEIN	DEG10100023	Rv0283		Mycobacterium tuberculosis H37Rv
Rv0282	COG0464O	hypothetical protein	DEG10100022	Rv0282		Mycobacterium tuberculosis H37Rv
Rv0236c	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100021	Rv0236c		Mycobacterium tuberculosis H37Rv
Rv0228	COG1835I	PROBABLE INTEGRAL MEMBRANE ACYLTRANSFERASE	DEG10100020	Rv0228		Mycobacterium tuberculosis H37Rv
Rv0227c	-	PROBABLE CONSERVED MEMBRANE PROTEIN	DEG10100019	Rv0227c		Mycobacterium tuberculosis H37Rv
Rv0226c	-	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100018	Rv0226c		Mycobacterium tuberculosis H37Rv
Rv0224c	COG0500QR	POSSIBLE METHYLTRANSFERASE (METHYLASE)	DEG10100017	Rv0224c		Mycobacterium tuberculosis H37Rv
trmB	COG0220R	tRNA (guanine-N(7))-methyltransferase	DEG10100016	Rv0208c	Rv0208c	Mycobacterium tuberculosis H37Rv
Rv0205	COG0628R	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN	DEG10100015	Rv0205		Mycobacterium tuberculosis H37Rv
ilvD	COG0129EG	dihydroxy-acid dehydratase	DEG10100014	Rv0189c	Rv0189c	Mycobacterium tuberculosis H37Rv
Rv0127	COG3281G	hypothetical protein	DEG10100013	Rv0127	Rv0127	Mycobacterium tuberculosis H37Rv
oxcA	COG0028EH	putative oxalyl-CoA decarboxylase	DEG10100012	Rv0118c		Mycobacterium tuberculosis H37Rv
gca	COG0451MG	POSSIBLE GDP-MANNOSE 4,6-DEHYDRATASE GCA (GDP-D-MANNOSE DEHYDRATASE)	DEG10100011	Rv0112	Rv0112	Mycobacterium tuberculosis H37Rv
Rv0102	COG3336S	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN	DEG10100010	Rv0102		Mycobacterium tuberculosis H37Rv
hycQ	COG0651CP	POSSIBLE HYDROGENASE HYCQ	DEG10100009	Rv0086		Mycobacterium tuberculosis H37Rv
hycP	COG4237C	POSSIBLE HYDROGENASE HYCP	DEG10100008	Rv0085		Mycobacterium tuberculosis H37Rv
Rv0060	COG2110R	hypothetical protein	DEG10100007	Rv0060		Mycobacterium tuberculosis H37Rv
dnaB	COG0305L,COG1372L	replicative DNA helicase	DEG10100006	Rv0058	Rv0058	Mycobacterium tuberculosis H37Rv
leuS	COG0495J	leucyl-tRNA synthetase	DEG10100005	Rv0041	Rv0041	Mycobacterium tuberculosis H37Rv
pknA	COG0515RTKL	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE A PKNA (PROTEIN KINASE A) (STPK A)	DEG10100004	Rv0015c		Mycobacterium tuberculosis H37Rv
pknB	COG0515RTKL,COG2815S	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE B PKNB (PROTEIN KINASE B) (STPK B)	DEG10100003	Rv0014c		Mycobacterium tuberculosis H37Rv
gyrB	COG0187L	DNA gyrase subunit B	DEG10100002	Rv0005	Rv0005	Mycobacterium tuberculosis H37Rv
dnaA	COG0593L	chromosomal replication initiation protein	DEG10100001	Rv0001	Rv0001	Mycobacterium tuberculosis H37Rv

Supplemental Table 2. RNA-seq analysis of *S. sanguinis* genes in both treatments. Statistically significant transcriptional variations are shown, with the stressor used (ampicillin or heat) at 10, 20, and 30 minutes post-stress exposure at T_{10} , T_{20} , and T_{30} respectively.

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_2140	ribonuclease P protein component	41	11	4	3	Ampicillin
SSA_0006	peptidyl-tRNA hydrolase	26		9	6	Ampicillin
SSA_0713	1-acyl-sn-glycerol-3-phosphate acyltransferase	36		17	10	Ampicillin
SSA_0575	HAD superfamily hydrolase	53	30	18	15	Ampicillin
SSA_1851	guanylate kinase	134	55	27	12	Ampicillin
SSA_0691	D-alanyl-alanine synthetase A	89	48	30	21	Ampicillin
SSA_0625	phosphopantetheine adenylyltransferase	60	45	32	26	Ampicillin
SSA_2375	tryptophanyl-tRNA synthetase II	104	57	34	25	Ampicillin
SSA_1091	thymidylate synthase	68	62	39	20	Ampicillin
SSA_1086	tRNA CCA-pyrophosphorylase	48	47	41	36	Ampicillin
SSA_1491	methionine aminopeptidase	54	48	41	34	Ampicillin
SSA_0720	DNA polymerase III subunit delta	57	51	42	34	Ampicillin
SSA_1806	replication initiation protein DnaB	46	53	48	43	Ampicillin
SSA_0801	Mur ligase family protein	66	63	55	51	Ampicillin
SSA_1872	cell division protein	115	69	55	45	Ampicillin
SSA_1452	second subunit of major exonuclease	53	52	56	59	Ampicillin
SSA_1529	lysyl-tRNA synthetase	129	91	56	44	Ampicillin
SSA_0063	Holliday junction DNA helicase RuvB	56	54	57	47	Ampicillin
SSA_0912	phenylalanyl-tRNA synthetase subunit alpha	80	74	57	45	Ampicillin
SSA_2360	tRNA-specific 2-thiouridylase MnmA	91	78	57	48	Ampicillin
SSA_1940	3-oxoacyl-ACP synthase	160	115	57	40	Ampicillin
SSA_1495	S-adenosylmethionine synthetase	73	69	61	52	Ampicillin
SSA_1721	DNA polymerase III subunit delta'	79	70	63	66	Ampicillin
SSA_1522	cell division protein FtsW	93	83	68	51	Ampicillin
SSA_1864	nicotinate phosphoribosyltransferase	80	71	71	73	Ampicillin
SSA_0333	mevalonate kinase	72	70	72	71	Ampicillin
SSA_0846	DNA polymerase III DnaE	48	55	74	92	Ampicillin
SSA_1784	glutamate racemase	100	92	77	62	Ampicillin
SSA_1152	peptide chain release factor 1	102	82	79	80	Ampicillin
SSA_1209	inorganic polyphosphate/ATP-NAD kinase	73	90	79	58	Ampicillin
SSA_0800	glutamine amidotransferase	79	90	82	85	Ampicillin
SSA_1848	methionyl-tRNA formyltransferase	76	75	83	88	Ampicillin
SSA_2350	30S ribosomal protein S4	507	188	83	59	Ampicillin
SSA_0653	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	96	92	88	81	Ampicillin
SSA_1223	30S ribosomal protein S1	655	278	88	52	Ampicillin
SSA_1213	pyridoxal-phosphate dependent aminotransferase	120	111	93	77	Ampicillin
SSA_2066	DNA polymerase III PolC	96	92	94	98	Ampicillin
SSA_1738	polysaccharide biosynthesis protein	89	95	94	79	Ampicillin
SSA_1430	ribonuclease Z	65	77	95	109	Ampicillin
SSA_1863	NAD synthetase	93	93	96	96	Ampicillin
SSA_0198	dihydrofolate synthetase	93	96	96	102	Ampicillin
SSA_1739	UDP-D-glutamate--L-lysine ligase	89	100	100	90	Ampicillin
SSA_1865	thioredoxin reductase	115	118	100	79	Ampicillin
SSA_0010	cell division protein DivIC	140	111	103		Ampicillin
SSA_1703	methionyl-tRNA synthetase	118	123	105		Ampicillin
SSA_1925	seryl-tRNA synthetase	117	127	108	104	Ampicillin
SSA_0824	DNA primase	152	139	110		Ampicillin
SSA_0999	biotin--protein ligase	25	63	113	141	Ampicillin
SSA_0199	GTP cyclohydrolase I	97	98	113	106	Ampicillin

