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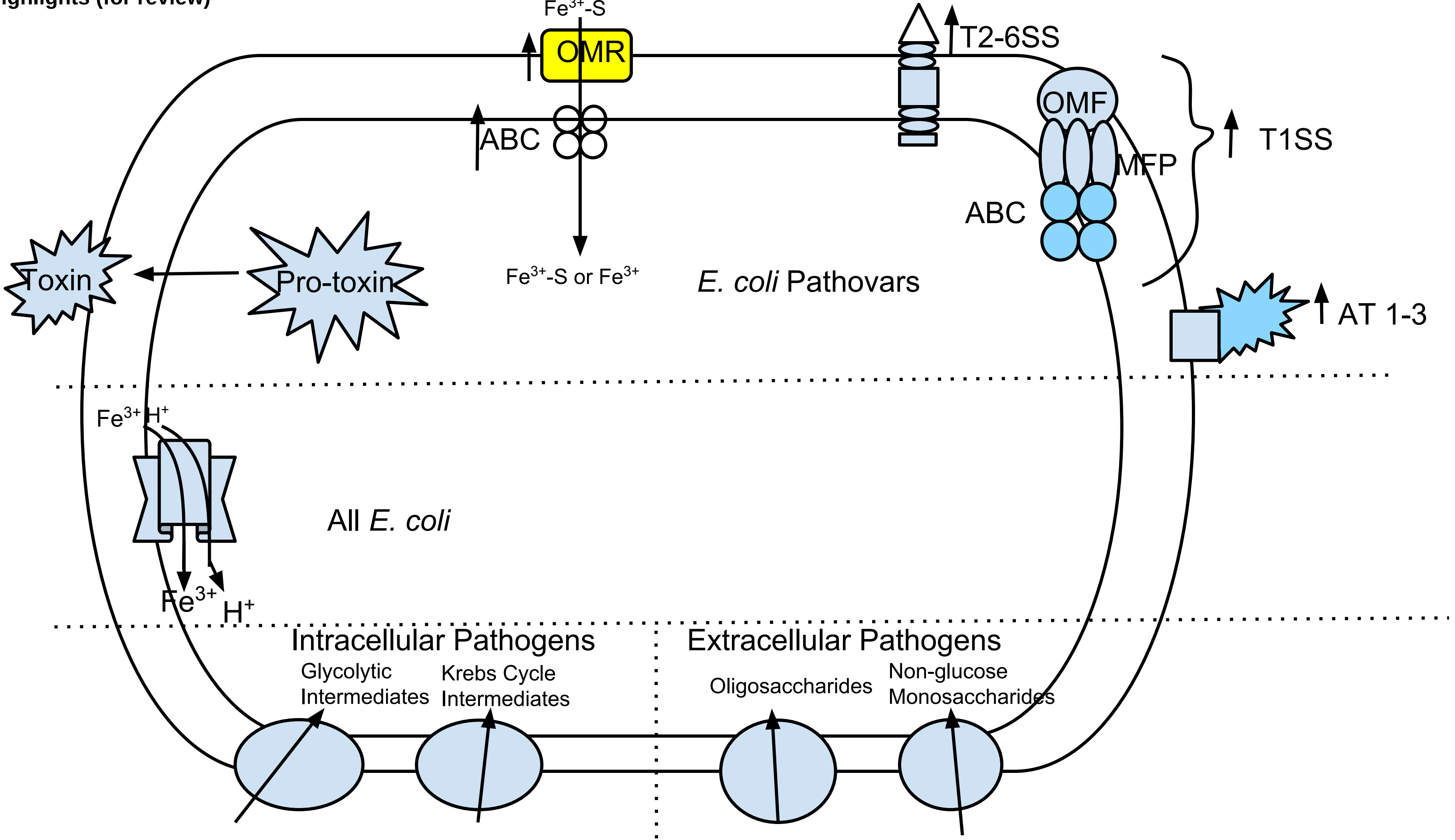
Abstract: Escherichia coli is a genetically diverse species infecting hundreds of millions of people worldwide annually. We examined seven well-characterized E. coli pathogens causing urinary tract infections, gastroenteritis, pyelonephritis and haemorrhagic colitis. Their transport proteins were identified and compared with each other and a non-pathogenic E. coli K12 strain to identify transport proteins related to pathogenesis. Each pathogen possesses a unique set of protein secretion systems for export to the cell surface or for injecting effector proteins into host cells. Pathogens have increased numbers of iron siderophore receptors and ABC iron uptake transporters, but the numbers and types of low-affinity secondary iron carriers were uniform in all strains. The presence of outer membrane iron complex receptors and high-affinity ABC iron uptake systems correlated, suggesting co-evolution. Each pathovar encodes a different set of pore-forming toxins and virulence-related outer membrane proteins lacking in K12. Intracellular pathogens proved to have a characteristically distinctive set of nutrient uptake porters, different from those of extracellular pathogens. The results presented in this report provide information about transport systems relevant to various types of E. coli pathogenesis that can be exploited in future basic and applied studies.

