

Intracellular/Surface Moonlighting Proteins

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THESIS

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I dedicate my dissertation work to my family, especially to my parents, Xiaowen and Minxue who have supported and encouraged me all the time even while they are in China. A special gratitude to all my cousins, for taking care of my parents and never making them feel lonely.

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LIST OF ABBREVIATIONS

COG	Clusters of Orthologous Groups of Proteins
EF	Elongation Factor
GAPDH	Glyceraldehyde-3-phosphate Dehydrogenase
IF	Initiation Factor
Hsp	Heat Shock Protein
GAS	Group A Streptococcus
GBS	Group B Streptococcus
NCBI	National Center for Biotechnology Information
PDB	Protein Data Bank
PGM	Phosphoglycerate Mutase
PspA	Pneumococcal Surface Protein A
TMBs	Transmembrane Beta-barrels
TMHs	Transmembrane Alpha-helices
TPI	Triosephosphate Isomerase
T1SS to T6SS	Type I-VI Secretion Systems
UniProtKB	Universal Protein Resource Knowledgebase

SUMMARY

Bacterial surface proteins play an important role in bacterial infection and virulence. More and more intracellular proteins have been found also to be located on the cell surface where they perform a second function. The intracellular proteins that perform a second function on the cell surface were defined as intracellular/surface moonlighting proteins in this work. These proteins have been commonly identified in cell surface proteomes or cell wall proteomes in proteomics studies. Published proteomics studies were used to collect information about proteins found on the cell surface in this work. Protein sequences were obtained from UniProtKB and NCBI databases and were then analyzed by bioinformatics tools. I found that more than 1,100 out of the 3,027 proteins that were found to be located on the cell surface through proteomics studies lack transmembrane alpha-helices, transmembrane beta-barrels and signal peptides for secretion. Many of these proteins are chaperones and proteins involved in carbohydrate metabolism and biogenesis.

This work shows that the presence of intracellular proteins on the cell surface is more common than previously expected. This large number of examples of intracellular/cell surface proteins will help scientists and researchers to learn more about the role the intracellular/surface moonlighting proteins play in bacterial infection and virulence. Additional information about proteins located on the cell surface can also be important in developing new vaccine or biomarkers.

I. INTRODUCTION

A. Moonlighting Proteins

Moonlighting proteins are a subset of multifunctional proteins in which the multiple functions are not due to gene fusions, families of homologous proteins, promiscuous enzyme activity or splice variants [1]–[3]. Also, proteins that have the same functions in different cell types are not counted as moonlighting proteins [3].

To date, around 300 moonlighting proteins have been identified [4]. More moonlighting proteins are likely to be found in the future. In terms of functions, many of the identified moonlighting proteins are receptors (e.g., Neuropilin, which is a VEGF receptor in endothelial cells but the receptor for semaphorin III in nerve axons [5]), metabolic enzymes (e.g., phosphoglucose isomerase is a glycolytic enzyme and also a neurotrophic factor, an autocrine motility factor and a differentiation and maturation mediator [6], [7]), chaperones (e.g., some ATP-dependent proteases, including Clp and FtsH in bacteria also act as chaperones [8]), ribosomal proteins (e.g., *E. coli* ribosomal protein S1 is also a subunit of the replicase of RNA phages [9]) and transmembrane channels (e.g., cystic fibrosis transmembrane-conductance regulator is a chloride channel and a regulator of the ENaC channel [10]).

B. Intracellular/Surface Moonlighting Proteins

Moonlighting proteins may perform different functions as a result of different localization in a cell, expression in different cell types, different oligomeric states, or changes in the cellular concentrations of a ligand, cofactor, substrate or product [1]. My

project is focused on proteins that have both functions inside the cell and on the cell surface. I will refer to these proteins as intracellular/surface moonlighting proteins.

1. Roles of Intracellular Proteins on the Cell Surface

After the first discovery of a glycolytic enzyme, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), on the surface of group A streptococci [11], [12], a lot of research has been done on the multiple functions of GAPDH found on the surfaces of several species of bacteria. On the cell surface, GAPDH can moonlight as an adhesin for cell binding in *Streptococcus suis* serotype 2 [13]. In *S. pyogenes*, GAPDH is a cell surface receptor for plasminogen [11], [14]. GAPDH has also been found to have multiple functions in other organisms. In gram-negative bacteria such as *E. coli*, GAPDH has been found to be secreted outside the cell where it plays a role in signal transduction [15]. Besides GAPDH, other cytoplasmic enzymes in glycolysis, such as enolase/phosphopyruvate hydratase, also moonlight on the cell surface. In *Lactobacillus plantarum*, surface located enolase has the ability to bind fibronectin, a major host component of the ECM [16]. In some group A *Streptococci* species, streptococcal surface enolase (SEN) also serves as a plasminogen-binding protein [17].

Glycolytic enzymes are not the only group of intracellular proteins that have been found to play a second role on the cell surface. In addition to playing a critical role in protein folding, some chaperones can be released onto the cell surface. Hsp70/DnaK from *Bifidobacterium* is a chaperone, generally thought to be intracellular, but it was also observed to be surface exposed by transmission electron microscopy and showed high

affinity to human plasminogen [18]. *Legionella pneumophila* Hsp 60/GroEL was identified as an adhesin and was shown to promote binding of this pathogenic bacterium to HeLa cells by which it can mediate invasion [19]. More examples of intracellular/surface moonlighting proteins are listed in Table 1.

Intracellular/surface moonlighting proteins not only exist in bacteria, but also in fungi, protozoan parasites and mammalian cells. For instance, Hsp 60/GroEL is displayed on the cell surface of eukaryotic Caco-2 cells and acts as host cell receptor for the *Listeria* adhesion protein (LAP) in the pathogen *Listeria monocytogenes* [20]. Hsp60 has been identified by internal microprotein sequencing to be the cell surface binding protein for HDL in human cell lines. Other examples are shown in Table 2. But in this project, we focus on the bacterial intracellular/surface moonlighting proteins in bacteria.

Table 1. Examples of previously identified bacterial intracellular/surface moonlighting proteins in the literature

Intracellular function	Surface function	Species	Gram type
6-phosphofructokinase	Binds plasminogen	<i>Streptococcus oralis</i> [21]	Positive
Enolase	Binds plasminogen and laminin	<i>Bacillus anthracis</i> [22]	Positive
GAPDH, Elongation factor Tu (EF-Tu) and triosephosphate isomerase (TPI)	Bind Caco-2 cells	<i>Lactobacillus plantarum</i> [23]	Positive
EF-Tu and GroEL	Adhere to mucin and human epithelial cells	<i>Lactobacillus Johnsonii</i> [24], [25]	Positive
Hsp60, GroEL	Adheres to eukaryotic host cells, binds glycosphingolipids	<i>Haemophilus ducreyi</i> [26], [27]	Negative
Hsp60, GroEL	Cell surface protein controlling bacterial growth	<i>Helicobacter pylori</i> [28]	Negative
Hsp60, GroEL	Cell adhesion	<i>Chlamydia pneumoniae</i> [29]	Negative
Hsp65, GroEL2	Cell surface protein that inhibits bacterial association with macrophages	<i>Mycobacterium tuberculosis</i> [30]	Acid-fast Gram-positive bacterium
Peroxiredoxin, DnaK and enolase	Bind plasminogen	<i>Neisseria meningitides</i> [31]	Negative
Ornithine carbamoyltransferase	Binds fibronectin	<i>Staphylococcus epidermidis</i> [32]	Positive
Glucosyltransferase	Adhesin to human endothelial cells	<i>Streptococcus gordonii</i> [33]	Positive
Malate synthase	Binds fibronectin and laminin	<i>Mycobacterium tuberculosis</i> [34]	Acid-fast Gram-positive bacterium
Glutamine synthetase	Binds laminin, fibronectin, collagen I, plasminogen	<i>Lactobacillus crispatus</i> [35]	Positive
TPI	Adhesion to fungal pathogen	<i>Staphylococcus aureus</i> [36]	Positive
Pyruvate kinase	Recognizes and binds to yeast mannan	<i>Lactococcus lactis</i> [37]	Positive

Table 2. Examples of intracellular/surface moonlighting proteins in non-bacterial species

Intracellular function	Surface function	Species	Kind of species
TPI	Binds laminin	<i>Candida albicans</i> [38]	Fungus
Enolase	Binds plasminogen	<i>Pneumocystis carinii</i> [39]	Fungus
GAPDH	Binds fibronectin and laminin	<i>Candida albicans</i> [40]	Fungus
Peroxisomal catalase	Binds plasminogen	<i>Candida albicans</i> [41]	Fungus
NADP ⁺ dependent malic enzyme	Adheres to erythrocytes and HeLa cells	<i>Trichomonas vaginalis</i> [42]	Protozoan parasite
Alcohol dehydrogenase	Binds fibronectin and laminin	<i>Entamoeba histolytica</i> [43]	Protozoan parasite
GAPDH	Binds fibronectin, plasminogen and collagen	<i>Trichomonas vaginalis</i> [44]	Protozoan parasite

The examples of intracellular/surface moonlighting proteins are by no means limited to the proteins listed above, but these examples prove that the presence of intracellular proteins at “unexpected” locations is not always because of coincidence or experimental artifacts. Some intracellular proteins in pathogenic bacteria, fungi and protozoa have the ability to get secreted onto the cell surface and interact with plasminogen and host components in the extracellular matrix (ECM), such as fibronectin and laminin [45] (Figure 1). This interaction enables pathogens to colonize host tissues and plays an essential role in infection and virulence [45].

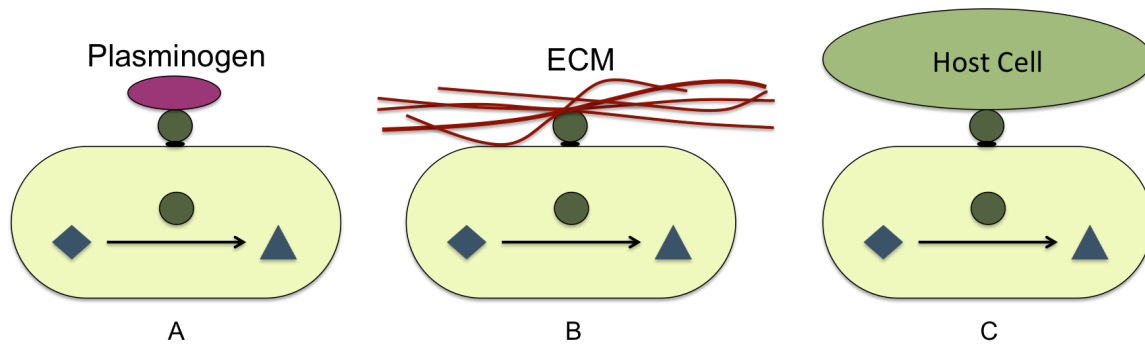


Figure 1. Intracellular proteins that perform another function on the cell surface. An intracellular/surface moonlighting protein can function as an enzyme inside of the cell, converting a substrate (diamond) to a product (triangle) (A-C) and can also present on the cell surface. Some of them can bind to plasminogen and convert plasminogen to plasmin (A), or bind to extracellular matrix (such as fibronectin, collagen and laminin), or interact with host cell surface proteins (C). These intracellular proteins on the cell surface often play an important role in invasion, infection and virulence.

2. Protein Secretion and Secretory Pathways

The correct subcellular localization is important for proteins to function properly. More than a third of all proteins synthesized in the cytoplasm need to be transported across the cell membrane upon synthesis to function as toxins, adhesins, invasins or for other roles [46]. Most secreted proteins are co-translationally transported across a membrane. These secreted pre-proteins carry a signal peptide at the N-terminus that can be recognized by the translocation system. For secreted proteins, the signal peptide is cleaved when the protein is translocated through the cell membrane.

Gram-negative bacteria have an inner plasma membrane as well as an outer membrane. This architecture requires secreted proteins to be transported through the inner membrane, periplasmic space and finally the outer membrane. So far, at least six

types of secretory pathways have been found in Gram-negative bacteria, named the type I-VI secretion systems (T1SS to T6SS). They can be classified as Sec dependent and Sec independent pathways. The Sec dependent secretion system generally relies on a signal peptide on the protein's N-terminus that leads to co-translational transport of proteins across the inner membrane to the periplasm [47]. In the Sec independent pathways, such as the type I secretion system (T1SS), also known as an ABC protein exporter-mediated secretion system, the secreted proteins are directed toward the secretory pathway because of a C-terminal secretion signal [48]. In an alternative Sec independent secretion system, the twin-arginine translocation pathway (Tat), the secreted proteins are targeted to the secretion pathway with highly conserved Tat signal peptides in a folded manner [49]. These secretory pathways transport secreted proteins across the inner membrane, other secretory systems are needed for the export across the outer membrane.

Unlike for Gram-negative bacteria, the protein secretory mechanisms in Gram-positive bacteria are less well understood. Gram-positive bacteria only have a single membrane with a thick peptidoglycan layer in the cell wall. In the signal peptide-mediated secretion system, the signal peptide directly leads secreted proteins from the cytoplasm into the extracellular environment. Some pre-proteins have a signal peptide at the N-terminus and a sorting signal at the C-terminus that can be recognized and cleaved by sortase. This latter process leads the attachment of these proteins to the cell wall.

However, some intracellular proteins without known signal peptides have also been found to be secreted [50]. This behavior, first discovered and identified in

eukaryotes, is defined as non-classical secretion [50]–[52]. The *Mycobacterium tuberculosis* glutamine synthetase was the first published intracellular protein to be observed to be secreted in the absence of a signal peptide in bacteria. Harth et al. [53] studied the targeting of recombinant *M. tuberculosis* glutamine synthetase in *M. smegmatis*. Glutamine synthetase lacks a signal peptide and was originally believed to be solely intracellular, but it was found that it can be secreted in pathogenic *M. tuberculosis*, but not in the non-pathogenic species *M. smegmatis*. Surprisingly, the recombinant *M. tuberculosis* glutamine synthetase is released extracellularly when expressed in *M. smegmatis*, even more efficiently than in *M. tuberculosis*. This result indicates that the protein is released with a novel signal peptide independent secretion pathway, and the release signal is within the amino acid sequences of the protein itself.

More and more intracellular proteins have been recently found to be secreted, but the mechanism of non-classical secretion is unknown. One hypothesis is that the proteins are released by cell lysis or cell death, supported by evidence such as the amount of GAPDH presence on the cell surface and in the supernatant were both impaired under conditions of low levels of cell lysis in group B Streptococcus [54]. However, many more studies showed that most of these cytoplasmic proteins are secreted from an intact cell instead of simply being released due to cell lysis. Dreisbach et al. [55] measured cell integrity using TrxA as an intracellular marker and discovered highly variable proteins on the cell surface of *S. aureus*, including a lot of predicted intracellular proteins. Katakura et al. [37] measured a negligible amount of lactate dehydrogenase (0.006 units/ml) in the cell supernatant and more than 1,000 times that amount of lactate dehydrogenase when

the cell suspension was treated with sonication, showing that the presence of intracellular proteins such as DnaK and GroEL on the *Lactococcus lactis* surface was not the result of cell leakage. Other groups found a discrepancy in the amount of abundant proteins in the cytoplasmic fraction and in the cell wall fraction using 2-D gel electrophoresis.

Boonjakuakul et al. [56] isolated cell membranes and identified the proteins in different subcellular fractions. The major protein spots in the cytoplasmic fraction on the gel are very different from the prominent bands in the outer membrane fraction. There are many of these intracellular/surface proteins that are somehow secreted from the cell and are not simply released from the cell due to cell lysis.

The secretion pathways that make use of a signal peptide, such as Sec dependent and Tat secretion pathways, cannot explain the non-classical secretion behavior of intracellular proteins. Some potential pathways have been proposed, yet the underlying mechanisms are still unknown. EAST-6 and CFP-10, two small proteins secreted by *M. tuberculosis*, lack signal peptides [57]. Pallen [57] used PSI-BLAST to identify many proteins containing homology with EAST-6's amino acid sequence and found that the small antigenic proteins apparently secreted by the same system as EAST-6 share a WXG motif but lack a signal peptide, suggesting a possible novel Gram-positive secretion pathway.

Another example of a non-classical secretion pathway is the SecA2 system. This accessory Sec system has been identified in several Gram-positive bacterial species. Braunstein and coworkers [58], [59] compared secreted proteins in wild-type and secA2

mutant *M. tuberculosis* and found three proteins including SodA that lack a signal peptide but still get secreted from the cytoplasm in a SecA2-dependent manner. It is interesting that two of the identified SecA2 dependent lipoproteins in *M. smegmatis* still possess a signal peptide [60]. In *L. monocytogenes*, SecA2-dependent proteins can also be classified into two categories —proteins with a signal peptide and without a signal peptide [59], [61]. It remains a question as to why the SecA2 secretion system can export proteins both with and without a signal peptide out of the cytoplasm.

Despite the fact that Gram-negative secretion pathways have been more intensively investigated, fewer proteins have been identified that are secreted in a non-classical manner in Gram-negative bacteria than in Gram-positive bacteria. T3SS is a Sec independent pathway responsible for export of various proteins in many gram-negative pathogens. Aguilera and coworkers [62] first reported the export of the housekeeping protein GAPDH through T3SS in enteropathogenic *E. coli* (EPEC) and the interaction between GAPDH and CesT, the general chaperone of this secretion system. But more effort is needed to investigate why GAPDH can only be secreted in pathogenic *E. coli* strains like EPEC and enterohemorrhagic *E. coli* (EHEC), but not in non-pathogenic *E. coli* strains. Before Aguilera's report, Egea and coworkers [63] demonstrated that the medium condition is a key factor for GAPDH secretion by EPEC. This result shows that there are several secretion pathways for GAPDH in *E. coli*, and it points to the complexity of secretion pathways in Gram-negative bacteria. There is no doubt that non-classical secretion pathways in Gram-negative bacteria may be more complicated and require more attention.