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_0804	phosphoglucosamine mutase	150	140	114		Ampicillin
SSA_0914	phenylalanyl-tRNA synthetase subunit beta	100	117	115	109	Ampicillin
SSA_1880	glycyl-tRNA synthetase subunit alpha	134	130	122	113	Ampicillin
SSA_1606	dephospho-CoA kinase	102	104	123	135	Ampicillin
SSA_0334	diphosphomevalonate decarboxylase	100	111	124	137	Ampicillin
SSA_1302	tRNA (guanine-N(1)-)-methyltransferase	154	154	124	82	Ampicillin
SSA_1819	valyl-tRNA synthetase	123	126	130	124	Ampicillin
SSA_1642	bifunctional N-acetylglucosamine-acetyltransferase	179	167	130	89	Ampicillin
SSA_0878	DNA gyrase subunit B	123	137	132	118	Ampicillin
SSA_0941	phosphate ABC transporter substrate-binding protein	126	132	134	135	Ampicillin
SSA_0869	peptide chain release factor 2	170	162	134	97	Ampicillin
SSA_0002	DNA polymerase III subunit beta	160	161	136	133	Ampicillin
SSA_1620	uridylate kinase	197	176	136	103	Ampicillin
SSA_1623	50S ribosomal protein L11	647	346	139	86	Ampicillin
SSA_0200	bifunctional folate synthesis protein	114	124	140	138	Ampicillin
SSA_0570	aspartyl/glutamyl-tRNA amidotransferase subunit A	132	142	140	132	Ampicillin
SSA_0337	hydroxymethylglutaryl-CoA reductase	122	142	141	148	Ampicillin
SSA_0174	tyrosyl-tRNA synthetase	152	151	141	126	Ampicillin
SSA_0336	isopentenyl pyrophosphate isomerase	103	123	142	145	Ampicillin
SSA_2072	phosphatidate cytidylyltransferase	134	151	142	134	Ampicillin
SSA_0128	adenylate kinase	211	172	142	77	Ampicillin
SSA_0335	phosphomevalonate kinase	111	129	145	161	Ampicillin
SSA_0289	leucyl-tRNA synthetase	175	158	146		Ampicillin
SSA_1871	penicillin-binding protein 2X	178	171	156	153	Ampicillin
SSA_1310	30S ribosomal protein S16	431	265	157	114	Ampicillin
SSA_2284	histidyl-tRNA synthetase	144	147	160	163	Ampicillin
SSA_0100	DNA polymerase I	97	135	161	172	Ampicillin
SSA_1484	NAD-dependent DNA ligase LigA	107	131	166	180	Ampicillin
SSA_0825	RNA polymerase sigma factor RpoD	182	187	166	156	Ampicillin
SSA_1803	GTP-binding protein EngA	132	157	167	163	Ampicillin
SSA_0770	ribonucleotide-diphosphate reductase subunit alpha	228	236	171		Ampicillin
SSA_1565	two-component response transcriptional regulator	223	210	173	116	Ampicillin
SSA_0862	MurM protein	108	136	174	223	Ampicillin
SSA_1226	DNA topoisomerase IV subunit A	143	152	175	183	Ampicillin
SSA_0943	phosphate ABC transporter permease	135	167	185	194	Ampicillin
SSA_2203	30S ribosomal protein S2	679	298	185	147	Ampicillin
SSA_1805	primosomal protein DnaI	143	174	186	176	Ampicillin
SSA_0106	30S ribosomal protein S10	481	317	187	139	Ampicillin
SSA_1220	DNA gyrase subunit A	182	196	190	168	Ampicillin
SSA_2044	cysteinyl-tRNA synthetase	140	161	193	209	Ampicillin
SSA_1419	hypothetical protein	157	198	200	193	Ampicillin
SSA_0944	phosphate ABC transporter ATP-binding protein	137	177	203	231	Ampicillin
SSA_0571	aspartyl/glutamyl-tRNA amidotransferase subunit B	182	204	209	207	Ampicillin
SSA_0870	cell division protein FtsE	215	225	210	181	Ampicillin