***Highlights (for review)**



- Each *E. coli* pathogen have an unique set of pore-forming toxins.
- Each pathogen has an unique set of transenvelope and outer membrane protein secretion systems.
- Pathogens have increased numbers of iron siderophore receptors and high affinity ABC uptake porters, and the two increase in parallel to promote pathogenesis.
- Low affinity iron uptake systems are present in invariant numbers and serve housekeeping functions unrelated to pathogenesis.
- Distinct nutrient uptake systems are present in intra- vs. extracellular pathovars, and these may serve as diagnostic tools in medicine.

Transport Proteins Promoting *E. coli* Pathogenesis

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ABSTRACT

***Escherichia coli* is a genetically diverse species infecting hundreds of millions of people worldwide annually. We examined seven well-characterized *E. coli* pathogens causing urinary tract infections, gastroenteritis, pyelonephritis and haemorrhagic colitis. Their transport proteins were identified and compared with each other and a non-pathogenic *E. coli* K12 strain to identify transport proteins related to pathogenesis. Each pathogen possesses a unique set of protein secretion systems for export to the cell surface or for injecting effector proteins into host cells. Pathogens have increased numbers of iron siderophore receptors and ABC iron uptake transporters, but the numbers and types of low-affinity secondary iron carriers were uniform in all strains. The presence of outer membrane iron complex receptors and high-affinity ABC iron uptake systems correlated, suggesting co-evolution. Each pathovar encodes a different set of pore-forming toxins and virulence-related outer membrane proteins lacking in K12. Intracellular pathogens proved to have a characteristically distinctive set of nutrient uptake porters, different from those of extracellular pathogens. The results presented in this report provide information about transport systems relevant to various types of *E. coli* pathogenesis that can be exploited in future basic and applied studies.**

1. Introduction

E. coli is a major source of infant mortality, adult diarrhoea and urinary tract infections worldwide [1] [2]. Uropathogenic strains are responsible for up to 80% of urinary tract infections (UTIs) and a majority of pyelonephritis cases [3]. Enteroaggregative and enterotoxic pathovars have been the leading causes of travellers' diarrhoea, which has significantly contributed to infant mortality [4]. Enterohaemorrhagic serotypes are currently the leading cause of haemorrhagic colitis which can lead to fatalities [5].

Some probiotic strains of *E. coli* including the *E. coli* Nissle and O83 strains contribute beneficially to human physiology [7, 8]. Current research on probiotic *E. coli* in humans has proven to be clinically useful in the treatment of colitis and inflammatory bowel disease (IBD) syndromes and in combating pathogenic *E. coli* strains [9,10]. *E. coli* can have tremendously varied effects on humans and other animals, a consequence of its genetic diversity.

Prominent types of *E. coli* pathogens have been identified based on varying mechanisms of infection. There are five types of diarrhoeagenic strains that pertain specifically to the alimentary system: enteropathogenic (EPEC), enterohaemorrhagic (EHEC), enterotoxic (ETEC), enteroinvasive (EIEC), and enteroaggregative (EAEC). Diffusely adherent (DAEC) strains can infect both the urinary tract and the gastrointestinal tract due in part to their diverse mechanisms of host adhesion [6]. In our study, seven representative *E. coli* pathogens as well as *E. coli* K12 were examined. We use the first three letters/numbers of these strain designations as abbreviations to refer to these strains. Table 1 presents these abbreviations as well as basic information about the eight strains of *E. coli* examined.

The general paradigm of the pathogenic mechanism associated with *E. coli* virulence involves (1) adhesion, (2) protein injection into host cells, (3) subversion of signaling mechanisms and (4) colonization leading to impaired immune responses, membrane potential disruption and cytoskeletal manipulation [11]. During the injection stage, *E. coli* typically secretes effectors into host cells using one or more protein secretion systems, either to escape the immune response or to alter signaling pathways. Host membrane potential disruption and apoptosis induction are employed by several pathovars.