3. Cell Surface Anchor Mechanisms

Pathogenic bacteria start bacterial infections by colonizing host tissues. These organisms have evolved adhesion and attachment mechanisms to interact with host tissues. A lot of surface proteins act as adhesins, which are the bacterial ligands that interact with host cell receptors, and invasins, which are produced by bacteria to promote their penetration into host cells. After secretion of these proteins by Gram-positive bacteria, they become anchored to the surface of the bacterial cells with several mechanisms.

Some pre-proteins in Gram-positive bacteria, including bacilli, listeria and staphylococci, harbor a signal peptide at the N-terminus and a sorting signal, the LPXTG motif, at the C-terminus [64]. These pre-proteins are targeted to the secretion pathway via the signal peptide and become anchored to the cell wall after the cleavage of the LPXTG sorting signal by sortase A in these bacteria, albeit the cleavage mechanisms are different in different species [65]. In addition to *isdA* and *isdB* that encode proteins with the LPXTG motif, *S. aureus* has an *isdC* locus that codes a protein with an NPQTN sorting signal at the C-terminus that can be recognized and cleaved by sortase B, thus anchoring the protein to murein [66]. The whole *isd* cluster helps the import of haem and liberates iron for the growth of *S. aureus* [65], [66]. Other species also have sortase B homologues, but the mechanisms are somewhat different; for example, sortase B anchors proteins with an NPKTG instead of NPQTN sorting signal on the *B. anthracis* cell wall [67]. There are other major anchor mechanisms in Gram-positive bacteria, including pilus assembly and the sortase C anchoring mechanism [65]. A different anchor mechanism was found in *S. pneumoniae*. PspA has a N-terminal signal peptide and C-terminal choline-binding

repeats, anchoring to the cell surface via a choline-mediated interaction [64], [68].

Almost all of these systems share a common character that the proteins get secreted through use of signal peptides at the N-terminus and then anchored on cell wall via a motif at the C-terminus.

Accompanied by the discovery of more and more non-classically secreted proteins, it has been found that some surface proteins perform their functions on the cell surface without LPXTG or NPKTG motifs or choline-binding repeats, suggesting an “anchorless” mechanism [64]. Pancholi and Fischetti [12] identified a 45 kDa surface protein with strong plasminogen binding activity as the streptococcal surface α -enolase (SEN). They further confirmed the importance of a SEN C-terminal lysine residue and an N-terminal region in performing its plasminogen-binding role. Bergmann and coworkers [69] characterized a 47 kDa surface protein in *S. pneumonia* as α -enolase, which shares 93% sequence identity to the sequence of SEN. This α -enolase gets secreted in an unknown non-classical secretion pathway and is able to reassociate to the pneumococcal cell surface, as confirmed by electron microscopy [69]. The lysine residue at the C-terminus has also been verified to be important in binding to plasminogen. In a following study, Bergmann and coworkers [70] identified another plasminogen-binding motif FYDKERKVY within the α -enolase sequence. The surface-reassociated enolase that binds to plasminogen has an essential role in bacterial pathogenicity. Chhatwal [64] listed some proteins, including *S. pneumonia* PavA, Eno and *S. pyogenes* FBP54, SEN and SDH that lack signal peptides and known membrane anchors, indicating that the reassociation of these secreted proteins could be a general but as-yet-unknown

mechanism.

There are not as many published studies about how intracellular proteins in Gram-negative bacteria become attached on the cell surface after secretion. There are fewer examples in the list of the intracellular/surface moonlighting proteins we've collected so far, with 61 proteins in Gram-positive bacteria but only 19 proteins in Gram-negative bacteria [4], [71], but it is very likely that these intracellular/surface moonlighting proteins adhere to the cell surface by reassociation in both Gram-positive and Gram-negative bacteria. Using electron microscopy, it was shown that the association behavior of 60 kDa Hsp in *H. ducreyi* [26] shares similarity with the reassociation of *S. pneumonia* α -enolase on the cell surface [69]. Similar transmission electron microscopy studies of *N. meningitides* also manifested the association of enolase, DnaK and peroxiredoxin with the outer membrane after secretion [31]. All of these data suggest that many of the intracellular/surface moonlighting proteins reassociate on cell surface of pathogens after secretion.

C. Outline of the Study

This project aims to find additional candidates for intracellular/surface moonlighting proteins using published proteomics studies and bioinformatics tools. Firstly, the amino acid sequences of proteins found to be localized in cell surface/cell wall proteomes have been gathered. Secondly, protein sequences were analyzed using bioinformatics tools in order to look for proteins that lack transmembrane domain and signal peptides. Finally, the candidate intracellular/surface proteins were categorized based on function.

II. METHODS

A. Selections of Proteins for Study

The process of selecting intracellular/surface moonlighting proteins is shown in Figure 2. First, information such as gene locus, Uniprot/NCBI accession numbers, and descriptions of proteins were collected from published proteomics studies that identified proteins on the cell surface. Second, the amino acid sequences were identified through use of the in NCBI [72] or Uniprot [73] databases. Third, proteins with unknown functions or putative functions were left out of the study because we focused on proteins with known intracellular functions. Fourth, transmembrane proteins were discarded because they span and attach to the cell membrane permanently and do not fit the intracellular/surface moonlighting protein category. Fifth, proteins with signal peptides were also ruled out because intracellular/surface moonlighting proteins are secreted with non-classical secretion pathways that lack signal peptide. Finally, PSORTb 3.0 [74] was used as a prediction of the subcellular localization. The programs and databases that were used in the project are shown in Table 3.

Table 3. Programs and database used in the work

Programs and databases	Function
UniProt [73]	Acquisition of amino acid sequences
NCBI [72]	Acquisition of amino acid sequences
TMHMM Server, v. 2.0 [75]	Transmembrane alpha-helices prediction
SignalP 4.0 [76]	Signal peptides prediction
PSORTb 3.0 [74]	Subcellular localization prediction

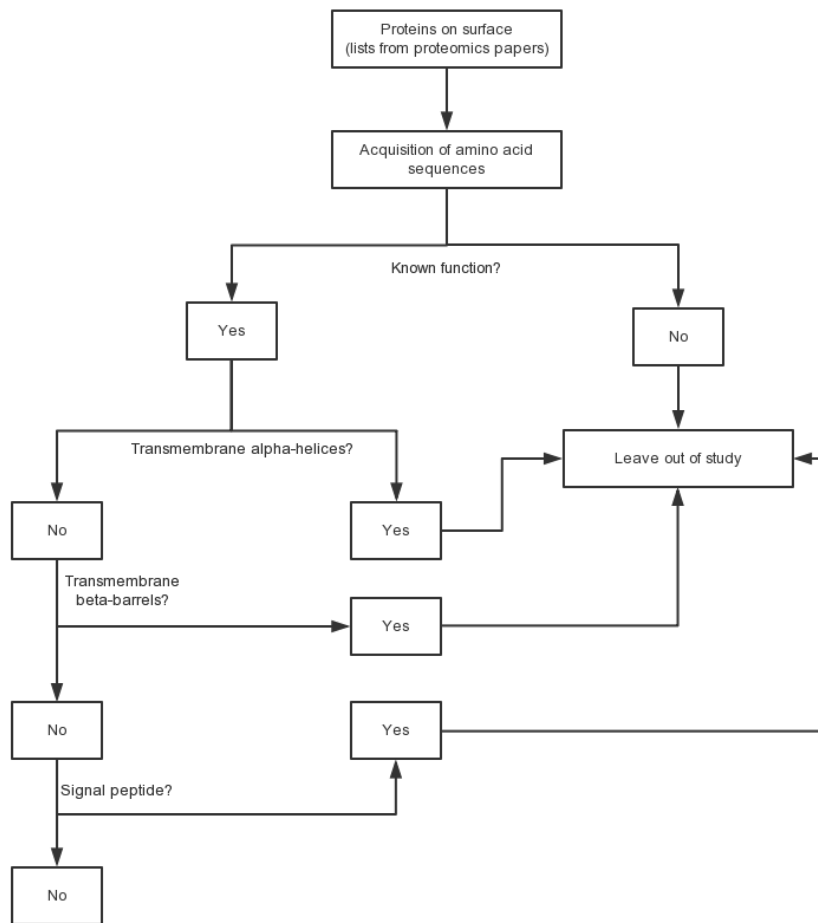


Figure 2. The process of selecting intracellular/surface moonlighting protein candidates.

B. Initial Data Acquisition

The initial data were obtained from published surface proteomics projects for two major reasons: 1) proteomics, the large-scale analysis of proteins fulfills the need for enough information about dozens or hundreds of proteins compared to the traditional laboratory methods; 2) the surface proteomics papers provide information about all of the

proteins present on the cell surface, which may include some proteins that are usually considered to be intracellular. Table 4 lists the proteomics papers from which the lists of surface proteins were gathered.

Table 4. Proteomics papers used in the study

Species	Gram type	Table Used
<i>Bartonella quintana</i> [56]	Negative	Table 2
<i>Clostridium acetobutylicum</i> [77]	Positive	Table S1
<i>Streptococcus suis</i> [78]	Positive	Table S2 and S3
<i>Escherichia Coli</i> [79]	Negative	Table S1 and S2
<i>Capnocytophaga canimorsus</i> [80]	Negative	Table 1
<i>Clostridium thermocellum</i> [81]	Positive	Table S1
<i>Enterococcus faecalis</i> [82]	Positive	Table 1
<i>Pseudomonas aeruginosa</i> [83]	Negative	Table 1 and 2
<i>Staphylococcus aureus</i> [84]	Positive	Table 1
<i>Streptococcus pneumoniae</i> [85]	Positive	Table 3
<i>Shewanella oneidensis</i> [86]	Gram-negative	Table S1
<i>Mycobacterium smegmatis</i> [87]	Acid-fast Gram-positive	Table S3
<i>Neorickettsia sennetsu</i> [88]	Gram-negative	Table 1
<i>Listeria monocytogenes</i> [89]	Gram-positive	Table S1
<i>Listeria monocytogenes</i> [90]	Gram-positive	Table 1
<i>Escherichia Coli</i> [91]	Gram-negative	Table S1
<i>Rickettsia typhi</i> [92]	Gram-negative	Table S3
<i>Rickettsia parkeri</i> [93]	Gram-negative	Table 2
<i>Group A Streptococcus</i> [94]	Gram-positive	Table S1
<i>Group B Streptococcus</i> [95]	Gram-positive	Table S1

C. Acquisition of Amino Acid Sequences

The UniProtKB [73] and the NCBI protein databases [72] were used to collect

protein amino acid sequences using the gene name, locus, UniProt accession number, and/or NCBI accession number provided in the proteomics papers. The amino acid sequences were obtained in FASTA format.

D. Prediction of Transmembrane Alpha-helices

TMHMM Server v.2.0 [75] was used in the study to predict the presence of TMHs. TMHMM, based on a hidden Markov model, has been tested to have the best performance in predicting TMHs among various prediction servers with almost 100 percent specificity and sensitivity [75]. FASTA sequences were used as input, and the proteins with TMHs were recorded and were separated from the other proteins.

E. Prediction of Signal Peptide

The SignalP 4.1 Server [76] was used to predict the presence and location of signal peptides. Protein sequences in FASTA format were used as input. The program was run with organism group information based on the cell type because the program was trained using different datasets for Gram-positive and Gram-negative proteins. Gram-negative bacteria also tend to have shorter signal peptides and different D-cutoff values. D-cutoff values were set to default. SignalP-TM network was used by default for Gram-positive bacteria. SignalP-noTM network was used for Gram-negative bacteria for a slightly better result.

F. Prediction of Subcellular Localization

The subcellular localization of proteins was predicted by PSORTb version 3.0.2 [74]. In choosing the cell type, Mycobacterium was input as “Advanced” and “Positive with outer membrane” in “Choose Gram stain”. A score out of ten was reported (high confidence with a high value). Five possible localizations are reported for Gram-negative bacteria and four possible localizations are reported for Gram-positive bacteria [74]. “Unknown” will be reported if no score is over 7.5.

G. Functional Analysis

COG annotation [96] was used to characterize the proteins’ functional categories. COG employed seventeen single letter abbreviations to represent different functional categories.

III. RESULTS

A. Initial Datasets

After removing duplicates, 3,027 proteins (data not shown) were collected from the 20 proteomics papers listed in Table 4. Proteins from eight Gram-negative bacterial species were included from the proteomics papers: *B. quintana*, *E. coli*, *C. canimorsus*, *P. aeruginosa*, *S. oneidensis*, *N. sennetsu*, *R. typhi* and *R. parkeri*. Proteins from nine Gram-positive bacterial species were analyzed: *C. acetobutylicum*, *S. suis*, *C. thermocellum*, *E. faecalis*, *S. aureus*, *S. pneumoniae*, *L. monocytogenes*, GAS (*S. pyogenes*), GBS (*S. agalactiae*). One special case is *Mycobacterium smegmatis*, a non-pathogenic bacterium that is considered as Gram-positive bacteria but has a thicker cell wall than most of the other Gram-positive bacteria.

The annotations of these proteins were recorded. 430 of these proteins have annotations such as “hypothetical proteins”, “uncharacterized proteins”, “protein of unknown function”, “conserved hypothetical protein” and etc. These proteins were discarded because they don’t have a distinct function, and I am looking for proteins with a known intracellular function that are also found on the cell surface. 72 proteins don’t have corresponding information in the UniProtKB/NCBI databases and therefore were left out of the study.

B. Prediction of Transmembrane Proteins

The rest of the proteins were then analyzed with TMHMM server v 2.0 [75], and 627 were predicted to have TMHs. Although TMHs are the majority group of transmembrane

proteins based on structure, the other transmembrane group, transmembrane beta-barrels (TMBs), is not negligible. Tusnády and coworkers [97] established a database called PDBTM, which collected transmembrane protein structures from the PDB. As of February 2015, more than 2,000 transmembrane proteins were found in the PDB, among which 14% are TMBs. Still, the prediction for TMBs is more difficult due to the nature of a TMB structure compared to a TMH structure, which results in insufficient prediction accuracy for TMBs [98]. I used TMBs predictors to predict TMBs, but none of them gave satisfactory results. For example, the FASTA sequence of maltoporin (LamB porins, formed by a TMB) from *E. coli* (gi| 253775338) was input into Pred-TMBB [98]. None of the methods, Viterbi, N-best and Posterior Decoding, predicted it as a protein with TMBs. Viterbi gave the sequence a score of 2.969, which is higher than the 2.965 threshold, indicating that the protein does not have TMBs. Also this predictor gave some false positive results: a lot of cytoplasmic proteins were predicted to be outer membrane proteins with beta-barrels (data not shown). Another limitation of TMB predictors is some of them, such as PROFtm and Pred-TMBB can be only used for Gram-negative bacteria. However, TMBs exist in both the outer membrane of Gram-negative bacteria and the membrane of Gram-positive bacteria [99]. Therefore, I manually selected proteins with TMBs based on SCOP (Structural Classification of Proteins) classification. SCOP classified TMBs into six superfamilies: OmpA-like, OmpT-like, OmpLA, porins, Txs-like channels and autotransporter [100]. Proteins with annotations similar to these superfamilies were picked out and carefully compared to the existing literature or the PDB database. 38 were classified as proteins with TMBs and thus left out of the study.

C. Prediction of Signal Peptides

The remaining proteins without transmembrane helices or transmembrane beta barrels were analyzed using SignalP 4.1 [76] for best performance. 349 of them were predicted to harbor a signal peptide within the amino acid sequences. SignalP is not able to identify bacterial lipoproteins because the lipoprotein signal peptide is cleaved by signal peptidase II (SPaseII) instead of signal peptide I (SPaseI). In bacteria, lipoproteins are abundant secretory proteins [101]. For example, in *E. coli*, most lipoproteins are attached to the outer membrane, and some are anchored to the inner membrane [102]. Therefore, lipoproteins can be left out of the study because they usually do not have an intracellular function. In fact, most lipoproteins were already left out of the study because they are localized within the cell membrane or periplasmic space. The list was manually checked for lipoproteins, and 17 lipoproteins were left out of the study.

D. Prediction of Subcellular Localization

Up to this point, most of the proteins left in the list are cytoplasmic proteins that may be candidates for intracellular/surface moonlighting proteins. In order to compare the prediction of the subcellular localization, PSORTb 3.0 [74] was used. PSORTb 3.0 not only uses the original six modules including HMMTOP, Signal and SCL-BLAST, but also uses host-associated, T3SS and flagellar spore as new modules [74], [103]. It is able to predict the cellular locations of more types of proteins. For example, flagellar hook protein FlgE from *C. acetobutylicum* (gi|15895423) was correctly predicted as “Flagellar”. Succinate dehydrogenase, a flavoprotein subunit from *E. coli* (gi|1786942) that is part of the electron transport chain, was also correctly predicted as “Cytoplasmic

Membrane”. But sometimes PSORTb was not able to predict the localization of a subunit of a big integral member protein complex correctly.

After careful examination of the localization scores and manual checking, some proteins associated with the cell membrane were grouped into the following categories: ABC transporters and other transmembrane transporters, ATP synthase subunits, flagellin and flagellar hook components, and electron transport chain subunits. Proteins involved with cell division were also considered to be cell membrane associated. “ABC transporters and other transmembrane transporters” include proteins annotated as: ABC transporter/ABC transporter related, metal ion or small molecule transporter (cobalt, iron, arginine transporter, etc.), efflux pump, and part of a translocation system. Alpha, beta, gamma, delta and epsilon subunits of the F1/F0 ATP synthase, located in the mitochondria matrix, were also grouped in the category of “ATP synthase subunits” because they are part of the big membrane complex. The category of “Electron transport chain subunits” includes NADH dehydrogenase, succinate dehydrogenase, cytochrome c dehydrogenase, etc. FtsE, ftsF, ftsZ, ftsY, ftsA, divIVA are proteins that are related to cell division machinery and considered to be cell membrane associated [104]. Other than *ftsA* and *ftsZ* which are intracellular proteins, the rest of the Fts proteins are all membrane proteins [105]. FtsE and ftsX, homologues of ABC transporter are associated with the cell membrane and are involved in translocation and transportation [104]. FtsZ is a GTPase [106] and an analogue of tubulin, and ftsA is an actin homologue. FtsA was found to localize in septum in the presence of the Z ring formed by ftsZ [105]. All of these proteins are part of the cell division machinery, and so I grouped them in the

category of “cell membrane acting” in my study. Figure 3 shows the distribution of the major cell membrane associated protein groups.