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_2005	molecular chaperone DnaJ	285	233	213	209	Ampicillin
SSA_1094	ribosome biogenesis GTP-binding protein YsxC	295	249	214		Ampicillin
SSA_0547	4'-phosphopantetheinyl transferase	156	173	215	250	Ampicillin
SSA_1571	threonyl-tRNA synthetase	187	231	219	203	Ampicillin
SSA_0548	alanine racemase	169	178	224	262	Ampicillin
SSA_2356	replicative DNA helicase	199	203	228	228	Ampicillin
SSA_1557	SRPR, signal recognition particle-docking protein	162	184	229	265	Ampicillin
SSA_1935	3-oxoacyl-ACP synthase	280	277	229	204	Ampicillin
SSA_1622	50S ribosomal protein L1	835	453	229	158	Ampicillin
SSA_0756	alanyl-tRNA synthetase	210	228	231	215	Ampicillin
SSA_2069	prolyl-tRNA synthetase	193	225	235	219	Ampicillin
SSA_0871	cell division protein FtsX	215	255	236	224	Ampicillin
SSA_2144	glutamyl-tRNA synthetase	249	253	238	230	Ampicillin
SSA_1879	glycyl-tRNA synthetase subunit beta	202	227	241	248	Ampicillin
SSA_2208	preprotein translocase subunit SecE	273	286	247	196	Ampicillin
SSA_0437	30S ribosomal protein S6	943	459	253	181	Ampicillin
SSA_1934	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	264	279	256	250	Ampicillin
SSA_0438	single-stranded DNA-binding protein	846	481	256	217	Ampicillin
SSA_1800	UDP-N-acetylmuramate--L-alanine ligase	233	240	263	294	Ampicillin
SSA_1933	(3R)-hydroxymyristoyl-ACP dehydratase	291	281	275	251	Ampicillin
SSA_2169	glucose-1-phosphate uridylyltransferase	166	241	281	284	Ampicillin
SSA_1870	phospho-N-acetylmuramoyl-pentapeptide-transferase	226	275	293	308	Ampicillin
SSA_0661	isoleucyl-tRNA synthetase	213	278	295	304	Ampicillin
SSA_1930	acetyl-CoA carboxylase subunit alpha	327	305	296		Ampicillin
SSA_1932	acetyl-CoA carboxylase biotin carboxylase subunit	316	308	315	270	Ampicillin
SSA_1931	acetyl-CoA carboxylase subunit beta	302	311	318	271	Ampicillin
SSA_2240	Holliday junction resolvase-like protein	274	323	335	278	Ampicillin
SSA_0771	glutaredoxin-like protein	580	572	338	113	Ampicillin
SSA_0782	ATP synthase F0F1 subunit C	509	386	345	188	Ampicillin
SSA_0768	ribonucleotide-diphosphate reductase subunit beta	329	444	376	386	Ampicillin
SSA_0109	50S ribosomal protein L23	544	501	393		Ampicillin
SSA_1498	50S ribosomal protein L20	496	474	398	342	Ampicillin
SSA_0859	triosephosphate isomerase	553	517	464		Ampicillin
SSA_0656	cell division protein FtsZ	529	565	503		Ampicillin
SSA_0312	metallo-beta-lactamase superfamily hydrolase	419	499	516	505	Ampicillin
SSA_0177	DNA-directed RNA polymerase subunit beta'	477	585	637	614	Ampicillin
SSA_0783	ATP synthase F0F1 subunit A	820	785	680		Ampicillin
SSA_0131	30S ribosomal protein S11	920	917	682	414	Ampicillin
SSA_1105	50S ribosomal protein L7/L12	872	819	689		Ampicillin
SSA_0112	50S ribosomal protein L22	672	713	693	738	Ampicillin
SSA_0111	30S ribosomal protein S19	784	784	701	670	Ampicillin
SSA_0113	30S ribosomal protein S3	742	774	773	738	Ampicillin
SSA_0117	50S ribosomal protein L14	700	742	812	781	Ampicillin
SSA_0127	preprotein translocase subunit SecY	595	657	851	887	Ampicillin
SSA_0133	50S ribosomal protein L17	1021	1106	869	501	Ampicillin
SSA_0785	ATP synthase F0F1 subunit delta	926	956	883	753	Ampicillin

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_0119	50S ribosomal protein L5	664	751	899	910	Ampicillin
SSA_1062	50S ribosomal protein L27	1069	1214	987		Ampicillin
SSA_0120	30S ribosomal protein S8	779	897	1095	1111	Ampicillin
SSA_0116	30S ribosomal protein S17	876	991	1128	1149	Ampicillin
SSA_0786	proton-translocating ATPase, F1 sector subunit alpha	1201	1170	1158		Ampicillin
SSA_0114	50S ribosomal protein L16	1056	1097	1166	1175	Ampicillin
SSA_0122	50S ribosomal protein L6	804	958	1218	1288	Ampicillin
SSA_0302	phosphoglycerate kinase	888	1107	1241	1205	Ampicillin
SSA_0784	ATP synthase F0F1 subunit B	1263	1302	1246	1103	Ampicillin
SSA_2391	30S ribosomal protein S14	917	1057	1302	1521	Ampicillin
SSA_0123	50S ribosomal protein L18	825	963	1308	1358	Ampicillin
SSA_0124	30S ribosomal protein S5	906	1010	1321	1349	Ampicillin
SSA_0787	ATP synthase F0F1 subunit gamma	1318	1339	1366		Ampicillin
SSA_0788	ATP synthase F0F1 subunit beta	1341	1394	1512	1435	Ampicillin
SSA_0789	ATP synthase F0F1 subunit epsilon	1562	1689	1879	1894	Ampicillin
SSA_1184	DNA topoisomerase I	51	40		22	Ampicillin
SSA_0936	bifunctional riboflavin kinase/FMN adenylyltransferase	70	40		24	Ampicillin
SSA_1047	UDP-N-acetylenolpyruvoylglucosamine reductase	58	45		27	Ampicillin
SSA_0997	DNA polymerase III subunits gamma and tau	69	50			Ampicillin
SSA_1722	thymidylate kinase	74	52		31	Ampicillin
SSA_0692	D-Ala-D-Ala adding enzyme	76	57			Ampicillin
SSA_0338	hydroxymethylglutaryl-CoA synthase	77	64		61	Ampicillin
SSA_0652	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	84	66			Ampicillin
SSA_2368	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	72	68		47	Ampicillin
SSA_0001	chromosomal replication initiation protein	110	70		40	Ampicillin
SSA_2263	flavoprotein NrdI	109	71		35	Ampicillin
SSA_0013	PP family ATPase	88	74			Ampicillin
SSA_0197	dihydropteroate synthase	90	74			Ampicillin
SSA_1167	SRP54, signal recognition particle GTPase protein	88	75		39	Ampicillin
SSA_2073	undecaprenyl pyrophosphate synthase	93	77		41	Ampicillin
SSA_0569	aspartyl/glutamyl-tRNA amidotransferase subunit C	94	92		66	Ampicillin
SSA_1604	preprotein translocase subunit SecG	132	93		51	Ampicillin
SSA_1232	DNA topoisomerase IV subunit B	124	94			Ampicillin
SSA_2061	peptide deformylase	127	94		55	Ampicillin
SSA_1903	hypothetical protein	141	94			Ampicillin
SSA_0807	GTPase ObgE	123	100		66	Ampicillin
SSA_1092	dihydrofolate reductase	140	101		44	Ampicillin
SSA_1555	glucose-6-phosphate 1-dehydrogenase	134	127		72	Ampicillin
SSA_1619	ribosome recycling factor	143	129		80	Ampicillin
SSA_2262	arginyl-tRNA synthetase	214	172			Ampicillin
SSA_1938	enoyl-acyl carrier protein(ACP) reductase	270	191		76	Ampicillin
SSA_1748	manganese-dependent inorganic pyrophosphatase	231	193			Ampicillin
SSA_1939	acyl carrier protein	257	211		116	Ampicillin
SSA_1937	malonyl-CoA:ACP transacylase	246	216		118	Ampicillin
SSA_1500	translation initiation factor IF-3	297	232		100	Ampicillin
SSA_1811	6-phosphogluconate dehydrogenase	273	234		115	Ampicillin

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_1936	3-ketoacyl-ACP reductase	282	251			Ampicillin
SSA_0225	co-chaperonin GroES	479	308			Ampicillin
SSA_2202	elongation factor Ts	422	334			Ampicillin
SSA_0176	DNA-directed RNA polymerase subunit beta	304	342			Ampicillin
SSA_0107	50S ribosomal protein L3	531	389		202	Ampicillin
SSA_2034	50S ribosomal protein L13	701	486		235	Ampicillin
SSA_1265	50S ribosomal protein L19	832	490		208	Ampicillin
SSA_0108	50S ribosomal protein L4	633	510			Ampicillin
SSA_2109	elongation factor G	642	588			Ampicillin
SSA_0688	phosphoglyceromutase	813	637			Ampicillin
SSA_2111	30S ribosomal protein S12	800	643			Ampicillin
SSA_0110	50S ribosomal protein L2	758	695			Ampicillin
SSA_0129	translation initiation factor IF-1	822	696		365	Ampicillin
SSA_0440	30S ribosomal protein S18	1142	712		382	Ampicillin
SSA_2183	glucose-6-phosphate isomerase	680	731			Ampicillin
SSA_2136	50S ribosomal protein L34	1049	734		453	Ampicillin
SSA_1104	50S ribosomal protein L10	980	794			Ampicillin
SSA_2110	30S ribosomal protein S7	981	844			Ampicillin
SSA_0848	pyruvate kinase	1051	949			Ampicillin
SSA_0683	DNA-binding protein HU	1443	1216			Ampicillin
SSA_1189	ribosomal biogenesis GTPase	25			17	Ampicillin

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_0999	biotin--protein ligase				25	Heat
SSA_0006	peptidyl-tRNA hydrolase	35	34	26	33	Heat
SSA_1233	glycerol-3-phosphate acyltransferase PlsY	91	94	77	34	Heat
SSA_1452	second subunit of major exonuclease	27	33	22	47	Heat
SSA_0912	phenylalanyl-tRNA synthetase subunit alpha	78	69	60	48	Heat
SSA_0575	HAD superfamily hydrolase	65	50	52	49	Heat
SSA_1047	UDP-N-acetylenolpyruvoylglucosamine reductase	79	71	62	50	Heat
SSA_0625	phosphopantetheine adenylyltransferase				50	Heat
SSA_1091	thymidylate synthase	76	55	56	52	Heat
SSA_0720	DNA polymerase III subunit delta	61	48	52	54	Heat
SSA_0713	1-acyl-sn-glycerol-3-phosphate acyltransferase	109	121	88	56	Heat
SSA_2140	ribonuclease P protein component	82	72	69	59	Heat
SSA_0692	D-Ala-D-Ala adding enzyme	83	73	72	62	Heat
SSA_1925	seryl-tRNA synthetase	142	172	116	68	Heat
SSA_1209	inorganic polyphosphate/ATP-NAD kinase	53	38	35	69	Heat
SSA_1184	DNA topoisomerase I	91	85	74	72	Heat
SSA_0914	phenylalanyl-tRNA synthetase subunit beta	114	135	93	76	Heat
SSA_1491	methionine aminopeptidase	116	136	94	76	Heat
SSA_1606	dephospho-CoA kinase	56	42	43	80	Heat
SSA_1522	cell division protein FtsW	96	105	82	85	Heat

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_2368	acylglycerol--glycerol-3-phosphate 3-phosphatidyltrans	103	107	87	87	Heat
SSA_0569	aspartyl/glutamyl-tRNA amidotransferase subunit C	111	127	89	89	Heat
SSA_2061	peptide deformylase	112	132	92	95	Heat
SSA_2375	tryptophanyl-tRNA synthetase II	113	135	93	95	Heat
SSA_1784	glutamate racemase	119	139	96	101	Heat
SSA_0807	GTPase ObgE	123	145	104	101	Heat
SSA_2360	tRNA-specific 2-thiouridylase MnmA	110	123	89	102	Heat
SSA_1232	DNA topoisomerase IV subunit B	123	149	105	103	Heat
SSA_0338	hydroxymethylglutaryl-CoA synthase				110	Heat
SSA_1703	methionyl-tRNA synthetase	176	238	133	112	Heat
SSA_1880	glycyl-tRNA synthetase subunit alpha	131	153	106	113	Heat
SSA_0941	phosphate ABC transporter substrate-binding protein	135	167	114	116	Heat
SSA_2072	phosphatidate cytidylyltransferase	144	176	120	117	Heat
SSA_2356	replicative DNA helicase	133	161	114	118	Heat
SSA_0878	DNA gyrase subunit B	139	171	116	122	Heat
SSA_0804	phosphoglucosamine mutase	151	177	122	122	Heat
SSA_0944	phosphate ABC transporter ATP-binding protein	143	175	119	124	Heat
SSA_1571	threonyl-tRNA synthetase	145	176	120	126	Heat
SSA_1529	lysyl-tRNA synthetase	178	250	142	128	Heat
SSA_0869	peptide chain release factor 2	204	282	150	134	Heat
SSA_0570	aspartyl/glutamyl-tRNA amidotransferase subunit A	154	182	125	135	Heat
SSA_2069	prolyl-tRNA synthetase	166	210	131	135	Heat
SSA_1865	thioredoxin reductase	243	433	165	136	Heat
SSA_0001	chromosomal replication initiation protein			3047	136	Heat
SSA_1851	guanylate kinase	209	312	154	137	Heat
SSA_0943	phosphate ABC transporter permease	160	197	129	140	Heat
SSA_2169	glucose-1-phosphate uridylyltransferase	148	176	120	143	Heat
SSA_1903	hypothetical protein	200	261	148	145	Heat
SSA_0174	tyrosyl-tRNA synthetase	212	316	158	149	Heat
SSA_1226	DNA topoisomerase IV subunit A	159	188	127	150	Heat
SSA_0289	leucyl-tRNA synthetase	195	258	148	151	Heat
SSA_0756	alanyl-tRNA synthetase	180	250	144	157	Heat
SSA_1620	uridylate kinase	282	533	180	157	Heat
SSA_0128	adenylate kinase	309	599	182	157	Heat
SSA_1619	ribosome recycling factor	202	278	150	161	Heat
SSA_0547	4'-phosphopantetheinyl transferase	101	107	86	165	Heat
SSA_1800	UDP-N-acetylmuramate--L-alanine ligase	207	286	153	165	Heat
SSA_0870	cell division protein FtsE	239	354	163	165	Heat
SSA_1879	glycyl-tRNA synthetase subunit beta	186	251	145	170	Heat
SSA_1604	preprotein translocase subunit SecG	310	603	183	171	Heat
SSA_0571	aspartyl/glutamyl-tRNA amidotransferase subunit B	205	286	152	177	Heat
SSA_0770	ribonucleotide-diphosphate reductase subunit alpha	364	791	232	178	Heat
SSA_0871	cell division protein FtsX	270	512	167	181	Heat
SSA_1940	3-oxoacyl-ACP synthase	530	885	375	182	Heat