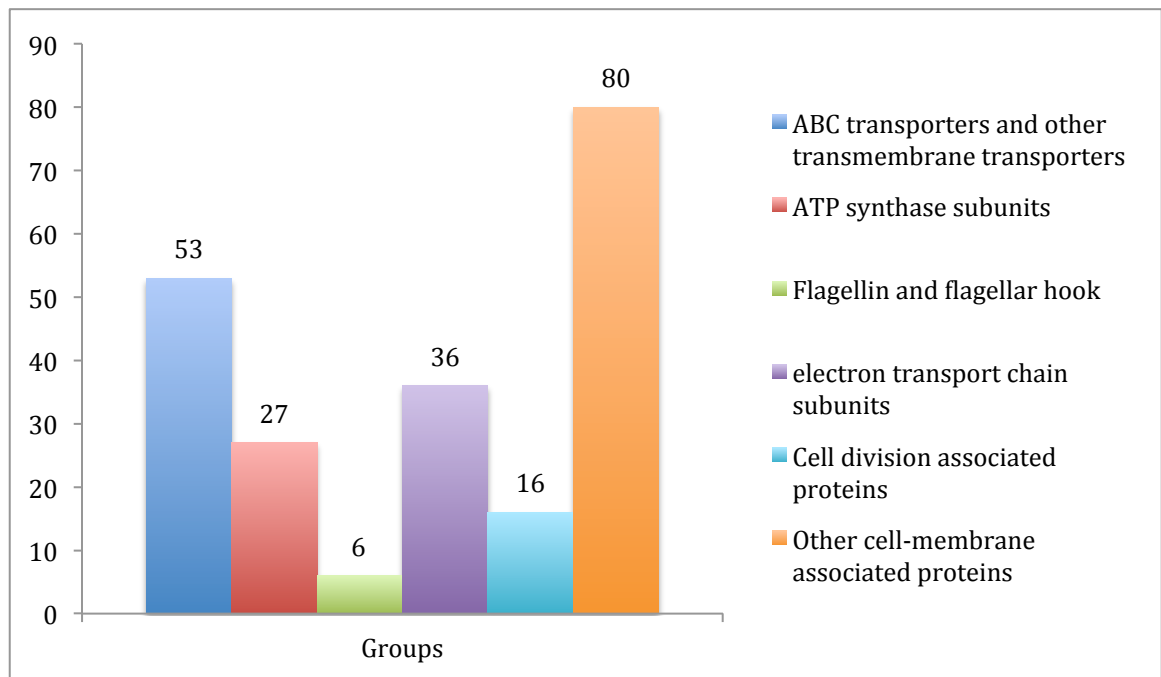


Figure 3. Distribution of the cell membrane-associated proteins. The numbers on each histogram bar represents the number of each group.

E. Statistics of the Selection Process

Figure 4 shows the statistics of the whole selection process. More than three thousand proteins were analyzed initially. More than 1,100 protein were predicted to be intracellular proteins that don't possess transmembrane domains or signal peptides. This result further confirms that some intracellular proteins have the ability to get secreted

across the cell membrane and perform another function on the cell surface.

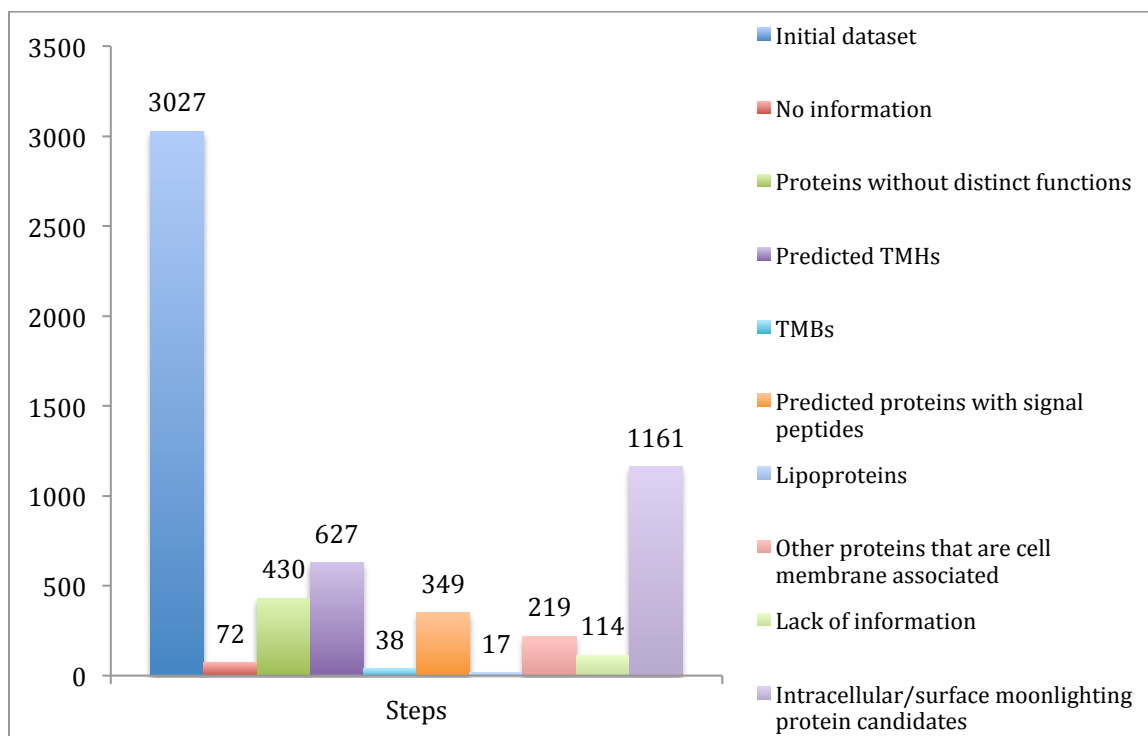


Figure 4. Statistics of the whole selection process. 1161 out of 3027 proteins in the cell surface/cell wall proteomes have been predicted to be intracellular proteins.

F. Intracellular/Surface Moonlighting Protein Candidates

Appendix I and II list all the predicted cytoplasmic proteins that were identified on the cell surface from the proteomics studies. The NCBI numbers of the proteins were used to search the COG database [96], and the proteins were classified based on COG annotation. The database covers the majority of genomes of the organisms in this study (Table 3) except *E. coli* BL21, *C. thermocellum*, *R. parkeri*, *L. monocytogenes*, *S. suis*, *S.*

aureus, GBS. The dominant functional category is J — translation, ribosomal structure and biogenesis [96]. This category consists of ribosomal proteins, tRNA synthetases, translation elongation factors/initiation factors and some other enzymes involved in mRNA degradation or tRNA processing. Another major functional category is O — post-translational modification, protein turnover, chaperones [96]. This group comprises a lot of molecular chaperones, including GroEL chaperonins, chaperone proteins DnaK and DnaJ, and Clp and Lon family proteases. Functional category G — carbohydrate transport and metabolism [96] is another big group, including proteins involved in glycolysis and the pentose phosphate pathway. The major functional groups are shown in Table 5.

Not all the proteins in my list can be found in the COG database. Figure 5 shows that almost three quarters of the intracellular/surface moonlighting protein candidates cannot be found in the COG database. Further investigation of the data (Appendix I and II) shows that the proteins that don't exist in the COG database fit into similar functional groups. Ribosomal/ribosomal associated proteins, molecular chaperones, aminoacyl tRNA synthetases, elongation/initiation/termination factors, enzymes involved in glycolysis, enzymes in replication and transcription, proteins involved in energy production, and proteins in nucleotide transport were also frequently found in the other species on the list.

Table 5. Major functional groups of intracellular/surface moonlighting protein candidates based on COG database classifications

COG code	Function description	Examples
J	Translation, ribosomal structure and biogenesis	30S/50S ribosomal protein; EF-G, EF-Ts, EF-Tu, EF-P, IF; aminoacyl tRNA synthetases
O	Post-translational modification, protein turnover, chaperones	Chaperonin GroEL; chaperone proteins DnaJ, DnaK; Lon/Clp family proteases
G	Carbohydrate transport and metabolism	Aldolase, TPI, GAPDH, phosphoglycerate kinase, phosphoglycerate mutase (PGM), enolase, pyruvate kinase; transketolase
E	Amino acid transport and metabolism	Acetylglutamate kinase, glutamine synthetase
C	Energy production and conversion	Alcohol dehydrogenase, acetate kinase, isocitrate lyase
K	Transcription	Transcription termination factor rho, transcription termination/antitermination protein NusA, DNA-directed RNA polymerase
F	Nucleotide transport and metabolism	GMP synthase, adenylate kinase, Phosphoribosylformylglycinamide synthase
L	Replication, recombination and repair	DNA polymerase I/III, ATP-dependent RNA helicase, DNA gyrase
I	Lipid transport and metabolism	Acetyl-CoA acetyltransferase, acetyl-CoA carboxylase

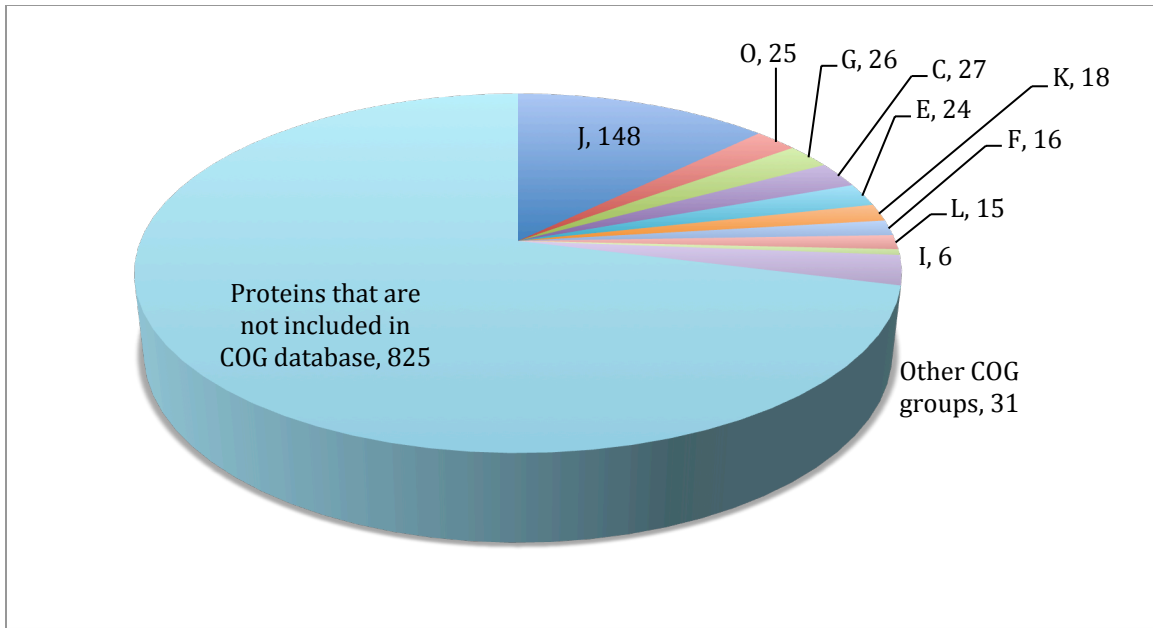


Figure 5. Distribution of the functional groups based on the COG database. The single letter is the COG code representing each functional group.

IV. DISCUSSIONS

A. Comparison of Proteomics Experimental Approaches

This study is based on bioinformatics analysis of data from published proteomics studies. A lot of proteins that are known to function in the cytoplasm have been found in the cell wall or cell surface subproteomes. The presence of known cytoplasmic proteins on the cell surface suggests they might be intracellular/surface moonlighting protein candidates.

The proteomics studies that were used in this analysis were based on two popular experimental approaches. The first method is separation of subcellular fractions followed by two-dimensional gel electrophoresis or one-dimensional gel electrophoresis [77], [79] coupled with mass spectrometry. The success of this approach in identifying only cell surface proteins depends on how well the cell membrane is separated from the other subcellular fractions. Some cytoplasmic proteins may “contaminate” the membrane fraction. For example, J. Boonjakuakul and coworkers [56] paid attention to the result that among the 60 identified proteins in the total membrane protein fraction of *B. quintana*, more cytoplasmic proteins were identified than membrane proteins. Yu and coworkers [81] also found a large amount of cytoplasmic proteins in the cell wall proteome.

The second proteomics technique uses proteolytic enzymes such as trypsin to digest proteins on the cell surface followed by mass spectrometry to identify the digested

peptides [78], [94]. This method has been proven to be more selective [94]. This shaving method is able to detect more surface proteins because weakly membrane-attached surface proteins (peripheral membrane proteins) may be lost during the membrane isolation steps of the first method, but fewer integral membrane proteins are identified because integral membrane proteins are embedded in the cell membrane. A good shaving technique should digest the surface proteins efficiently while not damaging the cell surface, which would result in a great amount of contamination from cytoplasmic proteins. However, some cytoplasmic proteins that are identified as being on the cell surface through these proteomics methods may be artifacts from imperfect separation of subfractions or over-digestion of the cell surface. But Schaumburg and coworkers [90] confirmed that a large amount of cytoplasmic proteins in the cell wall subproteomes are actually active on the surface, and they also visualized enolase on the cell surface of *L. monocytogenes*.

B. Proteins in DNA Binding and Replication

A lot of proteins involved in replication, recombination and repair (COG code: L) [96] such as DNA polymerase I, DNA polymerase III, DNA gyrase, RecA, DNA helicase, DnaA, DNA ligase, MutS, and DNA topoisomerases (I, II, IV), were identified in the study. DNA was found a long time ago to bind to the cell membrane and form a DNA-membrane complex during replication in prokaryotic cells [107]. The interaction between DNA and cell membrane is important for the transfer of the daughter chromosome during cell division [107], [108]. This may be an explanation for the presence of some of the proteins that interact with DNA, such as DNA-dependent RNA polymerase and RNA

termination factor Rho, on the cell surface (Appendix I and II).

C. Proteins in Protein Biogenesis

Ribosomal proteins comprise the most abundant functional group found on our list. Although a lot of ribosomal proteins exist in the MoonProt database [4], none of them are known to have a second function on the cell surface. Because ribosomes play an important role in the biogenesis of membrane proteins and secreted proteins and can be membrane associated, it is reasonable that many of the ribosomal proteins were identified in the surface proteome. Ribosomes interact with translocons with high affinity in the cotranslational assembly of membrane proteins or secreted proteins. This behavior has been proven to be evolutionarily conserved [109]. Aminoacyl tRNA synthetases are enzymes that link the proper amino acid to a tRNA that contains the corresponding anticodon. They are important enzymes in protein translation and biogenesis. Similar to ribosomal proteins, during protein synthesis of membrane proteins, they can be membrane associated. Many of them have been found to perform more than one function inside of the cell. But whether or not they can be on the cell surface and perform a second role is not clear. It is interesting that Olmedo-Verd and coworkers [110] found that four aminoacyl tRNA synthetases have putative transmembrane domains in cyanobacteria.

Four elongation factors EF-Tu, EF-Ts, EF-G and EF-P were identified by several of the proteomics studies. They are required for protein synthesis in prokaryotes. EF-Ts, EF-G and EF-P are not currently in the MoonProt database [4]. EF-Ts is the exchange factor that induces the release of GDP from EF-Tu [111]. EF-G binds to the ribosome and

helps the translocation of tRNA from the A site to P site [112]. EF-P is required in peptide bond synthesis on ribosomes [113]. The close relation of these three elongation factors in protein translation with ribosomes may explain why these elongation factors were identified in the surface proteomics studies, while whether they are moonlighting proteins on the cell surface requires more experimental evidence. However, *L. johnsonii* and *L. plantarum* EF-Tu have been identified to be intracellular/surface moonlighting proteins that mediate the attachment of the bacteria to human cells [25], [114].

Mycoplasma pneumonia EF-Tu on the cell surface has been found to bind host fibronectin [115]. *P. aeruginosa* EF-Tu has also been found to localize to the cell surface and bind to plasminogen [116]. The additional EF-Tu proteins on the list might be strong intracellular/surface moonlighting protein candidates.

D. Molecular Chaperones

Intracellular molecular chaperones are found in many species to also be found on the cell surface. Several of these intracellular/surface moonlighting proteins are found in the MoonProt database [4]. DnaK and GroEL are stress proteins that play a critical role in protein folding and help protect proteins from stress [117]. On the cell surface, several Hsp70/DnaK proteins show high affinity for plasminogen [18], [31], [90], and Hsp60/GroEL proteins function as adhesins [24], [26], [27], [29] that serve as cell signaling proteins and help the bacteria to interact with host cells [118]. Katakura and coworkers [37] found that DnaK and Hsp60/GroEL on the cell surface of *L. lactis* can bind to mannoprotein of yeast cells and might help reduce the stress on the yeast surface caused by lactic acid. DnaJ, Clp and Lon family proteases were also found on the cell

surface in several species. Despite lacking direct evidence of a second function of some of these chaperones on the cell surface, they have been proven to promote intracellular growth of intracellular pathogens and thus enhance the virulence of these pathogens [119], [120]. DjlA, a member of Hsp40/DnaJ family, was found to be important for the growth of *L. dumoffii* in host cells and probably was essential in folding and transporting the membrane protein Dot/Icm that is part of the type IV secretion system (T4SS) [121]. Therefore, it might be transiently associated with the cell membrane. Trigger factor is a cytoplasmic chaperone protein that can bind to and disassociate from the ribosome [122]. Ribosomal protein L23 has both binding sites for trigger factor and signal recognition particle and helps with protein targeting to the cell membrane [123]. This explains the appearance of trigger factor in the cell membrane proteomes.