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_0002	DNA polymerase III subunit beta			3494	187	Heat
SSA_1811	6-phosphogluconate dehydrogenase	228	337	162	188	Heat
SSA_2262	arginyl-tRNA synthetase	280	520	178	195	Heat
SSA_0824	DNA primase	178	247	134	198	Heat
SSA_1937	malonyl-CoA:ACP transacylase	341	693	210	208	Heat
SSA_1936	3-ketoacyl-ACP reductase	345	695	211	214	Heat
SSA_1938	enoyl-acyl carrier protein(ACP) reductase	365	833	252	214	Heat
SSA_1748	manganese-dependent inorganic pyrophosphatase	245	471	166	221	Heat
SSA_1934	tyl-CoA carboxylase biotin carboxyl carrier protein sub	314	633	190	232	Heat
SSA_2144	glutamyl-tRNA synthetase	276	517	167	234	Heat
SSA_1935	3-oxoacyl-ACP synthase	326	661	203	235	Heat
SSA_1933	(3R)-hydroxymyristoyl-ACP dehydratase	315	640	197	241	Heat
SSA_1932	acetyl-CoA carboxylase biotin carboxylase subunit	327	667	209	259	Heat
SSA_0768	ribonucleotide-diphosphate reductase subunit beta	575	946	391	264	Heat
SSA_0176	DNA-directed RNA polymerase subunit beta	355	699	225	267	Heat
SSA_2240	Holliday junction resolvase-like protein	315	643	202	282	Heat
SSA_1939	acyl carrier protein	950	1252	511	285	Heat
SSA_1930	acetyl-CoA carboxylase subunit alpha	364	813	243	286	Heat
SSA_1931	acetyl-CoA carboxylase subunit beta	364	817	247	288	Heat
SSA_1500	translation initiation factor IF-3	1109	1253	512	364	Heat
SSA_2005	molecular chaperone DnaJ	151	182	124	366	Heat
SSA_0656	cell division protein FtsZ	432	862	301	392	Heat
SSA_0312	metallo-beta-lactamase superfamily hydrolase	441	871	318	403	Heat
SSA_0177	DNA-directed RNA polymerase subunit beta'	570	895	375	448	Heat
SSA_0106	30S ribosomal protein S10	1384	1500	584	462	Heat
SSA_0107	50S ribosomal protein L3	1289	1394	544	489	Heat
SSA_0782	ATP synthase F0F1 subunit C	494	878	374	496	Heat
SSA_0109	50S ribosomal protein L23	1222	1313	535	502	Heat
SSA_0859	triosephosphate isomerase	721	1090	476	534	Heat
SSA_0771	glutaredoxin-like protein	800	1147	484	542	Heat
SSA_0112	50S ribosomal protein L22	1336	1428	553	554	Heat
SSA_0108	50S ribosomal protein L4	1438	1685	629	573	Heat
SSA_0127	preprotein translocase subunit SecY	1135	1267	516	579	Heat
SSA_0113	30S ribosomal protein S3	1326	1399	548	581	Heat
SSA_2202	elongation factor Ts	890	1225	511	589	Heat
SSA_0111	30S ribosomal protein S19	1471	1803	657	591	Heat
SSA_2109	elongation factor G	1224	1329	536	607	Heat
SSA_0847	6-phosphofructokinase	800	1161	491	614	Heat
SSA_0110	50S ribosomal protein L2	1482	1815	661	614	Heat
SSA_0688	phosphoglyceromutase	1214	1269	519	636	Heat
SSA_0117	50S ribosomal protein L14	1348	1430	583	636	Heat
SSA_2183	glucose-6-phosphate isomerase				642	Heat
SSA_0225	co-chaperonin GroES	191	255	147	662	Heat
SSA_0785	ATP synthase F0F1 subunit delta	573	918	389	662	Heat
SSA_0119	50S ribosomal protein L5	1437	1568	602	664	Heat

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_0783	ATP synthase F0F1 subunit A	644	1058	406	672	Heat
SSA_1498	50S ribosomal protein L20	1685	2347	700	677	Heat
SSA_1223	30S ribosomal protein S1	1400	1547	585	680	Heat
SSA_1310	30S ribosomal protein S16	1459	1769	640	686	Heat
SSA_0123	50S ribosomal protein L18	1584	2091	697	694	Heat
SSA_0122	50S ribosomal protein L6	1577	1918	681	704	Heat
SSA_0116	30S ribosomal protein S17	1691	2488	702	709	Heat
SSA_0114	50S ribosomal protein L16	1833		747	731	Heat
SSA_2350	30S ribosomal protein S4	1797	3979	718	738	Heat
SSA_0786	proton-translocating ATPase, F1 sector subunit alpha	607	969	401	746	Heat
SSA_0120	30S ribosomal protein S8	1701	2754	708	777	Heat
SSA_0133	50S ribosomal protein L17	2262		834	794	Heat
SSA_0787	ATP synthase F0F1 subunit gamma	631	969	404	803	Heat
SSA_0132	DNA-directed RNA polymerase subunit alpha	2043		825	807	Heat
SSA_0788	ATP synthase F0F1 subunit beta	650	1066	434	817	Heat
SSA_0784	ATP synthase F0F1 subunit B	765	1105	480	821	Heat
SSA_0124	30S ribosomal protein S5	1835		755	831	Heat
SSA_2391	30S ribosomal protein S14	2020		809	845	Heat
SSA_2203	30S ribosomal protein S2	1816	5347	736	851	Heat
SSA_0131	30S ribosomal protein S11	1999		796	857	Heat
SSA_0789	ATP synthase F0F1 subunit epsilon	721	1070	468	860	Heat
SSA_1623	50S ribosomal protein L11	1801	4838	723	873	Heat
SSA_0226	molecular chaperone GroEL	285	534	182	910	Heat
SSA_0438	single-stranded DNA-binding protein	2258		831	919	Heat
SSA_2034	50S ribosomal protein L13	1926		763	928	Heat
SSA_0848	pyruvate kinase	1284	1367	542	929	Heat
SSA_2007	molecular chaperone DnaK	361	725	227	933	Heat
SSA_2111	30S ribosomal protein S12	2048		826	961	Heat
SSA_0437	30S ribosomal protein S6	2553		975	987	Heat
SSA_2107	glucosamine--fructose-6-phosphate aminotransferase	404	859	289	1001	Heat
SSA_0129	translation initiation factor IF-1	2272		919	1005	Heat
SSA_1622	50S ribosomal protein L1	1962		763	1010	Heat
SSA_1104	50S ribosomal protein L10	2829		1028	1027	Heat
SSA_2110	30S ribosomal protein S7	2237		826	1054	Heat
SSA_1105	50S ribosomal protein L7/L12	2586		977	1064	Heat
SSA_0440	30S ribosomal protein S18	2779		1027	1236	Heat
SSA_1062	50S ribosomal protein L27	2392		930	1299	Heat
SSA_1265	50S ribosomal protein L19	2875		1032	1546	Heat
SSA_2136	50S ribosomal protein L34	3400		1417	1595	Heat
SSA_0683	DNA-binding protein HU	3288		1195	1782	Heat
SSA_1992	fructose-bisphosphate aldolase	2936		1070	2305	Heat
SSA_0886	phosphopyruvate hydratase	3363		1416	3796	Heat
SSA_1520	elongation factor Tu	5705		2118	3955	Heat
SSA_2108	glyceraldehyde 3-phosphate dehydrogenase	5680		1668	4178	Heat

Synonym	Product	Time 0	Time 10	Time 20	Time 30	Treatment
SSA_2066	DNA polymerase III PolC	60	46	47		Heat
SSA_0652	DP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetas	77	68	57		Heat
SSA_0653	hospho-muramoylpentapeptide beta-N- acetylglucosa	80	71	62		Heat
SSA_0548	alanine racemase	89	82	73		Heat
SSA_0862	MurM protein	93	95	78		Heat
SSA_1495	S-adenosylmethionine synthetase	93	97	78		Heat
SSA_0013	PP family ATPase	94	102	79		Heat
SSA_0336	isopentenyl pyrophosphate isomerase	94	103	81		Heat
SSA_0335	phosphomevalonate kinase	96	103	82		Heat
SSA_0691	D-alanyl-alanine synthetase A	97	105	84		Heat
SSA_1152	peptide chain release factor 1	97	107	85		Heat
SSA_1819	valyl-tRNA synthetase	101	107	86		Heat
SSA_2073	undecaprenyl pyrophosphate synthase	105	108	87		Heat
SSA_0010	cell division protein DivIC	118	138	96		Heat
SSA_1871	penicillin-binding protein 2X	132	157	108		Heat
SSA_1419	hypothetical protein	155	184	126		Heat
SSA_1220	DNA gyrase subunit A	170	223	132		Heat
SSA_0661	isoleucyl-tRNA synthetase	176	237	132		Heat
SSA_0825	RNA polymerase sigma factor RpoD	208	305	153		Heat
SSA_2208	preprotein translocase subunit SecE	402	849	261		Heat
SSA_0302	phosphoglycerate kinase	851	1222	506		Heat
SSA_0020	ribose-phosphate pyrophosphokinase			3641		Heat

Supplemental Table 3. Proteomic analysis of essential proteins in both treatments. Statistically significant proteomic variations with respect to control (T_0) are shown, with the stressor used (ampicillin or heat) at 10, 20, and 30 minutes post-stress exposure as T_{10} / T_0, T_{20} / T_0 , and T_{30} / T_0 respectively.

Locus tag	**Product**	**Paralogs**	**T10/T0**	**T20/T0**	**T30/T0**	**treatment**
SSA_1903	hypothetical protein	No			0.073749	Ampicillin
SSA_0870	cell division protein FtsE	Yes	0.655285	0.404556	0.272077	Ampicillin
SSA_0804	phosphoglucomutase/phosphomannomutase family protein	No	0.009648	0.024687		Ampicillin
SSA_2107	D-fructose-6-phosphate amidotransferase	Yes	0.31974	0.818653	1.003859	Ampicillin
SSA_2262	arginyl-tRNA synthetase	No	0.350381	0.445693	0.334065	Ampicillin
SSA_0174	tyrosyl-tRNA synthetase	No	0.170099			Ampicillin
SSA_2375	tryptophanyl-tRNA synthetase II	No	0.008841	0.192132		Ampicillin
SSA_2144	glutamyl-tRNA synthetase	No	0.442076	0.875678	0.191992	Ampicillin
SSA_0571	aspartyl/glutamyl-tRNA amidotransferase subunit B	No		0.571245		Ampicillin
SSA_0569	aspartyl/glutamyl-tRNA amidotransferase subunit C	No	0.165074	0.498775	0.262892	Ampicillin
SSA_1925	seryl-tRNA synthetase	Yes	0.648928	0.424951	0.480944	Ampicillin
SSA_2044	cysteinyl-tRNA synthetase	Yes		2.672498		Ampicillin
SSA_1571	threonyl-tRNA synthetase	Yes		0.607366		Ampicillin
SSA_2069	prolyl-tRNA synthetase	Yes	0.284362	0.275085	0.529658	Ampicillin
SSA_1529	lysyl-tRNA synthetase	Yes	0.147622	0.379166	0.219281	Ampicillin
SSA_2284	histidyl-tRNA synthetase	Yes	0.17083	0.72332	0.109667	Ampicillin
SSA_0656	cell division protein FtsZ	No	0.267969	0.734973	0.596965	Ampicillin
SSA_1872	cell division protein	No	0.41166			Ampicillin
SSA_0225	co-chaperonin GroES	No	0.484675	0.60199	0.653335	Ampicillin
SSA_2007	molecular chaperone DnaK	No	0.5	0.669767	0.587874	Ampicillin
SSA_0226	chaperonin GroEL	No	0.148883	0.277221	1.124138	Ampicillin
SSA_0683	DNA-binding protein HU	No	0.609223	0.6914	0.60596	Ampicillin
SSA_1419	hypothetical protein	No	0.243812	0.274854		Ampicillin
SSA_1938	enoyl-acyl carrier protein(ACP) reductase	No	0.252937	0.681252		Ampicillin
SSA_1937	malonyl-CoA:ACP transacylase	No	0.035334	0.312855	0.210202	Ampicillin
SSA_1935	3-oxoacyl-(acyl carrier protein) synthase II	No	0.013765	0.415299	0.4992	Ampicillin
SSA_1936	3-ketoacyl-(acyl-carrier-protein) reductase	Yes		0.450505		Ampicillin
SSA_0302	phosphoglycerate kinase	No	0.274229	0.542975	0.249353	Ampicillin
SSA_2108	glyceraldehyde 3-phosphate dehydrogenase	No	0.641549	0.835227	0.467241	Ampicillin
SSA_0859	triosephosphate isomerase	No	0.144384	0.35394	0.079689	Ampicillin
SSA_0688	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Yes	0.333178	1.22479	0.547126	Ampicillin
SSA_0886	phosphopyruvate hydratase	No	0.834862	0.359873	0.25656	Ampicillin
SSA_0847	6-phosphofructokinase	No	0.303351	0.59115	0.620767	Ampicillin