E. Metabolic Enzymes

It is interesting that most of the proteins used in glycolysis in bacteria can perform moonlighting functions on the cell surface. They bind to plasminogen, fibronectin, laminin and can also serve as adhesins [118]. The MoonProt database [4] includes a great number of cytoplasmic enzymes in central metabolism that are also surface moonlighting proteins in various species. Aldolase, TPI, GAPDH, phosphoglycerate kinase, PGM, enolase, and pyruvate kinase were identified from this proteomics project in many other species (Appendix I and II), possibly expanding this group of moonlighting proteins to more species.

F. Other Candidates for Intracellular/Surface Moonlighting Proteins

Some of the proteins on the list (Appendix I and II), enolase and GAPDH from *S. aureus* and *S. suis*, for instance, have been identified to be moonlighting proteins and were collected in the MoonProt database [4] already. As discussed before, proteins that belong to the molecular chaperones and carbohydrate metabolism categories but not yet identified to moonlight on the cell surface may be intracellular/surface moonlighting proteins. There are many other cytoplasmic proteins on the list (Appendix I and II) that don't belong to these two groups. Several alcohol dehydrogenases, involved in energy production and conversion [124], were found on the cell surface of *E. coli* BL21, *S. oneidensis*, *C. thermocellum*, *L. monocytogenes*, and *S. suis*. Among them, alcohol acetaldehyde dehydrogenase has been identified to act as an adhesin on the cell surface of *L. monocytogenes* [125] and is listed in the MoonProt database [4]. The rest of the alcohol dehydrogenases are strong candidates to be intracellular/surface moonlighting proteins as well. Similarly, 2-oxoglutarate dehydrogenase, an important complex in the TCA cycle that is also involved in energy production, was found on the cell surface in several species (Appendix I and II). Other than these proteins discussed above, proteins such as acetate kinase, acetylglutamate kinase, aconitate hydratase, adenylate kinase, carbamoyl-phosphate synthase, citrate synthase, dihydrolipoamide dehydrogenase were also commonly found on the cell surface (Appendix I and II). They may play a distinct role on the cell surface, although there's no evidence as to a second function currently.

G. Reproducibility of Different Proteomics Methods

Among the proteomic papers we've used in our study (Table 2), two of them used *L.*

monocytogenes. Schuamburg and coworkers [90] identified the cell wall subproteome using MALDI-TOF mass spectrometry (MS). Portillo and coworkers [89] used high resolution MS to study the cell wall proteome of intracellular and extracellular *L. monocytogenes*. Some of the proteins were found in the proteomes of both studies, suggesting the reproducibility of these proteomics results. Fourteen proteins were found in both studies with the gene names: Lmo2653, Lmo2068, Lmo1473, Lmo2459, Lmo2455, Lmo1657, Lom2556, Lmo0223, Lmo2458, Lmo2654, Lmo1055, Lmo1634, Lmo2456 and Lmo1314. They are EF-Tu, GroEL, DnaK, GAPDH, enolase, EF-Ts, fructose-1,6-bisphosphate aldolase, cysteine synthase, phosphoglycerate kinase, EF-G, and dihydrolipoamide dehydrogenase, alcohol-acetaldehyde dehydrogenase, PGM and ribosome recycling factors, respectively. EF-Tu, EF-Ts, EF-G and ribosome recycling factors are associated with the ribosome. GroEL and DnaK are molecular chaperones. The rest are mainly metabolic enzymes. Most of these proteins have been discussed above and further support the model that the presence of these cytoplasmic proteins on the cell surface are not artifacts.

V. Conclusions and Future Work

This work selected candidates for intracellular/surface moonlighting proteins in many bacterial species from proteomics studies. Bioinformatics analysis has been extensively used throughout this work. The availability of bioinformatics tools makes it easier and less time-consuming to analyze the localization of proteins, but they are not always accurate. Careful use of the software or servers is required. Whether or not these proteins are real moonlighting proteins needs experimental verification. This work helps scientists to identify potential additional localizations of intracellular proteins and suggests candidates that also might play additional roles on the cell surface, such as a plasminogen binding protein or an adhesin.

The known intracellular/surface moonlighting proteins don't possess signal peptides or cell surface anchor motifs. One major question remaining to be elucidated is how these intracellular/surface moonlighting proteins get secreted. In the introduction, some potential secretion pathways have been illustrated. However, more experimental evidence is needed to verify which non-classical secretion pathways might be involved. Different proteins in different species may adopt different secretion pathways, adding the complexity of the research on secretion pathways.

Another question is how these proteins adhere onto the cell surface without an anchor motif. Although a lot of experiments have proved that some intracellular proteins have the ability to “stay” on the cell surface and perform another function there, how

these proteins get re-associated on the cell surface and how they can adhere there and perform a second function is still unknown.

The reason that these proteins can perform another role can be explained as follows: most of the intracellular/surface moonlighting protein candidates are chaperones or proteins involved in carbohydrate metabolisms. These proteins are ubiquitous in almost every bacterial species (and in many cases eukaryotic and archael species as well) and have been evolving for a very long time. Organisms tend to use the proteins that they already have instead of making a new proteins [126].

Future work includes but is not limited to searching for a common sequence or structural motif among all the identified intracellular/surface moonlighting proteins. They may share some common secretion motif or anchor motif within their protein sequences. Searching for such a sequence might be done by using bioinformatics prediction programs. But those predictions have some limitations. Different settings of parameters change the prediction results greatly. So when the length of the motif is unknown, it is very hard to select the best range of lengths of the potential motif sequences. Also, some predictors cannot identify sequence motifs containing gaps, such as LPXTG where X is any amino acid. “Wet work” needs to be combined with bioinformatics programs in order to look for sequence motifs that might be involved in selecting these intracellular/surface proteins for secretion and/or attachment to the cell surface.

APPENDICIES

Appendix I – List of Protein Cellular Roles Based on COG Database Classifications

Group J: Translation, ribosomal structure and biogenesis [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene Locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0F8		rplY	50S ribosomal protein L25
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0X5		rpsA	30S ribosomal protein s1
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896369		30S ribosomal protein S8
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895083		30S ribosomal protein S15
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895036		50S ribosomal protein L19
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896394		50S ribosomal protein L10
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896348		30S ribosomal protein S9
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896384		30S ribosomal protein S10
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896354		50S ribosomal protein L17
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894556		30S ribosomal protein S20 subunits
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896349		50S ribosomal protein L13
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896366		30S ribosomal protein S5
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896374		30S ribosomal protein S17
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896372		50S ribosomal protein L24
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896379		30S ribosomal protein S19
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895626		50S ribosomal protein L20
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894570		30S ribosomal protein S21
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896377		30S ribosomal protein S3
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896365		50S ribosomal protein L30
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896381	rplW	50S ribosomal protein L23
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896393		50S ribosomal protein L7/L12
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896383		50S ribosomal protein L3
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896378		50S ribosomal protein L22
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896388		30S ribosomal protein S7
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896356		30S ribosomal protein S4
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896380		50S ribosomal protein L2
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896375		50S ribosomal protein L29
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895063	rpsB	30S ribosomal protein S2
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896395	rplA	50s ribosomal protein L1
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YRQ8	340621193	Ccan_04150	50S ribosomal protein L21
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YRT1	340621216	Ccan_04380	30S ribosomal protein S12
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YS35	340621244	Ccan_04660	30S ribosomal protein S4
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YS02	340622458	Ccan_16870	50S ribosomal protein L7/L12
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YS04	340622460	Ccan_16890	50S ribosomal protein L1

Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YSG9	340622549	Ccan_17780	50S ribosomal protein L9
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839H0	29374845	EF0199	30S ribosomal protein S7
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839G5	29374850	EF0205	30S ribosomal protein S10
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839G4	29374851	EF0206	50S ribosomal protein L3
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839G3	29374852	EF0207	50S ribosomal protein L4
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839F9	29374856	EF0211	50S ribosomal protein L22
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839F2	29374863	EF0218	50S ribosomal protein L5
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839E9	29374866	EF0221	50S ribosomal protein L6
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839E8	29374867	EF0223	50S ribosomal protein L18
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839E5	29374870	EF0226	50S ribosomal protein L15
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839D8	29374878	EF0234	50S ribosomal protein L17
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q837C7	29375500	EF0916	50S ribosomal protein L20
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q836X4	29375553	EF0970	50S ribosomal protein L27
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q833P5	29376426	EF1898	50S ribosomal protein L19
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q831U9	29376895	EF2398	30S ribosomal protein S2
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q830Q6	29377196	EF2718	50S ribosomal protein L1
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWE9	15599445	rpsH PA4249	30S ribosomal protein S8
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWC7	15599468	rplJ PA4272	50S ribosomal protein L10
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HTN8	15600509	rpmB PA5316	50S ribosomal protein L28
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWE1	15599453	rpsC PA4257	30S ribosomal protein S3
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	O82850	15598852	rpsB PA3656	30S ribosomal protein S2
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HXP9	15598940	rpsP PA3745	30S ribosomal protein S16
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWD0	15599464	rpsL PA4268	30S ribosomal protein S12
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWF8	15599436	rpsK PA4240	30S ribosomal protein S11
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	O52759	15599435	rpsD PA4239	30S ribosomal protein S4
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWE7	15599447	rplE PA4251	50S ribosomal protein L5
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HVV2	15599629	rplM PA4433	50S ribosomal protein L13
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9I5V8	15595776	rpsU PA0579	30S ribosomal protein S21
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWF1	15599443	rplR PA4247	50S ribosomal protein L18
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWD7	15599457	rplW PA4261	50S ribosomal protein L23
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWE8	15599446	rpsN PA4250	30S ribosomal protein S14
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWE4	15599450	rpsQ PA4254	30S ribosomal protein S17
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWD8	15599456	rplB PA4260	50 S ribosomal protein L2

Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWF3	15599441	rpmD PA4245	50S ribosomal protein L30
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HXQ2	15598937	rplS PA3742	50S ribosomal protein L19
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HZN4	15598166	rpmF PA2970	50S ribosomal protein L32
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HZ71	15598358	rpsA PA3162	30S ribosomal protein S1
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWF2	15599442	rpsE PA4246	30S ribosomal protein S5
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1790418	RplL	50S ribosomal subunit protein L7/L12
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1787140	RpsA	30S ribosomal subunit protein S1
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1786365	RpsB	30S ribosomal subunit protein S2
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GCI4	88608048	NSE_0948	30S ribosomal protein S2
Rodriguez-Ortega 2006	<i>S. pyogenes</i>	Positive			spy0717	50S ribosomal protein L31
Rodriguez-Ortega 2006	<i>S. pyogenes</i>	Positive			spy1073	50S ribosomal protein L7/L12
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK77	24371819	SO_0221	50S ribosomal protein L1
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK76	24371820	SO_0222	50S ribosomal protein L10
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK75	24371821	SO_0223	50S ribosomal protein L7/L12
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK72	24371825	SO_0227	30S ribosomal protein S7
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK68	24371829	SO_0231	50S ribosomal protein L3
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK67	24371830	SO_0232	50S ribosomal protein L4
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK65	24371832	SO_0234	50S ribosomal protein L2
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK63	24371834	SO_0236	50S ribosomal protein L22
Zhang, 2010	<i>S. oneidensis</i>	Negative	P59183	24371835	SO_0237	30S ribosomal protein S3
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK62	24371836	SO_0238	50S ribosomal protein L16
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK59	24371839	SO_0241	50S ribosomal protein L14
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK57	24371841	SO_0243	50S ribosomal protein L5
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK54	24371844	SO_0246	50S ribosomal protein L6
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK53	24371845	SO_0247	50S ribosomal protein L18
Zhang, 2010	<i>S. oneidensis</i>	Negative	P59124	24371846	SO_0248	30S ribosomal protein S5
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK51	24371848	SO_0250	50S ribosomal protein L15
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK48	24371851	SO_0253	30S ribosomal protein S13
Zhang, 2010	<i>S. oneidensis</i>	Negative	P59375	24371852	SO_0254	30S ribosomal protein S11
Zhang, 2010	<i>S. oneidensis</i>	Negative	P59131	24371853	SO_0255	30S ribosomal protein S4
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EH70	24372938	SO_1360	50S ribosomal protein L19
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EGH5	24373197	SO_1629	30S ribosomal protein S2
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EER6	24373855	SO_2302	50S ribosomal protein L20
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EEI0	24373949	SO_2402	30S ribosomal protein S1
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EB80	24375151	SO_3652	50S ribosomal protein L21
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EAH5	24375415	SO_3927	50S ribosomal protein L9
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EAH2	24375418	SO_3930	30S ribosomal protein S6

Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EAG3	24375427	SO_3939	30S ribosomal protein S9
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EAG2	24375428	SO_3940	50S ribosomal protein L13
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8E9M3	24375731	SO_4247	50S ribosomal protein L28
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK46	24371855	SO_0257	50S ribosomal protein L17
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZC0		tufI	Elongation factor Tu
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q9XCM5		tsf	Elongation factor Ts
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZB9	49474407	fusA	Elongation factor G
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896387		Elongation factor G (EF-G)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896386	tufA	Elongation factor Tu (EF-Tu)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895364	efp	Elongation factor P
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YRT3	340621218	Ccan_04400	Elongation factor G
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YS08	340622464	Ccan_16930	Elongation factor Tu
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839G9	29374846	EF0200	Elongation factor G
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839G8	29374847	EF0201	Elongation factor Tu
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	O82851	15598851	tsf PA3655	Elongation factor EF-Ts
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1789737	TufA	Protein chain elongation factor EF-Tu (duplicate of TufB)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GEY8	88608486	NSE_0057	Polyribonucleotide nucleotidyltransferase (Pnp)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GCI5	88608372	NSE_0947	Translation elongation factor Ts (Tsf)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GD82	88608233	NSE_0687	Translation elongation factor G (FusA)
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK81	24371815	SO_0217	Elongation factor Tu 1
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EK71	24371826	SO_0228	Elongation factor G 1 (EF-G 1)
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EGH4	24373198	SO_1630	Elongation factor Ts
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EIJ7	24372431	SO_0842	Elongation factor G 2
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZF1	49474375	alaS	Alanyl-tRNA synthetase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G036	49474113	serS	Seryl tRNA synthetase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895623		Phenylalanyl-tRNA synthetase beta chain
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895624		Phenylalanyl-tRNA synthetase alpha chain
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896444		Lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896289		Isoleucyl-tRNA synthetase (Isoleucine--tRNA ligase) (IleRS)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895665		Valyl-tRNA synthetase (Valine--tRNA ligase) (ValRS)
Bøhle, 2011	<i>E. faecalis</i>	Positive	P0DM33	29375234	EF0633	Tyrosine--tRNA ligase
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q835J8	29375946	EF1379	Alanine--tRNA ligase
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9I553	15596100	alaS PA0903	Alanyl-tRNA synthetase AlaS

Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	Q51422	15596160	aspS PA0963	Aspartyl-tRNA synthetase AspS
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EKS6	24371614	SO_0014	Glycine--tRNA ligase beta subunit
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EFA0	24373645	SO_2085	Phenylalanine--tRNA ligase alpha subunit
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EF99	24373646	SO_2086	Phenylalanine--tRNA ligase beta subunit
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EEZ1	24373772	SO_2218	Asparagine--tRNA ligase
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8EEE9	24373980	SO_2433	Aspartate--tRNA ligase
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8ECI8	24374667	SO_3154	Proline--tRNA ligase
Zhang, 2010	<i>S. oneidensis</i>	Negative	Q8E9Y7	24375609	SO_4123	Arginine--tRNA ligase
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	Q9I0A0	15597939	infC PA2743	Translation initiation factor IF-3
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	Q9HV55	15599938	infB PA4744	Translation initiation factor IF-2

Group O: Post-translational modification, protein turnover, chaperones [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene Locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZK6	49474320	tig	Trigger factor
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	O33964	49474597	mopA	Chaperonin protein GroEL
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G1F9	49473743	dnaK	Heat shock protein 70 Dna K
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G134	49474627	clpB	ATP-dependent Clp protease
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896437		ATPase with chaperone activity ClpC, two ATP-binding domain
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895960		60 kDa chaperonin (groEL protein)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893936		Molecular chaperone, DnaJ family
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YU57	340622830	Ccan_20590	Thioredoxin
Böhle, 2011	<i>E. faecalis</i>	Positive	Q835R7	29375876	EF1308	Chaperone protein DnaK
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9HV44	15599954	dnaJ PA4760	Chaperone protein DnaJ
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9HYX8	15598458	PA3262	Peptidyl-prolyl cis-trans isomerase
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9I2T9	15597000	lon PA1803	Lon protease
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9I2U0	15596999	clpX PA1802	Clp protease ClpX
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9I742	15595288	clpV1 PA0090	Protein ClpV
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GDC6	88608250	NSE_0642	Heat shock protein 60 (GroEL)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GF34	88608598	NSE_0019	Heat shock protein 70 (DnaK)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GES7	88608018	NSE_0119	Heat shock protein ClpB protein
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8CX48	24372295	SO_0704	60 kDa chaperonin
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHT7	24372709	SO_1126	Chaperone protein DnaK
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EG20	24373359	SO_1793	Trigger factor
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EG18	24373361	SO_1795	ATP-dependent Clp protease ATP-binding subunit ClpX
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EG17	24373362	SO_1796	Lon protease
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFF7	24373579	SO_2016	Chaperone protein HtpG
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBE6	24375079	SO_3577	Chaperone protein ClpB
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8E9U9	24375649	SO_4163	ATP-dependent protease ATPase subunit HslU