Locus tag	Product	Paralogs	T10/T0	T20/T0	T30/T0	treatment
SSA_1992	fructose-bisphosphate aldolase	No	0.2125	0.899563	0.324103	Ampicillin
SSA_2183	glucose-6-phosphate isomerase	No	0.62	0.34058	0.037155	Ampicillin
SSA_0848	pyruvate kinase	No	0.428358	0.245802	0.585915	Ampicillin
SSA_1094	GTPase EngB	Yes	0.100179			Ampicillin
SSA_0692	D-Ala-D-Ala adding enzyme	Yes	0.667939	0.627635	0.181782	Ampicillin
SSA_1748	putative manganese-dependent inorganic pyrophosphatase	No	2.908333	0.65873	0.223283	Ampicillin
SSA_0789	F0F1 ATP synthase subunit epsilon	No	1.165182	0.554109		Ampicillin
SSA_0788	F0F1 ATP synthase subunit beta	Yes	1.386651	0.373684	0.139202	Ampicillin
SSA_0786	proton-translocating ATPase, F1 sector, alpha subunit	Yes	0.35931	1.638037	0.35575	Ampicillin
SSA_2169	glucose-1-phosphate uridylyltransferase	Yes	0.751751	0.002083	0.590011	Ampicillin
SSA_1811	6-phosphogluconate dehydrogenase	No	0.444448	0.8	0.351281	Ampicillin
SSA_0020	ribose-phosphate pyrophosphokinase	Yes	0.344099	0.288609		Ampicillin
SSA_0013	PP family ATPase	No	0.084913	0.498801		Ampicillin
SSA_2061	peptide deformylase	Yes	6.327501	0.055231	0.028605	Ampicillin
SSA_0543	preprotein translocase subunit SecA	Yes	0.543841	0.668991	0.501244	Ampicillin
SSA_1167	SRP54, signal recognition particle GTPase protein	Yes	0.236258	0.52796	0.453871	Ampicillin
SSA_0128	adenylate kinase	No	0.123899	0.350267	0.161429	Ampicillin
SSA_0770	ribonucleotide-diphosphate reductase subunit alpha	No	0.401353	0.791165	0.065575	Ampicillin
SSA_0768	ribonucleotide-diphosphate reductase subunit beta	No	0.426017	0.460737	0.630547	Ampicillin
SSA_0002	DNA polymerase III subunit beta	No	0.48555	0.6	0.642951	Ampicillin
SSA_0176	DNA-directed RNA polymerase subunit beta	No	0.660057	0.805955	2.063871	Ampicillin
SSA_0177	DNA-directed RNA polymerase subunit beta'	No	0.308139	0.475096	0.176715	Ampicillin
SSA_0132	DNA-directed RNA polymerase subunit alpha	No	0.361496	1.767123	0.705939	Ampicillin
SSA_0771	glutaredoxin-like protein	No	0.400136	0.588302	0.503819	Ampicillin
SSA_1620	uridylate kinase	No	0.888149	4.270677	0.264632	Ampicillin
SSA_1865	thioredoxin reductase	Yes	0.065259	0.233502	0.351308	Ampicillin
SSA_1932	acetyl-CoA carboxylase biotin carboxylase subunit	Yes	0.237504	0.409092	1.640307	Ampicillin
SSA_1622	50S ribosomal protein L1	No	0.572563	0.686131	0.365206	Ampicillin
SSA_0123	50S ribosomal protein L18	No	0.25328	0.356719		Ampicillin
SSA_0109	50S ribosomal protein L23	No	0.453559	0.684874	0.5648	Ampicillin
SSA_0119	50S ribosomal protein L5	No	0.127666	0.573171	0.074437	Ampicillin
SSA_2034	50S ribosomal protein L13	No	0.258342	0.818713	0.332795	Ampicillin
SSA_0117	50S ribosomal protein L14	No	0.580348	0.71978	1.311321	Ampicillin
SSA_0122	50S ribosomal protein L6	No	0.723473	0.487952	0.088699	Ampicillin