Group G: Carbohydrate transport and metabolism [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene Locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0B6	49474016	ppdK	Pyruvate phosphate kinase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894114		Fructose-bisphosphate aldolase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893997	gapC	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894001		Enolase (2-phosphoglycerate dehydratase)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893999		Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894627		Transketolase, TKT
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893775		Phosphomannomutase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894231	tkt	Transketolase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893999	tpi	Triosephosphate isomerase
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YV92	340621792	Ccan_10210	Glyceraldehyde-3-phosphate dehydrogenase A
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839H4	29374841	EF0195	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q836R2	29375625	EF1046	Pyruvate kinase
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q836E7	29375743	EF1167	Fructose-bisphosphate aldolase
Bøhle, 2011	<i>E. faecalis</i>	Positive	P0DM31	29376483	EF1961	Enolase
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q833I8	29376486	EF1964	Glyceraldehyde-3-phosphate dehydrogenase
Han, 2012	<i>E. coli K-12</i>	Negative		gi 87082041	GatY	D-Tagatose 1,6-bisphosphate aldolase 2, catalytic subunit
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1788411	GatZ	D-Tagatose 1,6-bisphosphate aldolase 2, catalytic subunit
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GEE9	88608298	NSE_0254	Triosephosphate isomerase (TpiA)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GDX7	88608457	NSE_0434	Glyceraldehyde-3-phosphate dehydrogenase, type I (Gap)
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EIB3	24372517	SO_0930	Transketolase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EIB0	24372520	SO_0933	Fructose-bisphosphate aldolase class II Calvin cycle subtype Fba
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEN3	24373892	SO_2345	Glyceraldehyde-3-phosphate dehydrogenase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEN1	24373894	SO_2347	Glyceraldehyde-3-phosphate dehydrogenase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EE96	24374035	SO_2491	Pyruvate kinase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EDU9	24374185	SO_2644	Phosphoenolpyruvate synthase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBH1	24375051	SO_3547	Glucose-6-phosphate isomerase

Group C: Energy production and conversion [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FYD2		sucD	Succinyl-coenzyme A synthetase alpha chain
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FYD4		sucB	Dihydrolipoamide succinyltransferase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G169	49474128	pdhB	Pyruvate dehydrogenase E1 component beta subunit
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0V8	49473786	acnA	Aconitate hydratase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894267		Pyruvate-formate lyase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896832		Rubrerythrin
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896341		Fumerate hydratase, subunit B (C-terminal domain of FumA E. coli) class I
Böhle, 2011	<i>E. faecalis</i>	Positive	Q834N1	29376172	EF1613	Formate acetyltransferase
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q59638	15600209	aceF aceB PA5016	Dihydrolipoyllysine-residue acetyltransferase
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1790445	AceA	Isocitrate lyase
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GEF1	88608589	NSE_0251	Succinyl-coenzyme A synthetase, β -subunit (SucC)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GDI7	88608632	NSE_0578	2-Oxoglutarate dehydrogenase (SucA)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GD40	88608282	NSE_0730	Citrate synthase (GltA)
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJN9	24372019	SO_0424	Pyruvate dehydrogenase E1 component
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJN1	24372027	SO_0432	Aconitate hydratase 2
Zhang 2010	<i>S. oneidensis</i>	Negative	P82177	24372359	SO_0770	Malate dehydrogenase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EGV1	24373064	SO_1490	Alcohol dehydrogenase II AdhB
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EGS3	414561917	SO_1521	Respiratory FAD-dependent D-lactate dehydrogenase Dld
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFP4	24373490	SO_1926	Citrate synthase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFP0	24373494	SO_1930	2-oxoglutarate dehydrogenase complex dehydrogenase E1 component SucA
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFN9	24373495	SO_1931	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFN8	24373496	SO_1932	Succinyl-CoA ligase [ADP-forming] subunit beta
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFN7	24373497	SO_1933	Succinyl-CoA ligase [ADP-forming] subunit alpha
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EDW2	24374171	SO_2629	Isocitrate dehydrogenase NADP-dependent Icd
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8ED58	24374439	SO_2912	Pyruvate formate-lyase PflB
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8ED55	24374442	SO_2915	Acetate kinase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EAP2	24375344	SO_3855	NAD-dependent malic enzyme

Group E: Amino acid transport and metabolism [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G009	49474159	glyA	Serine hydroxymethyltransferase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G010	49473952	lysC	Aspartokinase, alpha and beta subunit
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895916		Glutamine synthetase type III
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896499	proA	Gamma-glutamyl phosphate reductase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893858	asd	Aspartate semialdehyde dehydrogenase
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YQF7	340620981	Ccan_02030	Glycine cleavage system H protein
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GEI3	88608618	NSE_0218	Serine hydroxymethyltransferase (GlyA)
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GE57	88608432	NSE_0350	Glutamine synthetase, type I (GlnA)
Zhang 2010	<i>S. oneidensis</i>	Negative	P59301	24371874	SO_0276	Acetylglutamate kinase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJZ2	24371912	SO_0314	Ornithine decarboxylase SpeF
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHU1	24372705	SO_1122	Gamma-glutamyl phosphate reductase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFU5	24373435	SO_1870	Biosynthetic arginine decarboxylase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFB0	24373634	SO_2074	ATP phosphoribosyltransferase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEU9	24373817	SO_2264	Cysteine desulfurase IscS
Zhang 2010	<i>S. oneidensis</i>	Negative	K4PU16	414562022	SO_2304	Alanine dehydrogenase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEM8	24373897	SO_2350	Aspartate aminotransferase AspC
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEH8	24373951	SO_2404	3-phosphoshikimate 1-carboxyvinyltransferase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EDZ7	24374136	SO_2593	Glutamate dehydrogenase (NAD ⁺) Gdh
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EDI2	24374305	SO_2767	Asparagine synthase glutamine-hydrolyzing AsnB
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBT6	24374923	SO_3413	Threonine synthase ThrC
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBT4	24374925	SO_3415	Bifunctional aspartokinase I / homoserine dehydrogenase I ThrA
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBN8	24374977	SO_3471	Serine hydroxymethyltransferase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EAC1	24375473	SO_3986	Aspartokinase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8E976	24375890	SO_4410	Glutamine synthetase

Group K: Transcription [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FYB7		rho	Transcription terminator factor rho
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZL4		nusG	Transcription antitermination protein
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZE6		rpoA	DNA-directed RNA polymerase alpha chain
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0P0	49473872	nusA	N utilization substance protein A
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q9KJM5	49474307	rpoB	DNA-directed RNA polymerase beta chain
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896391		DNA-directed RNA polymerase subunit beta' (RNAP subunit beta')
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896392		DNA-directed RNA polymerase subunit beta (RNAP subunit beta)
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q82ZX2	29377389	EF2925	Cold shock-like protein CspLA
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9HWC4	15599471	nusG PA4275	Transcription antitermination protein NusG
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9HTV1	15600432	rho PA5239	Transcription termination factor Rho
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	P26480	15595773	rpoD PA0576	RNA polymerase sigma factor RpoD
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	Q9HV54	15599939	nusA PA4745	N utilization substance protein A NusA
Vecchiatti, 2012	<i>P. aeruginosa</i>	Negative	O52760	15599434	rpoA PA4238	RNA polymerase subunit alpha RpoA
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EK74	24371822	SO_0224	DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EK73	24371823	SO_0225	DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EK47	24371854	SO_0256	DNA-directed RNA polymerase subunit alpha
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJQ7	24372001	SO_0405	Transcription termination factor Rho
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHL6	24372786	SO_1203	N utilization substance protein A NusA

Group F: Nucleotide transport and metabolism [96]

Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZJ2		purC	Phosphoribosylaminoimidazole-succinocarboxamide synthase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZJ4	49474332	purB	Adenylosuccinate lyase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G197	49473838	guaA	GMP synthase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895957		GMP synthase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894932		Bifunctional enzyme phosphoribosylformylglycinamide (FGAM) synthase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894670		Phosphoribosylaminoimidazole-succinocarboxamide synthase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895097	purB	Adenylosuccinate lyase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896827	purA	Adenylosuccinate synthase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894160	xpt	Xanthine phosphoribosyltransferase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896133	upp	Uracil phosphoribosyltransferase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893771	nrdD	Oxygen-sensitive ribonucleoside triphosphate reductase nrdD
Bøhle, 2011	<i>E. faecalis</i>	Positive	Q839E3	29374872	EF0228	Adenylate kinase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHC7	24372879	SO_1301	Aspartate carbamoyltransferase PyrB
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEG7	24373962	SO_2415	Ribonucleoside-diphosphate reductase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EC57	24374798	SO_3287	Phosphoribosylformylglycinamide synthase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8ECR8	24374586	SO_3064	Amidophosphoribosyltransferase

Group L: Replication, recombination and repair [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZF9		ssb	Single-strand binding protein
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZF0		recA	Recombinase A protein
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0V5	49473789	dnaN	DNA polymerase III, beta chain
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G1I9	49473721	gyrB	DNA gyrase subunit B
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893305		DNA gyrase subunit A
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895224		Site-specific recombinases, DNA invertase Pin homolog
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893421	dnaX	DNA-directed DNA polymerase, III chain (dnaX)
Han, 2012	<i>E. coli K-12</i>	Negative		gi 1789051	RecA	DNA strand exchange and recombination protein with protease and nuclease activity
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	Q9I7C2	15595202	gyrB PA0004	DNA gyrase subunit B
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EKS9	24371611	SO_0011	DNA gyrase subunit B
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EIQ4	24372372	SO_0783	Superfamily I DNA and RNA helicase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EEH1	24373958	SO_2411	DNA gyrase subunit A
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EBS0	24374940	SO_3430	Protein RecA
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EA75	24375521	SO_4034	ATP-dependent RNA helicase DeaD
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8E8J5	24376141	SO_4669	DNA polymerase I PolA

Group I: Lipid transport and metabolism [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Mao, 2011	<i>C. cetobutylicum</i>	Positive		gi 15896127		Acetyl-CoA acetyltransferase
Mao, 2011	<i>C. cetobutylicum</i>	Positive		gi 15895965		3-hydroxybutyryl-CoA dehydrogenase
Mao, 2011	<i>C. cetobutylicum</i>	Positive		gi 15896803		Acetyl-CoA carboxylase beta subunit
Mao, 2011	<i>C. cetobutylicum</i>	Positive		gi 15895968	bcd	Acyl-CoA dehydrogenase, short-chain specific (SCAD)
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	Q9HXZ2	15598835	accA PA3639	Acetyl-coenzyme A carboxylase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EFR9	24373462	SO_1897	Isovaleryl-CoA dehydrogenase LiuA

The other groups based on COG Classification [96]

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description	COG code ^a
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G181	49473836	guaB	Inosine-5'-monophosphate dehydrogenase	T
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G180	499492646	ntrX	Nitrogen regulation protein	T
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0R7	49473827	typA	GTP-binding protein TypA	T
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJ49	24372215	SO_0624	cAMP-responsive regulator of catabolite repression Crp	T
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHW1	24372685	SO_1101	S-ribosylhomocysteine lyase	T
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8ED82	24374411	SO_2882	Serine protein kinase PrkA	T
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893882	ribH	Riboflavin synthase beta chain	H
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJM8	24372030	SO_0435	Uroporphyrinogen decarboxylase	H
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EIB4	24372516	SO_0929	S-adenosylmethionine synthase	H
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHC8	24372878	SO_1300	Glutamate-1-semialdehyde 2,1-aminomutase	H
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EH88	24372919	SO_1341	L-aspartate oxidase component of quinolinate synthetase NadB	H
Zhang 2010	<i>S. oneidensis</i>	Negative	K4PSH5	414562066	SO_2756	Peroxiredoxin TsaA	V
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0U6	49473798	fabB	3-Oxyacyl-(acyl-carrier-protein) synthase I	I, Q
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YQW2	340621055	Ccan_02770	Acyl carrier protein	I, Q
Gibson 2010	<i>N. sennetsu</i>	Negative	Q2GDV8	88608089	NSE_0453	3-Oxoacyl-(acyl carrier protein) synthase II (FabF)	I, Q
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZ64	49474483	carB	Carbamoyl-phosphate synthase large chain	E, F
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895902		Carbamoyl-phosphate synthase large chain	E, F
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EHS5	24372725	SO_1142	Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	E, F
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8E9E1	414562267	SO_4343	Serine-pyruvate aminotransferase AgxT	E, F
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894106		Phosphoribosylpyrophosphate synthetase	F, E
Vecchiotti, 2012	<i>P. aeruginosa</i>	Negative	O87124	15596655	PA1458	CheA homolog	N, T
Han, 2012	<i>E. coli BL21</i>	Negative		gi 1788197	CheA	Fused chemotactic sensory histidine kinase in two-component regulatory system with CheB and CheY: sensory histidine kinase/signal sensing protein	N, T
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8ECD6	24374719	SO_3207	Histidine kinase	N, T
Manfredi, 2011	<i>C. canimorsus</i>	Negative	F9YTR2	340622762	Ccan_19910	Branched-chain-amino-acid transaminase, Vegetative protein 85 homologue	E, H
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EET7	24373832	SO_2279	Acetolactate synthase	E, H

Zhang 2010	<i>S. oneidensis</i>	Negative	Q8E9D5	24375830	SO_4349	Ketol-acid reductoisomerase	E, H
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15893467		Response regulator, CheY-like receiver domain and HTH-type DNA binding domain	T, K
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896682		DNA/RNA helicase, SNF2	K, L
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15894801		Fructokinase	K, G
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EIH7	24372451	SO_0862	D-3-phosphoglycerate dehydrogenase SerA	H, R
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EGQ7	24373111	SO_1538	Isocitrate dehydrogenase NAD-dependent	C, E

^aCOG code [96]

- C Energy production and conversion
- E Amino acid transport and metabolism
- F Nucleotide transport and metabolism
- G Carbohydrate transport and metabolism
- H Coenzyme transport and metabolism
- I Lipid transport and metabolism
- K Transcription
- L Replication, recombination and repair
- N Cell motility
- Q Secondary metabolites biosynthesis, transport and catabolism
- R General function prediction only
- T Signal transduction mechanisms
- V Defense mechanisms

**Appendix II – The Other Intracellular/Surface Moonlighting Protein Candidates
that are not Included in the COG Database**

Author, Year	Species	Gram type	UniProt #	NCBI #	Gene locus	Function description
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6FZ43		ctrA	Cell cycle transcriptional regulator
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G0F7		prsA	Ribose-phosphate pyrophosphokinase
Boonjakuakul, 2007	<i>B. quintana</i>	Negative	Q6G1E5		hrcA	Heat-inducible transcription repressor
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896327		Phosphate butyryltransferase (Phosphotransbutyrylase)
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 18266735		Pyruvate kinase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 3914324		Phosphoglycerate kinase alpha
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895958		Inositol-5'-monophosphate dehydrogenase
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895341	spo0A	Stage 0 sporulation protein A homolog
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15895023	plsX	Glycerol-3-phosphate acyltransferase PlsX
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896376		50S ribosomal protein L16
Mao, 2011	<i>C. acetobutylicum</i>	Positive		gi 15896396		50S ribosomal protein L11
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	P15276		algP algR3 PA5253	Transcriptional regulatory protein AlgP
Vecchietti, 2012	<i>P. aeruginosa</i>	Negative	G3XCY4		amrZ PA3385	Alginate and motility regulator Z AmrZ
Gibson, 2010	<i>N. sennetsu</i>	Negative	Q2GDR7		NSE_0495	Heat shock protein HtpG
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EKR9	24371621	SO_0021	Fatty acid oxidation complex subunit alpha
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EK30		SO_0274	Phosphoenolpyruvate carboxylase
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EJ61	24372202	SO_0611	Transcriptional activator SspA
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EGS5	24373093	SO_1519	L-lactate dehydrogenase iron-sulfur cluster-binding protein LldF
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EGS4	24373094	SO_1520	L-lactate dehydrogenase complex protein LldE
Zhang 2010	<i>S. oneidensis</i>	Negative	Q8EAQ9	24375327	SO_3837	Ribose-phosphate pyrophosphokinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773763		Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771754		Glycogen/starch/alpha-glucan phosphorylase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775592		Transcription termination factor Rho
Thein, 2010	<i>E. coli</i> BL21	Negative		253775172		50S ribosomal protein L9
Thein, 2010	<i>E. coli</i> BL21	Negative		253771436		Chromosomal replication initiator protein DnaA
Thein, 2010	<i>E. coli</i> BL21	Negative		253771438		DNA replication and repair protein RecF
Thein, 2010	<i>E. coli</i> BL21	Negative		253771439		DNA gyrase, B subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253771451		Heat shock protein Hsp20

Thein, 2010	<i>E. coli</i> BL21	Negative		253771508		(p)ppGpp synthetase I, SpoT/RelA
Thein, 2010	<i>E. coli</i> BL21	Negative		253773135		Excinuclease ABC, C subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253771522		50S ribosomal protein L28
Thein, 2010	<i>E. coli</i> BL21	Negative		253771523		50S ribosomal protein L33
Thein, 2010	<i>E. coli</i> BL21	Negative		253771526		Three-deoxy-D-manno-octulosonic-acid transferase domain protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253771540		2-amino-3-ketobutyrate coenzyme A ligase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771541		L-threonine 3-dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771605		Glycyl-tRNA synthetase, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253771606		Glycyl-tRNA synthetase, beta subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253771742		Glycogen/starch synthase, ADP-glucose type
Thein, 2010	<i>E. coli</i> BL21	Negative		253771745		FAD dependent oxidoreductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771755		4-alpha-glucanotransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771768		Phosphoenolpyruvate carboxykinase (ATP)
Thein, 2010	<i>E. coli</i> BL21	Negative		253771813		Glutamine amidotransferase of anthranilate synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771832		30S ribosomal protein S12
Thein, 2010	<i>E. coli</i> BL21	Negative		253771833		30S ribosomal protein S7
Thein, 2010	<i>E. coli</i> BL21	Negative		253771834		Translation elongation factor G
Thein, 2010	<i>E. coli</i> BL21	Negative		253771835		Translation elongation factor Tu
Thein, 2010	<i>E. coli</i> BL21	Negative		253771855		30S ribosomal protein S10
Thein, 2010	<i>E. coli</i> BL21	Negative		253771856		50S ribosomal protein L3
Thein, 2010	<i>E. coli</i> BL21	Negative		253771857		50S ribosomal protein L4
Thein, 2010	<i>E. coli</i> BL21	Negative		253771858		50S ribosomal protein L23
Thein, 2010	<i>E. coli</i> BL21	Negative		253771859		50S ribosomal protein L2
Thein, 2010	<i>E. coli</i> BL21	Negative		253771860		30S ribosomal protein S19
Thein, 2010	<i>E. coli</i> BL21	Negative		253771861		50S ribosomal protein L22
Thein, 2010	<i>E. coli</i> BL21	Negative		253771862		30S ribosomal protein S3
Thein, 2010	<i>E. coli</i> BL21	Negative		253771863		50S ribosomal protein L16
Thein, 2010	<i>E. coli</i> BL21	Negative		253771865		30S ribosomal protein S17
Thein, 2010	<i>E. coli</i> BL21	Negative		253771866		50S ribosomal protein L14
Thein, 2010	<i>E. coli</i> BL21	Negative		253771867		50S ribosomal protein L24
Thein, 2010	<i>E. coli</i> BL21	Negative		253771868		50S ribosomal protein L5
Thein, 2010	<i>E. coli</i> BL21	Negative		253771869		30S ribosomal protein S14
Thein, 2010	<i>E. coli</i> BL21	Negative		253771870		30S ribosomal protein S8
Thein, 2010	<i>E. coli</i> BL21	Negative		253771871		50S ribosomal protein L6
Thein, 2010	<i>E. coli</i> BL21	Negative		253771872		50S ribosomal protein L18
Thein, 2010	<i>E. coli</i> BL21	Negative		253771873		30S ribosomal protein S5
Thein, 2010	<i>E. coli</i> BL21	Negative		253771874		50S ribosomal protein L30
Thein, 2010	<i>E. coli</i> BL21	Negative		253771875		50S ribosomal protein L15

Thein, 2010	<i>E. coli</i> BL21	Negative		253771877		50S ribosomal protein L36
Thein, 2010	<i>E. coli</i> BL21	Negative		253771878		30S ribosomal protein S13
Thein, 2010	<i>E. coli</i> BL21	Negative		253771879		30S ribosomal protein S11
Thein, 2010	<i>E. coli</i> BL21	Negative		253771880		30S ribosomal protein S4
Thein, 2010	<i>E. coli</i> BL21	Negative		253771881		DNA-directed RNA polymerase, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253771882		50S ribosomal protein L17
Thein, 2010	<i>E. coli</i> BL21	Negative		253771914		Acetyl-CoA carboxylase, biotin carboxylase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771915		Acetyl-CoA carboxylase, biotin carboxyl carrier protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253771923		maf protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253771924		Ribonuclease, Rne/Rng family
Thein, 2010	<i>E. coli</i> BL21	Negative		253771940		50S ribosomal protein L13
Thein, 2010	<i>E. coli</i> BL21	Negative		253771941		30S ribosomal protein S9
Thein, 2010	<i>E. coli</i> BL21	Negative		253771980		50S ribosomal protein L21
Thein, 2010	<i>E. coli</i> BL21	Negative		253771981		50S ribosomal protein L27
Thein, 2010	<i>E. coli</i> BL21	Negative		253771987		Ribosomal RNA large subunit methyltransferase J
Thein, 2010	<i>E. coli</i> BL21	Negative		253771993		Argininosuccinate synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253771995		NusA antitermination factor
Thein, 2010	<i>E. coli</i> BL21	Negative		253771996		Translation initiation factor IF-2
Thein, 2010	<i>E. coli</i> BL21	Negative		253771999		30S ribosomal protein S15
Thein, 2010	<i>E. coli</i> BL21	Negative		253772000		Polyribonucleotide nucleotidyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772018		Uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin) methyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772097		RNA polymerase, sigma 70 subunit, RpoD
Thein, 2010	<i>E. coli</i> BL21	Negative		253772099		30S ribosomal protein S21
Thein, 2010	<i>E. coli</i> BL21	Negative		253772110		Adenylate cyclase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772112		rfaE bifunctional protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253772132		DNA topoisomerase IV, B subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772143		DNA topoisomerase IV, A subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772151		2,5-didehydrogluconate reductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772220		S-adenosylmethionine synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772225		Transketolase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772234		Phosphoglycerate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772235		Fructose-bisphosphate aldolase, class II
Thein, 2010	<i>E. coli</i> BL21	Negative		253772256		Glycine dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772269		Lysyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772290		PAS modulated sigma54 specific transcriptional regulator, Fis family
Thein, 2010	<i>E. coli</i> BL21	Negative		253772317		PTSINtr with GAF domain, PtsP
Thein, 2010	<i>E. coli</i> BL21	Negative		253772319		Thymidylate synthase

Thein, 2010	<i>E. coli</i> BL21	Negative		253772328		Amino-acid N-acetyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772337		SAM-dependent methyltransferase-like protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253772365		(p)ppGpp synthetase I, SpoT/RelA
Thein, 2010	<i>E. coli</i> BL21	Negative		253772370		Enolase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772411		DNA mismatch repair protein MutS
Thein, 2010	<i>E. coli</i> BL21	Negative		253772418		Hydrogenase accessory protein HypB
Thein, 2010	<i>E. coli</i> BL21	Negative		253772440		Short-chain dehydrogenase/reductase SDR
Thein, 2010	<i>E. coli</i> BL21	Negative		253772446		recA protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253772448		Alanyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772497		30S ribosomal protein S16
Thein, 2010	<i>E. coli</i> BL21	Negative		253772498		16S rRNA processing protein RimM
Thein, 2010	<i>E. coli</i> BL21	Negative		253772500		50S ribosomal protein L19
Thein, 2010	<i>E. coli</i> BL21	Negative		253772512		ATP-dependent chaperone ClpB
Thein, 2010	<i>E. coli</i> BL21	Negative		253772518		Thioredoxin
Thein, 2010	<i>E. coli</i> BL21	Negative		253772519		tRNA/rRNA methyltransferase (SpoU)
Thein, 2010	<i>E. coli</i> BL21	Negative		253772524		DEAD/DEAH box helicase domain protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253772534		Ribonuclease III
Thein, 2010	<i>E. coli</i> BL21	Negative		253772553		Glycine hydroxymethyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772571		Inositol monophosphatase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772574		cysteine desulfurase IscS
Thein, 2010	<i>E. coli</i> BL21	Negative		253772581		PepB aminopeptidase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772588		Nucleoside-diphosphate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772589		radical SAM enzyme, Cfr family
Thein, 2010	<i>E. coli</i> BL21	Negative		253772591		1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772592		Histidyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772598		Inosine-5'-monophosphate dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772599		Transcriptional regulator, XRE family
Thein, 2010	<i>E. coli</i> BL21	Negative		253772606		Ppx/GppA phosphatase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772610		Uracil phosphoribosyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772632		Phosphoribosylaminoimidazole-succinocarboxamide synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772684		Phosphoenolpyruvate-protein phosphotransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772690		DNA ligase, NAD-dependent
Thein, 2010	<i>E. coli</i> BL21	Negative		253772695		Glutamyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772753		Beta-ketoacyl synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772760		Acetyl-CoA carboxylase, carboxyl transferase, beta subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772779		Phosphate acetyltransferase

Thein, 2010	<i>E. coli</i> BL21	Negative		253772780		Acetate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772786		Aminotransferase class I and II
Thein, 2010	<i>E. coli</i> BL21	Negative		253772820		Polysaccharide deacetylase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772836		Glycerol-3-phosphate dehydrogenase, anaerobic, A subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772843		Ribonucleoside-diphosphate reductase, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772846		DNA gyrase, A subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772856		Two component, sigma 54 specific, transcriptional regulator, Fis family
Thein, 2010	<i>E. coli</i> BL21	Negative		253772883		Two component transcriptional regulator, LuxR family
Thein, 2010	<i>E. coli</i> BL21	Negative		253772888		50S ribosomal protein L25
Thein, 2010	<i>E. coli</i> BL21	Negative		253772890		Pseudouridine synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772921		GTP cyclohydrolase I
Method 2	<i>E. coli</i> BL21	Negative		253772967		Hydroxyethylthiazole kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772968		Phosphomethylpyrimidine kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253772976		D-tagatose-bisphosphate aldolase, class II, non-catalytic subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253772980		Alcohol dehydrogenase GroES domain protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253773002		Uridine kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773042		6-phosphogluconate dehydrogenase, decarboxylating
Thein, 2010	<i>E. coli</i> BL21	Negative		253773049		Histidinol-phosphatase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773140		Ferroxidase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773167		Arginyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773189		Pyruvate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773190		Transcriptional regulator, RpiR family
Thein, 2010	<i>E. coli</i> BL21	Negative		253773192		Glucose-6-phosphate 1-dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773214		ProQ activator of osmoprotectant transporter ProP
Thein, 2010	<i>E. coli</i> BL21	Negative		253773233		L-serine dehydratase 1
Thein, 2010	<i>E. coli</i> BL21	Negative		253773266		Glyceraldehyde-3-phosphate dehydrogenase, type I
Thein, 2010	<i>E. coli</i> BL21	Negative		253773281		Selenide, water dikinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773298		Acetylornithine and succinylornithine aminotransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773326		Threonyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773327		Translation initiation factor IF-3
Thein, 2010	<i>E. coli</i> BL21	Negative		253773328		50S ribosomal protein L35
Thein, 2010	<i>E. coli</i> BL21	Negative		253773329		50S ribosomal protein L20
Thein, 2010	<i>E. coli</i> BL21	Negative		253773333		Integration host factor, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253773340		Phospho-2-dehydro-3-deoxyheptonate aldolase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773343		Phosphoenolpyruvate synthase

Thein, 2010	<i>E. coli</i> BL21	Negative		253773380		Cyclopropane-fatty-acyl-phospholipid synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773403		Pyridoxamine 5'-phosphate oxidase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773404		Tyrosyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773420		Adenosine deaminase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773433		Fumarate hydratase, class II
Thein, 2010	<i>E. coli</i> BL21	Negative		253773612		ATP-dependent helicase HrpA
Thein, 2010	<i>E. coli</i> BL21	Negative		253773712		Exoribonuclease II
Thein, 2010	<i>E. coli</i> BL21	Negative		253773729		DNA topoisomerase I
Thein, 2010	<i>E. coli</i> BL21	Negative		253773734		Pseudouridine synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773739		Anthranilate phosphoribosyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773763		D-tagatose-bisphosphate aldolase, class II, non-catalytic subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253773766		UTP-glucose-1-phosphate uridylyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773794		Ribose-phosphate pyrophosphokinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773798		GTP-binding protein YchF
Thein, 2010	<i>E. coli</i> BL21	Negative		253773882		3-oxoacyl-(acyl-carrier-protein) synthase 2
Thein, 2010	<i>E. coli</i> BL21	Negative		253773884		3-oxoacyl-(acyl-carrier-protein) reductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773886		3-oxoacyl-(acyl-carrier-protein) synthase III
Thein, 2010	<i>E. coli</i> BL21	Negative		253773887		Fatty acid/phospholipid synthesis protein PlsX
Thein, 2010	<i>E. coli</i> BL21	Negative		253773888		50S ribosomal protein L32
Thein, 2010	<i>E. coli</i> BL21	Negative		253773891		Pseudouridine synthase, RluA family
Thein, 2011	<i>E. coli</i> BL21	Negative		253773892		Ribonuclease, Rne/Rng family
Thein, 2010	<i>E. coli</i> BL21	Negative		253773910		Ribosomal-protein-alanine N-acetyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253773956		Delta-1-pyrroline-5-carboxylate dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774008		UvrD/REP helicase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774041		Asparaginyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774043		Aspartate transaminase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774047		Chromosome segregation and condensation protein MukB domain protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253774059		Integration host factor, beta subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774060		30S ribosomal protein S1
Thein, 2010	<i>E. coli</i> BL21	Negative		253774068		Formate acetyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774082		Transcriptional regulator, AsnC family
Thein, 2010	<i>E. coli</i> BL21	Negative		253774088		ATP-dependent Clp protease, ATP-binding subunit clpA
Thein, 2010	<i>E. coli</i> BL21	Negative		253774141		RNA-directed DNA polymerase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774218		Excinuclease ABC, B subunit

Thein, 2010	<i>E. coli</i> BL21	Negative		253774281		Phosphoglycerate mutase 1 family
Thein, 2010	<i>E. coli</i> BL21	Negative		253774302		Succinyl-CoA synthetase, beta subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774303		2-oxoglutarate dehydrogenase, E2 subunit, dihydrolipoamide succinyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774304		2-oxoglutarate dehydrogenase, E1 subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774310		Citrate synthase I
Thein, 2010	<i>E. coli</i> BL21	Negative		253774355		tRNA-i(6)A37 thiotransferase enzyme MiaB
Thein, 2010	<i>E. coli</i> BL21	Negative		253774372		Leucyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774386		Lipoic acid synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774410		Peroxisredoxin
Thein, 2010	<i>E. coli</i> BL21	Negative		253774487		Peptidyl-prolyl cis-trans isomerase cyclophilin type
Thein, 2010	<i>E. coli</i> BL21	Negative		253774537		Heat shock protein Hsp90
Thein, 2010	<i>E. coli</i> BL21	Negative		253774569		Histone family protein DNA-binding protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253774573		ATP-dependent Clp protease, ATP-binding subunit ClpX
Thein, 2010	<i>E. coli</i> BL21	Negative		253774574		ATP-dependent Clp protease, proteolytic subunit ClpP
Thein, 2010	<i>E. coli</i> BL21	Negative		253774592		Thiamine biosynthesis/tRNA modification protein ThiI
Thein, 2010	<i>E. coli</i> BL21	Negative		253774595		Deoxyxylulose-5-phosphate synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774599		NusB antitermination factor
Thein, 2010	<i>E. coli</i> BL21	Negative		253774646		Porphobilinogen synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774666		Transcriptional regulator, LacI family
Thein, 2010	<i>E. coli</i> BL21	Negative		253774731		Glutamate 5-kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774738		Aminoacyl-histidine dipeptidase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774778		Prolyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774788		Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774789		DNA polymerase III, alpha subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774793		Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ
Thein, 2010	<i>E. coli</i> BL21	Negative		253774802		Uridylate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774803		Translation elongation factor Ts
Thein, 2010	<i>E. coli</i> BL21	Negative		253774804		30S ribosomal protein S2
Thein, 2010	<i>E. coli</i> BL21	Negative		253774807		2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774812		Deoxyguanosinetriphosphate triphosphohydrolase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774818		Glutamate-1-semialdehyde-2,1-aminomutase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774829		poly(A) polymerase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774838		3-methyl-2-oxobutanoate hydroxymethyltransferase

Thein, 2010	<i>E. coli</i> BL21	Negative		253774851		Spermidine synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774854		Aconitate hydratase 2
Thein, 2010	<i>E. coli</i> BL21	Negative		253774856		Dihydrolipoamide dehydrogenase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774857		Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774858		2-oxo-acid dehydrogenase E1 subunit, homodimeric type
Thein, 2010	<i>E. coli</i> BL21	Negative		253774859		Regulatory protein GntR HTH
Thein, 2010	<i>E. coli</i> BL21	Negative		253774874		UDP-3-0-acyl N-acetylglucosamine deacetylase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774879		UDP-N-acetylmuramate/alanine ligase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774888		S-adenosyl-methyltransferase MrwW
Thein, 2010	<i>E. coli</i> BL21	Negative		253774901		extracellular solute-binding protein family 5
Thein, 2010	<i>E. coli</i> BL21	Negative		253774911		SNF2-related protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253774920		Dihydrofolate reductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774934		Carbamoyl-phosphate synthase, large subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774935		Carbamoyl-phosphate synthase, small subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253774937		Dihydrodipicolinate reductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774942		Isoleucyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774945		30S ribosomal protein S20
Thein, 2010	<i>E. coli</i> BL21	Negative		253774954		Chaperone protein DnaJ
Thein, 2010	<i>E. coli</i> BL21	Negative		253774955		Chaperone protein DnaK
Thein, 2010	<i>E. coli</i> BL21	Negative		253774960		Transaldolase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774966		Aspartate kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253774980		Transcriptional regulator, XRE family
Thein, 2010	<i>E. coli</i> BL21	Negative		253775000		rRNA (guanine-N(2)-)-methyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775029		Type I site-specific deoxyribonuclease
Thein, 2010	<i>E. coli</i> BL21	Negative		253775117		Leucyl aminopeptidase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775119		Valyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775135		Alpha, alpha-phosphotrehalase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775137		Anaerobic ribonucleoside-triphosphate reductase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775173		30S ribosomal protein S18
Thein, 2010	<i>E. coli</i> BL21	Negative		253775175		30S ribosomal protein S6
Thein, 2010	<i>E. coli</i> BL21	Negative		253775195		RNA methyltransferase, TrmH family, group 3
Thein, 2010	<i>E. coli</i> BL21	Negative		253775196		VacB and RNase II family 3'-5' exoribonuclease
Thein, 2010	<i>E. coli</i> BL21	Negative		253775198		Adenylosuccinate synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775202		GTP-binding protein HflX
Thein, 2010	<i>E. coli</i> BL21	Negative		253775203		RNA chaperone Hfq