Locus tag	Product	Paralogs	T10/T0	T20/T0	T30/T0	treatment
SSA_0106	30S ribosomal protein S10	No	0.477509	0.920523	0.429872	Ampicillin
SSA_1062	50S ribosomal protein L27	No	0.365068	0.626263	0.394774	Ampicillin
SSA_0116	30S ribosomal protein S17	No	0.0605	0.219095	0.115806	Ampicillin
SSA_1265	50S ribosomal protein L19	No	0.225006	2.694524	0.337376	Ampicillin
SSA_0113	30S ribosomal protein S3	No	0.062283	1.501916	0.13692	Ampicillin
SSA_0107	50S ribosomal protein L3	No	0.519203	0.504673	0.146391	Ampicillin
SSA_0124	30S ribosomal protein S5	No	0.42158	0.647059	0.677686	Ampicillin
SSA_0120	30S ribosomal protein S8	No	0.146749	0.295841	0.052314	Ampicillin
SSA_2111	30S ribosomal protein S12	No	0.684307	0.747678	0.86828	Ampicillin
SSA_0108	50S ribosomal protein L4	No	0.59434	0.906504	2.208756	Ampicillin
SSA_1310	30S ribosomal protein S16	No	0.261495	0.715163	0.016683	Ampicillin
SSA_1105	50S ribosomal protein L7/L12	No	0.2646	1.176471	0.051328	Ampicillin
SSA_0111	30S ribosomal protein S19	No	0.650716	0.055465		Ampicillin
SSA_0110	50S ribosomal protein L2	No	0.399533	1.309309	0.331395	Ampicillin
SSA_0112	50S ribosomal protein L22	No	0.480851	0.809249	0.576419	Ampicillin
SSA_2110	30S ribosomal protein S7	No	0.395259	0.765546	0.019217	Ampicillin
SSA_1623	50S ribosomal protein L11	No	0.272389	0.497908	0.466195	Ampicillin
SSA_0114	50S ribosomal protein L16	No	0.137425	0.756757	0.209936	Ampicillin
SSA_2350	30S ribosomal protein S4	No	0.379228	0.856338	0.305862	Ampicillin
SSA_1104	50S ribosomal protein L10	No	0.638498	1.904412	0.227318	Ampicillin
SSA_2203	30S ribosomal protein S2	No	0.319588	0.803571	0.189453	Ampicillin
SSA_0131	30S ribosomal protein S11	No	0.273932	0.404181	0.540104	Ampicillin
SSA_1498	50S ribosomal protein L20	No	0.275444	0.509325	0.720027	Ampicillin
SSA_0133	50S ribosomal protein L17	No	0.251553	0.354041	0.628571	Ampicillin
SSA_0440	30S ribosomal protein S18	No	0.385594	0.765152	0.745235	Ampicillin
SSA_0437	30S ribosomal protein S6	No	0.712	0.785563	0.354854	Ampicillin
SSA_1223	30S ribosomal protein S1	Yes	0.784314	0.754206	0.38266	Ampicillin
SSA_0312	metallo-beta-lactamase superfamily hydrolase putative	Yes	0.247899	0.295159		Ampicillin
SSA_0825	RNA polymerase sigma factor RpoD	No	0.445952	0.723259	0.424286	Ampicillin
SSA_2202	elongation factor Ts	No	0.278203	0.371743	0.349309	Ampicillin
SSA_1500	translation initiation factor IF-3	No	0.495522	0.312086	0.430805	Ampicillin
SSA_1619	ribosome recycling factor	No	0.152234	0.516624	0.114228	Ampicillin
SSA_1520	elongation factor Tu	Yes	0.452703	1.278351	0.674877	Ampicillin
SSA_2109	elongation factor G	Yes	0.181217	0.499029	0.2625	Ampicillin

Locus tag	Product	Paralogs	T10/T0	T20/T0	T30/T0	treatment
SSA_1784	glutamate racemase	No	1.493953623		475.51	heat
SSA_1062	50S ribosomal protein L27	No	0.91173913		167.91	heat
SSA_0120	30S ribosomal protein S8	No	3.574463565		136.92	heat
SSA_2262	arginyl-tRNA synthetase	No			91.88	heat
SSA_0886	phosphopyruvate hydratase	No	0.770386676	1.001351	20.32	heat
SSA_0825	RNA polymerase sigma factor RpoD	No	0.740904041		10.91046	heat
SSA_2109	elongation factor G	Yes	1.064865173	0.350986	3.765464	heat
SSA_0110	50S ribosomal protein L2	No	2.154318058	0.098649	3.305554	heat
SSA_1520	elongation factor Tu	Yes	1.736	0.337867	1.244625	heat
SSA_1623	50S ribosomal protein L11	No	1.309068672	0.228982	0.794916	heat
SSA_0688	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Yes	2.220370868	0.239902	0.644632	heat
SSA_1209	inorganic polyphosphate/ATP-NAD kinase	No	0.437114988	0.242037	0.627101	heat
SSA_0131	30S ribosomal protein S11	No	7.233011912	0.564525	0.575203	heat
SSA_2111	30S ribosomal protein S12	No	2.079040033	0.28027	0.377758	heat
SSA_0302	phosphoglycerate kinase	No	1.820977109	0.062235	0.359923	heat
SSA_1992	fructose-bisphosphate aldolase	No	1.424274667	0.369661	0.353304	heat
SSA_0109	50S ribosomal protein L23	No	1.16752787	0.590794	0.345929	heat
SSA_0117	50S ribosomal protein L14	No	0.781553398	0.424502	0.328784	heat
SSA_1105	50S ribosomal protein L7/L12	No	0.774556617	0.147104	0.263772	heat
SSA_0122	50S ribosomal protein L6	No	0.25035712	0.529564	0.21076	heat
SSA_1104	50S ribosomal protein L10	No	2.966196919	0.301618	0.177537	heat
SSA_0124	30S ribosomal protein S5	No	1.023551399	0.449187	0.144706	heat
SSA_0132	DNA-directed RNA polymerase subunit alpha	No	0.842214623	0.687412	0.013556	heat
SSA_0225	co-chaperonin GroES	No	2.643621894	0.203503	0.006051	heat
SSA_1310	30S ribosomal protein S16	No	2.060722717		0.005086	heat
SSA_0226	chaperonin GroEL	No	3.415957075		0.003353	heat
SSA_0683	DNA-binding protein HU	No	3.040446467	0.831545	0.003194	heat
SSA_0133	50S ribosomal protein L17	No	0.873557773	0.279579	0.002876	heat
SSA_0106	30S ribosomal protein S10	No	1.879242701	0.129131	0.00059	heat
SSA_0656	cell division protein FtsZ	No	1.478773719	0.674723	0.000348	heat
SSA_0437	30S ribosomal protein S6	No	0.519787437	0.030913	0.000143	heat
SSA_0848	pyruvate kinase	No	0.807763014	0.578022	7.99E-06	heat

Locus tag	Product	Paralogs	T10/T0	T20/T0	T30/T0	treatment
SSA_2108	glyceraldehyde 3-phosphate dehydrogenase	No	0.570621469	1.141026	1.18E-06	heat
SSA_1419	hypothetical protein	No		2.398288		heat
SSA_0847	6-phosphofructokinase	No	0.980723392	0.929064		heat
SSA_1498	50S ribosomal protein L20	No	30.97			heat
SSA_0128	adenylate kinase	No	11.37099494			heat
SSA_0112	50S ribosomal protein L22	No	3.972335898			heat
SSA_2203	30S ribosomal protein S2	No	2.871401152			heat
SSA_0113	30S ribosomal protein S3	No	2.718928044			heat
SSA_2202	elongation factor Ts	No	2.693261369			heat
SSA_2034	50S ribosomal protein L13	No	2.272107809			heat
SSA_1938	enoyl-acyl carrier protein(ACP) reductase	No	1.846979417			heat
SSA_0116	30S ribosomal protein S17	No	1.746993272			heat
SSA_2350	30S ribosomal protein S4	No	1.712919705			heat
SSA_1223	30S ribosomal protein S1	Yes	1.40727542			heat
SSA_1622	50S ribosomal protein L1	No	1.397341987			heat
SSA_0440	30S ribosomal protein S18	No	1.343714009			heat
SSA_1721	DNA polymerase III subunit delta'	Yes	1.219287847			heat
SSA_1265	50S ribosomal protein L19	No	1.212196246			heat
SSA_0107	50S ribosomal protein L3	No	1.057142857			heat

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