Thein, 2010	<i>E. coli</i> BL21	Negative		253775229		Chaperonin GroEL
Thein, 2010	<i>E. coli</i> BL21	Negative		253775230		Chaperonin Cpn10
Thein, 2010	<i>E. coli</i> BL21	Negative		253775233		Aspartate ammonia-lyase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775242		Lysyl-tRNA synthetase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775303		Acetate/CoA ligase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775313		Excinuclease ABC, A subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253775320		Replicative DNA helicase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775357		Methionine synthase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775358		Transcriptional regulator, IclR family
Thein, 2010	<i>E. coli</i> BL21	Negative		253775360		Isocitrate lyase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775362		Homoserine O-succinyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775370		Histone family protein DNA-binding protein
Thein, 2010	<i>E. coli</i> BL21	Negative		253775383		DNA-directed RNA polymerase, beta' subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253775384		DNA- directed RNA polymerase, beta subunit
Thein, 2010	<i>E. coli</i> BL21	Negative		253775385		50S ribosomal protein L7/L12
Thein, 2010	<i>E. coli</i> BL21	Negative		253775386		50S ribosomal protein L10
Thein, 2010	<i>E. coli</i> BL21	Negative		253775387		50S ribosomal protein L1
Thein, 2010	<i>E. coli</i> BL21	Negative		253775388		50S ribosomal protein L11
Thein, 2010	<i>E. coli</i> BL21	Negative		253775391		Translation elongation factor Tu
Thein, 2010	<i>E. coli</i> BL21	Negative		253775395		Glutamate racemase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775405		Phosphoenolpyruvate carboxylase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775430		Heat shock protein HslVU, ATPase subunit HslU
Thein, 2010	<i>E. coli</i> BL21	Negative		253775435		Glycerol kinase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775436		Fructose-1,6-bisphosphatase, class II
Thein, 2010	<i>E. coli</i> BL21	Negative		253775496		Nitrogen metabolism transcriptional regulator, NtrC, Fis Family
Thein, 2010	<i>E. coli</i> BL21	Negative		253775545		5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775594		Thioredoxin
Thein, 2010	<i>E. coli</i> BL21	Negative		253775597		ATP-dependent DNA helicase Rep
Thein, 2010	<i>E. coli</i> BL21	Negative		253775605		Acetolactate synthase, large subunit, biosynthetic type
Thein, 2010	<i>E. coli</i> BL21	Negative		253775621		Aspartate/ammonia ligase
Thein, 2010	<i>E. coli</i> BL21	Negative		253775657		Tryptophanase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975384		50S ribosomal protein L3
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975203		50S ribosomal protein L1
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975212		Elongation factor Tu(EF-Tu)
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974466		Alkyl hydroperoxide reductase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972577		Ribonucleotide-diphosphate reductase subunitalpha

Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972625		Iron-containing alcohol dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972661		Glyceraldehyde-3-phosphate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972662		Phosphoglycerate kinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972663		Triosephosphate isomerase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972667		Enolase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972703		Argininosuccinate synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972738		Phenylalanyl-tRNA synthetase, alpha subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972741		Glucose-6-phosphate isomerase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972807		Isocitrate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972816		Phosphoserine aminotransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972865		Malate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972866		Malate dehydrogenase (NAD)
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972868		6-phosphofructokinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972870		Fructose-bisphosphate aldolase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972895		Glutamate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972896		Bifunctional GMP synthase/glutamineamidotransferase protein
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972939		Polynucleotide phosphorylase/polyadenylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125972944		Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973133		Phenylacetate-CoA ligase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973219		Oxaloacetate decarboxylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973232		4-hydroxy-3-methylbut-2-enyl diphosphatereductase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973238		Aminotransferase, class V
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973240		tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973250		Chorismate synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973273		Aspartate aminotransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973382		3-methyl-2-oxobutanoate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973418		Pantothenate synthetase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973439		Diaminopimelate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973468		Orotidine 5'-phosphate decarboxylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973478		Aspartate semialdehyde dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973520		Translation elongation factor Ts (EF-Ts)
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973521		SSU ribosomal protein S2P
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973543		Acetate kinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973544		Phosphotransacetylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973550		DNA ligase, NAD-dependent

Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973573		Serine hydroxymethyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973608		Methenyltetrahydrofolate cyclohydrolase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973678		Phosphoglucosamine mutase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973726		Tryptophan synthase subunit beta
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973761		Bifunctional phosphoribosylaminoimidazolecarboxamide formyl transferase/IMP cyclohydrolase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973776		6-phosphofructokinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973823		Pyruvate phosphate dikinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973837		Molecular chaperone DnaK
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125973926		Tryptophan synthase subunit beta
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974068		Cystathionine gamma-lyase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974069		Cystathionine beta-synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974074		Nitrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974075		Nitrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974078		O-acetylhomoserine aminocarboxypropyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974082		Nitrogenase iron protein subunit NifH
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974298		Translation elongation factor 2 (EF-2/EF-G)
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974299		3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974344		Cysteine synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974346		O-acetylhomoserine/O-acetylserine sulfhydrylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974367		N-acetyl-gamma-glutamyl-phosphate reductase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974368		Acetylglutamate kinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974371		Carbamoyl-phosphate synthase small subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974373		Ornithine carbamoyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974447		FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974547		CRISPR-associated TM1812 family protein
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974586		Methionyl-tRNA synthetase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974659		Transcription termination factor Rho
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974668		UDP-glucose pyrophosphorylase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974696		3-isopropylmalate dehydratase large subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974736		Methionine adenosyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974841		Quinolinate synthetase A
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974857		DNA polymerase III subunit beta
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974866		Seryl-tRNA synthetase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974875		Pyruvate ferredoxin oxidoreductase,

						gamma subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125974877		Pyruvate ferredoxin oxidoreductase, alpha subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975003		Ketol-acid reductoisomerase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975076		Peptide chain release factor 1
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975111		UDP-N-acetylglucosamine pyrophosphorylase /glucosamine-1-phosphate N-acetyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975112		Ribose-phosphate pyrophosphokinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975186		Transketolase subunit A
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975195		Dihydroxyacid dehydratase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975207		DNA-directed RNA polymerase subunit beta
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975211		Translation elongation factor 2 (EF-2/EF-G)
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975355		Phosphoenolpyruvate carboxykinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975373		Chaperonin GroEL
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975405		Adenylate kinase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975413		DNA-directed RNA polymerase, alpha subunit
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975506		Methylcitrate synthase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975514		D-3-phosphoglycerate dehydrogenase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975571		Adenylosuccinate synthetase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975635		Pyruvate carboxyltransferase
Yu, 2012	<i>C. thermocellum</i>	Positive		gi 125975636		Aconitate hydratase
Sears, 2012	<i>R. typhi</i>	Negative	Q68XV6		RT0049	Elongation factor Ts, tfs
Sears, 2012	<i>R. typhi</i>	Negative	Q68XR2		RT0094	ATP-binding ClpB chaperone
Sears, 2012	<i>R. typhi</i>	Negative	Q8KTB2		RT0121	Elongation factor G, fusA
Sears, 2012	<i>R. typhi</i>	Negative	Q68XI2		RT0176	Chaperone protein DnaK
Sears, 2012	<i>R. typhi</i>	Negative	Q68XG5		RT0193	Excinuclease ABC subunit B, uvrB
Sears, 2012	<i>R. typhi</i>	Negative	O33582		RT0198	Methionyl-tRNA formyltransferase, fmt
Sears, 2012	<i>R. typhi</i>	Negative	Q68XE8		RT0212	Threonine--tRNA ligase, thrS
Sears, 2012	<i>R. typhi</i>	Negative	Q68XB3		RT0248	Ribonuclease E, rne
Sears, 2012	<i>R. typhi</i>	Negative	Q68XA9		RT0252	Pyruvate decarboxylase, pdhA
Sears, 2012	<i>R. typhi</i>	Negative	Q68WU5		RT0420	Succinyl-CoA synthetase subunit beta, sucC
Sears, 2012	<i>R. typhi</i>	Negative	Q68WR9		RT0447	Dihydrolipoamide dehydrogenase, pdhD1
Sears, 2012	<i>R. typhi</i>	Negative	Q68WN2		RT0488	30S ribosomal protein S15
Sears, 2012	<i>R. typhi</i>	Negative	Q68WM5		RT0495	tRNA delta(2)-isopentenylpyrophosphate transferase
Sears, 2012	<i>R. typhi</i>	Negative	Q68WK2		RT0521	Biotin-protein ligase, birA
Sears, 2012	<i>R. typhi</i>	Negative	Q68WF6		RT0569	DNA topoisomerase II subunit B, gyrB
Sears, 2012	<i>R. typhi</i>	Negative	Q68WE3		RT0584	D-alanine ligase, murF

Sears, 2012	<i>R. typhi</i>	Negative	Q68WD4		RT0593	Peptidyl-tRNA hydrolase, pth
Sears, 2012	<i>R. typhi</i>	Negative	O85754		RT0617	60 kDa chaperonin/chaperonin GroEL
Sears, 2012	<i>R. typhi</i>	Negative	Q68W91		RT0638	30S ribosomal protein S14, rpsN
Sears, 2012	<i>R. typhi</i>	Negative	Q8KT95		RT0653	Elongation factor Tu, tuf
Sears, 2012	<i>R. typhi</i>	Negative	Q68W74		RT0657	Fumarase C, fumC
Sears, 2012	<i>R. typhi</i>	Negative	Q68W66		RT0666	Dimethyladenosine transferase, ksgA
Sears, 2012	<i>R. typhi</i>	Negative	Q68W63		RT0669	Exodeoxyribonuclease VII large subunit, xseA
Sears, 2012	<i>R. typhi</i>	Negative	Q68W61		RT0671	Exodeoxyribonuclease III, xthA2
Sears, 2012	<i>R. typhi</i>	Negative	Q68W54		RT0678	Methionine--tRNA ligase, metG
Sears, 2012	<i>R. typhi</i>	Negative	Q68W53		RT0679	Thymidylate kinase, tmk
Sears, 2012	<i>R. typhi</i>	Negative	Q68W07		RT0728	Serine hydroxymethyltransferase, glyA
Sears, 2012	<i>R. typhi</i>	Negative	Q68VY6		RT0749	Acyl carrier protein, acpP
Sears, 2012	<i>R. typhi</i>	Negative	Q68VT2		RT0805	Site-specific tyrosine recombinase, xerC
Sears, 2012	<i>R. typhi</i>	Negative	Q68Y04		RT0817	Ferredoxin, fdxA
Sears, 2012	<i>R. typhi</i>	Negative	Q68VQ5		RT0847	RNA polymerase sigma factor, rpoD
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		15892097		Elongation factor G
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34580431		Polyribonucleotide nucleotidyltransferase
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34580431		Polyribonucleotide nucleotidyltransferase
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34580814		DnaK protein
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		15892891		Chaperonin GroEL
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34580862		Aminopeptidase A
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34581103		Trigger factor
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		15893105		Recombinase A
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34580487		Succinyl-CoA synthetase alpha chain
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		15892374		Thioredoxin peroxidase 1
Pornwiroon, 2009	<i>R. parkeri</i>	Negative		34581077		Transcription elongation factor EF
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q9AGE6		lmo2068	Class I heat-shock protein (chaperonin) GroEL (groEL)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P0DJM2		lmo1473	Class I heat-shock protein (molecular chaperone) DnaK (dnaK)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4I1		lmo2459	Glyceraldehyde 3-phosphate dehydrogenase (gap)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P64074		lmo2455	Enolase (eno)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6M7		lmo1657	Translation elongation factor (tsf)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8G1		lmo0943	Non-heme iron-binding ferritin (fri)

Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6W1		lmo1570	Pyruvate kinases (pykA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y498		lmo2556	Similar to fructose-1,6-bisphosphate aldolase (fbaA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q92A74		lmo1934	Similar to non-specific DNA-binding protein HU (hup)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y570		lmo2206	Chaperon protein ClpB
Portillo, 2011	<i>L. monocytogenes</i>	Positive	C6ZWF9		lmo1054	Pyruvate dehydrogenase (dihydrolipoamide acetyltransferase E2 subunit) (pdhC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAC3		lmo0223	Cysteine synthase (cysK)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y440		lmo2632	50S ribosomal protein L3 (rplC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P0DJP0		lmo1398	Recombination protein recA (recA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P60426		lmo2629	50S ribosomal protein L2 (rplB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y3P9		lmo2785	Catalase (kat)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7L0		lmo1267	Trigger factor (prolyl isomerase) (tig)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6W0		lmo1571	ATP-dependent 6-phosphofructokinase (pfk)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4I2		lmo2458	Phosphoglycerate kinase (pgk)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6T2		lmo1600	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (aroA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y421		lmo2654	Translation elongation factor G (fus)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y862		lmo1055	Dihydrolipoamide dehydrogenase, E3 subunit of pyruvate dehydrogenase complex (PdhD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6M6		lmo1658	30S ribosomal protein S2 (rpsB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y9G8		lmo0560	Glutamate dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y458		lmo2597	50S ribosomal protein L13 (rplM)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7H4		lmo1305	Transketolase (tkt)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y9I9		lmo0539	Tagatose-1,6-diphosphate aldolase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6Y9		lmo1542	50S ribosomal protein L21 (rplU)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5X5		lmo1928	Chorismate synthase (aroF)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q926Y9		lmo2758	Inosine-monophosphate dehydrogenase (guaB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8D0		lmo0978	Branched-chain amino acid aminotransferase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8N0		lmo0866	ATP-dependent RNA helicase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y446		lmo2615	30S ribosomal protein S5 (rpsE)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4R7		lmo2367	Glucose-6-phosphate isomerase (pgi)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q9AGE7		lmo2069	Class I heat-shock protein (chaperonin) GroES (groES)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAA3		lmo0251	50S ribosomal protein L12 (rplL)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAB6		lmo0232	Endopeptidase Clp ATP-binding chain C (clpC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66352		lmo2607	30S ribosomal protein S11 (rpsK)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4M3		lmo2414	Aminotransferase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6L1		lmo1673	Dihydroxynaphthoic acid synthetase (menB)

Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YA96		lmo0259	RNA polymerase (beta subunit) (rpoC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y846		lmo1072	Pyruvate carboxylase (pycA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P33380		lmo0210	L-lactate dehydrogenase (ldh)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7B0		lmo1376	6-phosphogluconate dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y722		lmo1504	Alanyl-tRNA synthetase (alaS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66699		lmo2606	RNA polymerase (alpha subunit) (rpoA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAA4		lmo0249	50S ribosomal protein L1 (rplA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66330		lmo2633	30S ribosomal protein S10 (rpsJ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5W7		lmo1938	ribosomal protein S1 like protein
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66372		lmo2656	30S ribosomal protein S12 (rpsL)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q9RQI6		lmo2468	ATP-dependent Clp protease proteolytic subunit (clpP)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66611		lmo2655	30S ribosomal protein S7 (rpsG)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q9RLT9		lmo0258	RNA polymerase (beta subunit) (rpoB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y709		lmo1519	Aspartyl-tRNA synthetase (aspS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66042		lmo0250	50S ribosomal protein L10 (rplJ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6C5		lmo1765	Bifunctional phosphoribosylaminoimidazole carboxy formyl formyltransferase and inosine-monophosphate cyclohydrolase (purH)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6V2		lmo1579	Alanine dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6D3		lmo1754	Glutamyl-tRNA(Gln) amidotransferase (subunit B) (gatB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7Y1		lmo1138	ATP-dependent Clp protease proteolytic component
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7F6		lmo1325	Translation initiation factor IF-2 (infB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66054		lmo0248	50S ribosomal protein L11 (rplK)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	O53083		lmo1787	50S ribosomal protein L19 (rplS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4I3		lmo2457	Triose phosphate isomerase (tpi)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7J7		lmo1280	GTP-sensing transcriptional pleiotropic repressor CodY
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7F1		lmo1331	Polynucleotide phosphorylase (PNPase) (pnpA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6D2		lmo1755	Glutamyl-tRNA(Gln) amidotransferase (subunit A) (gatA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8I9		lmo0913	Succinate semialdehyde dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q92AU6		lmo1711	Aminopeptidases
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q927L9		lmo2620	50S ribosomal protein L5 (rplE)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66548		lmo2626	30S ribosomal protein S3 (rpsC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6T6		lmo1596	30S ribosomal protein S4 (rpsD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66484		lmo2628	30S ribosomal protein S19 (rpsS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y822		lmo1096	GMP synthetase (guaA)

Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAB3		lmo0237	Glutamyl-tRNA synthetase (gltX)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y766		lmo1435	Dihydrodipicolinate synthase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y665		lmo1835	Carbamoyl-phosphate synthetase (catalytic subunit) (pyrAB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y971		lmo0662	Phosphomethylpyrimidine kinase thiD (thiD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y450		lmo2605	50S ribosomal protein L17 (rplQ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4G8		lmo2475	Phosphomannomutase and phosphoglucomutase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6R4		lmo1620	Xaa-His dipeptidase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7I0		lmo1299	Glutamine synthetases (glnA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6V0		lmo1581	Acetate kinase (ackA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y583		lmo2188	Oligoendopeptidase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7K9		lmo1268	ATP-dependent Clp protease ATP-binding subunit ClpX (clpX)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6B1		lmo1780	Aminotripeptidase (peptidase T)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6B8		lmo1773	Adenylosuccinate lyase (purB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5B2		lmo2155	Ribonucleoside-diphosphate reductase, subunit alpha
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6X9		lmo1552	Valyl-tRNA synthetase (valS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAB8		lmo0228	Lysyl-tRNA synthetase (lysS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P0A3L1		lmo1785	Translation initiation factor IF-3 (infC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y915		lmo0727	L-glutamine-D-fructose-6-phosphate amidotransferase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8A1		lmo1011	Tetrahydrodipicolinate succinylase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y789		lmo1403	DNA mismatch repair (recognition) (mutS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6N9		lmo1645	ATP-dependent dsDNA exonuclease SbcC
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66383		lmo2608	30S ribosomal protein S13 (rpsM)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAW1		lmo0002	DNA polymerase III, beta chain (dnaN)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66103		lmo1783	50S ribosomal protein L20 (rplT)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y493		lmo2561	Arginyl-tRNA synthetase (argS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y423		lmo2652	Transcriptional antiterminator
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7Q1		lmo1222	Phenylalanyl-tRNA synthetase beta subunit (pheT)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7I4		lmo1293	Glycerol 3-phosphate dehydrogenase (glpD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y447		lmo2613	50S ribosomal protein L15 (rplO)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5N8		lmo2019	Isoleucyl-tRNA synthetase (ileS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7B3		lmo1373	Branched-chain alpha-keto acid dehydrogenase E1 subunit (2-oxoisovalerate dehydrogenase beta subunit)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6T4		lmo1598	Tyrosyl-tRNA synthetase (tyrS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P58695		lmo1896	Asparaginyl-tRNA synthetases (ansB)

Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7F9		lmo1322	N utilization substance protein A (NusA protein) (nusA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6X2		lmo1559	Threonyl-tRNA synthetase (thrS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6Q0		lmo1634	Alcohol-acetaldehyde dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4H1		lmo2471	NADH oxidase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66461		lmo0046	30S ribosomal protein S18 (rpsR)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAR1		lmo0055	Adenylosuccinate synthetase (purA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y764		lmo1437	Aspartate-semialdehyde dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4I4		lmo2456	Phosphoglycerate mutase (pgm)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAR9		lmo0044	30S ribosomal protein S6 (rpsF)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7G7		lmo1314	Ribosome recycling factors (frr)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6Z2		lmo1538	Glycerol kinase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4F5		lmo2489	Excinuclease ABC (subunit B) (uvrB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y3W1		lmo2720	Acetate-CoA ligase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P60384		lmo2072	REX_LISMO Redox-sensing transcriptional repressor
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7G2		lmo1319	Prolyl-tRNA synthetase (proS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y689		lmo1808	Malonyl CoA-acyl carrier protein transacylase (fabD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6X8		lmo1553	Glutamate-1-semialdehyde 2,1-aminotransferases (hemL)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P66623		lmo2618	30S ribosomal protein S8 (rpsH)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P0DJM1		lmo1472	Heat shock protein DnaJ (dnaJ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y690		lmo1807	3-ketoacyl-acyl carrier protein reductase (fabG)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y730		lmo1493	Oligopeptidase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y838		lmo1080	Similar to <i>B. subtilis</i> minor teichoic acids biosynthesis protein GgaB
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4B2		lmo2539	Glycine hydroxymethyltransferase (glyA)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5E6		lmo2118	Phosphoglucomutase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q927L7		lmo2622	50S ribosomal protein L14 (rplN)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y664		lmo1836	Carbamoyl-phosphate synthetase (glutaminase subunit) (pyrAa)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8A5		lmo1005	3-hydroxyisobutyrate dehydrogenase (<i>B. subtilis</i> YkwC protein)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAB1		lmo0239	Cysteinyl-tRNA synthetase (cysS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q927L2		lmo2627	50S ribosomal protein L22 (rplV)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7C7		lmo1357	Acetyl-CoA carboxylase subunit (biotin carboxylase subunit)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6W5		lmo1566	Isocitrate dehydrogenases (citC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6J6		lmo1688	Glucose 1-dehydrogenase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y606		lmo1897	Aspartate aminotransferases (aspB)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	P61055		lmo2631	50S ribosomal protein L4 (rplD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y708		lmo1520	Histidyl-tRNA synthetase (hisS)

Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y825		lmo1093	NH(3)-dependent NAD(+) synthetases, nitrogen regulatory protein
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5L9		lmo2038	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (murE)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8YAR2		lmo0053	50S ribosomal protein L9 (rplI)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q48793		lmo0199	Phosphoribosyl pyrophosphate synthetase (prs)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q9ZEY0		lmo0265	Succinyldiaminopimelate desuccinylase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y964		lmo0669	Oxidoreductase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y8R6		lmo0829	Pyruvate-flavodoxin oxidoreductase (nifJ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y837		lmo1081	Glucose-1-phosphate thymidyl transferase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y7Q2		lmo1221	Phenylalanyl-tRNA synthetase alpha subunit (pheS)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6T0		lmo1603	Aminopeptidase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y6C1		lmo1769	Phosphoribosylformylglycinamide synthetase I (purQ)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5V7		lmo1948	Two-component response regulator (ResD) (resD)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5S0		lmo1986	Ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) (ilvC)
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y5Q1		lmo2005	Oxidoreductase
Portillo, 2011	<i>L. monocytogenes</i>	Positive	Q8Y4U2		lmo2340	Similar to <i>Erwinia chrysanthemi</i> IndA protein
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8YAD0		Lmo0214	mfd, transcription-repair coupling factor
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8YAC3		Lmo0223	cysK, cysteine synthase
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y862		Lmo1055	pdhD, dihydrolipoamide dehydrogenase, E3 subunit of pyruvate dehydrogenase complex
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y7G7		Lmo1314	frr, ribosome recycling factors
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	P0DJM2		Lmo1473	dnaK, class I heat-shock protein (molecular chaperone) DnaK
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y6Q0		Lmo1634	Alcohol-acetaldehyde dehydrogenase
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y6M7		Lmo1657	tsf, translation elongation factor
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q9AGE6		Lmo2068	groEL, class I heat-shock protein (chaperonin) GroEL
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y4L2		Lmo2425	Glycine cleavage system protein H
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	P64074		Lmo2455	eno, enolase
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y4I4		Lmo2456	pgm, phosphoglycerate mutase
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y4I2		Lmo2458	pgk, phosphoglycerate kinase

2004						
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y4I1		Lmo2459	Glyceraldehyde-3-phosphate dehydrogenase
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y498		Lmo2556	fbaA, fructose-1,6-bisphosphate aldolase type II
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y422		Lmo2653	tufA, translation elongation factor EF-Tu
Schaumburg, 2004	<i>L. monocytogenes</i>	Positive	Q8Y421		Lmo2654	fus, translation elongation factor G
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753118	SSU0320	GTP-sensing transcriptional pleiotropic repressor
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752830	SSU0008	Transcription-repair coupling factor
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752842	SSU0021	Ribose-phosphate pyrophosphokinase 1
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752848	SSU0027	Phosphoribosylformylglycinamide synthase protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752858	SSU0037	Adenylosuccinate lyase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752880	SSU0062	RecA recombinase (recombinase A)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752886	SSU0069	30S ribosomal protein S10
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752887	SSU0070	50S ribosomal protein L3
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752888	SSU0071	50S ribosomal protein L4
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752889	SSU0072	50S ribosomal protein L23
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752890	SSU0073	50S ribosomal protein L2
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752892	SSU0075	50S ribosomal protein L22
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752893	SSU0076	30S ribosomal protein S3
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752894	SSU0077	50S ribosomal protein L16
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752895	SSU0078	50S ribosomal protein L29
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752897	SSU0080	50S ribosomal protein L14
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752898	SSU0081	50S ribosomal protein L24
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752899	SSU0082	50S ribosomal protein L5
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752902	SSU0085	30S ribosomal protein S8
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752904	SSU0088	50S ribosomal protein L6
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752905	SSU0089	50S ribosomal protein L18
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752906	SSU0090	30S ribosomal protein S5
Gómez-	<i>S. suis</i>	Positive		gi 253752907	SSU0091	50S ribosomal protein L30

Gascón, 2012						
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752908	SSU0092	50S ribosomal protein L15
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752910	SSU0094	Adenylate kinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752913	SSU0097	30S ribosomal protein S13
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752914	SSU0098	30S ribosomal protein S11
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752915	SSU0099	DNA-directed RNA polymerase alpha chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752916	SSU0100	50S ribosomal protein L17
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752935	SSU0120	Tyrosyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752937	SSU0122	DNA-directed RNA polymerase beta chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752938	SSU0123	160 kD subunit/DNA-directed RNA polymerase beta' chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752955	SSU0142	tRNA-binding protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752959	SSU0146	10 kDa chaperonin
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752960	SSU0147	60 kDa chaperonin
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752961	SSU0148	30S ribosomal protein S12
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752962	SSU0149	30S ribosomal protein S7
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752963	SSU0151	Elongation factor G (EF-G)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752965	SSU0153	Glyceraldehyde-3-phosphate dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752966	SSU0154	Phosphoglycerate kinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752969	SSU0157	Glutamine synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253752999	SSU0191	Formate acetyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753027	SSU0223	Thioredoxin
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753038	SSU0234	NADP-specific glutamate dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753062	SSU0261	Aldehyde-alcohol dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753063	SSU0262	Threonine synthase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753080	SSU0279	GrpE protein (HSP-70 cofactor)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753081	SSU0280	Chaperone protein DnaK (heat shock protein 70)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753082	SSU0281	Chaperone protein DnaJ
Gómez-	<i>S. suis</i>	Positive		gi 253753084	SSU0283	Amidase

Gascón, 2012						
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753106	SSU0306	Trigger factor (prolyl isomerase)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753110	SSU0310	DNA-directed RNA polymerase, delta subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753112	SSU0312	Fructose-bisphosphate aldolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753117	SSU0319	Aminotransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753122	SSU0325	Glutamyl-tRNA amidotransferase subunit A
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753123	SSU0326	Glutamyl-tRNA amidotransferase subunit B
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753146	SSU0352	ATP-dependent protease ATP-binding subunit ClpL
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753147	SSU0353	4-alpha-glucanotransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753148	SSU0354	Glycogen phosphorylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753172	SSU0379	DNA-directed RNA polymerase omega chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753176	SSU0383	Protein phosphatase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753183	SSU0391	Cysteine synthase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753187	SSU0395	Sigma 54 modulation protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753204	SSU0412	Valyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753207	SSU0416	DEAD/DEAH box family helicase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753211	SSU0420	Aspartate--ammonia ligase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753229	SSU0441	isoleucyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753232	SSU0244	ATP-dependent Clp protease ATP-binding subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753236	SSU0448	Bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753244	SSU0458	Peptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753256	SSU0470	Lysyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753268	SSU0482	Elongation factor Tu (EF-Tu)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753269	SSU0483	Triosephosphate isomerase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753270	SSU0484	Haloacid dehalogenase-like hydrolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753280	SSU0494	6-phosphofructokinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753281	SSU0495	Pyruvate kinase

Gascón, 2012						
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753286	SSU0500	Glucosamine--fructose-6-phosphate aminotransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753294	SSU0510	Pyrroline-5-carboxylate reductase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753335	SSU0570	Asparaginyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753346	SSU0582	Ornithine carbamoyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753352	ssu0589	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753353	SSU0591	Glucosamine-6-phosphate isomerase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753360	SSU0598	D-alanyl carrier protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753382	SSU0621	Phosphoserine aminotransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753395	SSU0642	Type III restriction-modification system, restriction enzyme
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753396	SSU0644	Phosphomannomutase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753400	SSU0648	Formate--tetrahydrofolate ligase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753420	SSU0671	Aspartate-semialdehyde dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753421	SSU0672	Dihydrodipicolinate synthase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753428	SSU0680	Oligopeptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753430	SSU0682	NADH oxidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753457	SSU0710	Topoisomerase IV subunit B
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753465	SSU0721	30S ribosomal protein S1
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753470	SSU0726	Thiamine biosynthesis protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753472	SSU0728	50S ribosomal protein L21
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753473	SSU0732	50S ribosomal protein L27
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753479	SSU0735	PyrR bifunctional protein [includes: pyrimidine operon regulatory protein; uracil phosphoribosyltransferase]
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753480	SSU0736	Aspartate carbamoyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753482	SSU0738	Carbamoyl-phosphate synthase large chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753486	SSU0742	30S ribosomal protein S16
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753491	SSU0747	Homoserine dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753502	SSU0760	GMP reductase

Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753511	SSU0771	Dihydrodipicolinate reductase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753515	SSU0775	Sugar kinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753525	SSU0785	GTP-binding protein LepA
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753530	SSU0790	Peptide chain release factor 1
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753556	SSU0816	GMP synthase [glutamine-hydrolyzing]
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753563	SSU0826	Phosphoglucomutase/phosphomannomutase family protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753582	SSU0845	50S ribosomal protein L7/L12
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753583	SSU0846	50S ribosomal protein L10
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753598	SSU0861	Dihydroorotase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753601	SSU0864	Orotate phosphoribosyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753648	SSU0918	Ribose-phosphate pyrophosphokinase 2
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753656	SSU0926	DNA gyrase subunit A
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753657	SSU0927	L-lactate dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753663	SSU0936	Deoxyribose-phosphate aldolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753664	SSU0937	Thymidine phosphorylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753667	SSU0940	30S ribosomal protein S20
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753693	SSU0972	Haloacid dehalogenase-like hydrolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753694	SSU0973	Peptidase T
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753716	SSU0995	Phenylalanyl-tRNA synthetase beta chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753759	SSU1038	Phosphoenolpyruvate-protein phosphotransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753760	SSU1039	Histidine-containing phosphocarrier protein (HPr)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753765	SSU1044	Ribonucleoside-diphosphate reductase alpha chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753767	SSU1046	Ribonucleoside-diphosphate reductase beta chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753793	SSU1076	Alanyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753799	SSU1082	Oligopeptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753801	SSU1084	Methionyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753812	SSU1095	Tagatose 1,6-diphosphate aldolase 2

Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753821	SSU1104	50S ribosomal protein L20
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753823	SSU1106	Translation initiation factor IF-3
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753824	SSU1107	Cytidylate kinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753846	SSU1130	dTDP-glucose-4,6-dehydratase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753849	SSU1133	Glucose-1-phosphate thymidyl transferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753855	SSU1139	Adenine phosphoribosyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753873	SSU1159	Ribosome recycling factor
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753878	SSU1164	50S ribosomal protein L1
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753879	SSU1165	50S ribosomal protein L11
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753910	SSU1196	Threonyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753916	SSU1202	Catabolite control protein A
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753963	SSU1255	RNA polymerase sigma factor RpoD
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753974	SSU1266	Purine nucleoside phosphorylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753977	SSU1269	Phosphopentomutase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753990	SSU1283	Xaa-His dipeptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253753997	SSU1290	Phosphoglucosamine mutase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754027	SSU1320	Enolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754034	SSU1327	DNA gyrase subunit B
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754055	SSU1348	50S ribosomal protein L31
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754073	SSU1366	ATP-dependent Clp protease proteolytic subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754074	SSU1367	Uracil phosphoribosyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754102	SSU1396	ADP-ribose pyrophosphatase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754137	SSU1433	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754139	SSU1435	S-adenosylmethionine synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754145	SSU1441	DNA polymerase III subunit gamma/tau
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754153	SSU1451	Phosphoglyceromutase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754160	SSU1458	DNA-binding protein HU

Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754169	SSU1467	Exodeoxyribonuclease VII large subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754176	SSU1478	Manganese-dependent inorganic pyrophosphatase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754177	SSU1479	Oligopeptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754184	SSU1486	NH(3)-dependent NAD(+) synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754211	SSU1513	Tyrosine recombinase XerD
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754217	SSU1519	Pyridoxal-dependent decarboxylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754218	SSU1520	Aminopeptidase C
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754224	SSU1526	Transcription elongation factor
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754232	SSU1534	GTP-binding protein EngA
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754238	SSU1541	6-phosphogluconate dehydrogenase, decarboxylating
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754267	SSU1570	Glycyl-tRNA synthetase beta chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754284	SSU1587	Seryl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754293	SSU1598	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754294	SSU1599	Biotin carboxylase subunit of acetyl-CoA carboxylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754296	SSU1601	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754297	SSU1602	3-oxoacyl-[acyl-carrier-protein] synthase II
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754298	SSU1603	3-oxoacyl-[acyl-carrier protein] reductase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754300	SSU1605	Enoyl-ACP reductase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754301	SSU1606	Acyl carrier protein (ACP)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754306	SSU1611	Aspartate kinase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754318	SSU1623	Elongation factor P (EF-P)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754319	SSU1624	Metallopeptidase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754320	SSU1625	UvrABC system protein A (UvrA protein)
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754324	SSU1629	Single strand binding protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754325	ssu1630	30S ribosomal protein S6
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754329	SSU1634	Dihydrolipoamide dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754330	SSU1635	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex

Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754331	SSU1636	Pyruvate dehydrogenase E1 component, beta subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754332	SSU1637	Pyruvate dehydrogenase E1 component, alpha subunit
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754337	SSU1642	Translation initiation factor IF-2
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754340	SSU1645	N utilization substance protein A
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754371	SSU1679	Threonine dehydratase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754372	SSU1680	Ketol-acid reductoisomerase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754378	SSU1686	Dihydroxy-acid dehydratase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754381	SSU1691	30S ribosomal protein S9
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754382	SSU1692	50S ribosomal protein L13
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754410	SSU1721	Polyribonucleotide nucleotidyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754415	SSU1728	30S ribosomal protein S15
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754429	SSU1743	Aminopeptidase PepS
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754432	SSU1746	DNA polymerase III PolC-type
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754439	SSU1753	Prolyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754444	SSU1758	Adenylosuccinate synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754452	SSU1766	Stress response-related Clp ATPase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754456	SSU1770	Elongation factor Ts
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754457	SSU1771	30S ribosomal protein S2
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754490	SSU1804	ssDNA-binding protein
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754501	SSU1815	Glutamyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754513	SSU1827	Glycerol-3-phosphate dehydrogenase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754518	SSU1832	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754522	SSU1836	Glucose-6-phosphate isomerase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754525	SSU1839	Transketolase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754549	SSU1863	Leucyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754550	SSU1864	Endopeptidase O
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754581	SSU1903	Anaerobic ribonucleoside-triphosphate reductase

Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754588	SSU1910	Arginyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754601	SSU1923	Aspartyl-tRNA synthetase
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754613	SSU1935	30S ribosomal protein S4
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754626	SSU1948	L-serine dehydratase, beta chain
Gómez-Gascón, 2012	<i>S. suis</i>	Positive		gi 253754638	SSU1960	Inosine-5'-monophosphate dehydrogenase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 1368	Catalase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 1385	Aconitrate hydratase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 1448	2-oxoglutarate dehydrogenase, E2
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 1449	2-oxoglutarate dehydrogenase, E1
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 1838	Phosphoenolpyruvate carboxykinase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 2048	3-isopropylmalate dehydratase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 2049	3-isopropylmalate dehydratase
Hempel, 2011	<i>S. aureus</i>	Positive			SACOL 2154	Arginase
Doro, 2009	<i>S. agalactiae</i>	Positive			SAN_1636	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
Doro, 2009	<i>S. agalactiae</i>	Positive			SAN_0083	ribosomal protein L2 (rplB)
Doro, 2009	<i>S. agalactiae</i>	Positive			SAN_0854	Translation elongation factor Tu (tuf)
Doro, 2009	<i>S. agalactiae</i>	Positive			SAN_1390	ribosomal protein L10

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