Virulence genes are often clustered in "pathogenicity islands" that reflect horizontal transfer [13]. Horizontal gene transfer has allowed *E. coli* to survive under a variety of *in vivo* conditions, increasing the virulence of existing pathogens and creating new ones [14]; [15]. Because the pan genome of *E. coli* far exceeds the core genome, perhaps by as much as 20-fold [16], this increase in genetic plasticity allows for fluctuations in gene content, further contributing to divergence of *E. coli* pathogenic mechanisms [17].

2. Methods

2.1. G-BLAST search of E. coli proteomes

The proteomes of eight *E. coli* strains were screened for homologues of all proteins contained in the Transporter Classification Database (TCDB; www.tcdb.org) as of September, 2012 using a program designed for this purpose, G-BLAST [18]. The program retrieves information for both the genome query and the TC top hit sequences, TC#, protein size in number of amino acyl residues, number of predicted TMSs using the HMMTop 2.0 Program, e-value for the query and hit proteins, regions of sequence similarity and regions of TMS overlap. FASTA-formatted protein sequences from the completed genome were used. Each putative open-reading frame was used as a query in the BLASTP software to search for homologous proteins in TCDB. The low complexity filter was not used as it is normally of value only for larger datasets including proteins with multiple repeat elements. In addition, each open reading frame [19] was scanned with the HMMTOP 2.0 program [20] to predict the number of putative transmembrane segments (TMSs). The Web-based Hydropathy, Amphipathicity and Topology (WHAT) program [21] was used with a window size of 19 residues and an angle of 100 degrees to display the hydropathy plot for individual proteins in order to resolve the differences in the numbers of TMSs between the proteins retrieved and their TCDB homologues. The plot generated by WHAT allows the user to judge if a program such as HMMTOP has missed a TMS or has predicted a TMS inappropriately. A cut-off value of 0.0001 was used with the G-BLAST program so proteins retrieved with larger values (greater sequence divergence) were not recorded. Proteins with no predicted TMSs were eliminated so that only integral membrane proteins, primarily multispanning membrane proteins, were retrieved. Proteins with only an N-terminal signal sequence are numerous because these proteins include almost all periplasmic, outer membrane and secreted proteins that are exported via the general secretory pathway (Sec) or twin arginine translocase (TAT). The topological prediction programs often miss these TMSs, recording them to have zero TMSs. Consequently, the numbers retrieved were not reliable and were therefore not always recorded. For example, single TMS proteins such as extracytoplasmic solute binding receptors of ABC transport systems were often predicted to lack a TMS, and therefore these proteins were not included in our study of the integral membrane transport proteins.

2.2. Identification of distant transport protein homologs

Proteins retrieved between the values of 0.0001 and 0.1 were examined manually to determine the likelihood that these proteins were members of recognized transport protein families, or if they might comprise representatives of novel families of putative transport proteins. A total of 82 non-orthologous homologous proteins were retrieved using the 0.0001 to

0.1 cutoff, but only 10 proved to be recognizable transport proteins. These were incorporated into TCDB. The 10 proteins were manually examined by conducting searches as follows. (1) TC-BLAST searches provided preliminary evidence for family assignment. (2) NCBI BLAST searches provided confirmation or refutation of family assignment based on the conserved domain database (CDD) and hits obtained with values to the query sequence of less than 1×10^{-7}. (3) Topological analyses revealed similarities and differences between the query sequence and members of the assigned family. (4) Proteins proving to represent new potential families were included in TC subclass 9.B.

Candidate proteins were subsequently examined in greater detail to estimate their substrate specificities. On the basis of the numbers and locations of TMSs as well as degrees of sequence similarity with entries of known function in TCDB, transport proteins were classified into families and subfamilies of homologous transporters according to the classification system presented in TCDB. Regions of sequence similarity were examined using the WHAT program which shows hydropathy plots to ensure that homology was in a transmembrane region of 3 or more TMSs and not only in hydrophilic domains. Proteins encoded within single multi-cistronic operons were often identified in order to gain evidence for multicomponent systems and to help deduce functions. Operon analyses (genome context, a.k.a., synteny analyses) were performed for candidate proteins with assigned or unassigned transport functions as described in Castillo and Saier (2010) and Reddy et al. (2012) [22] and [23].

2.3. Overview of programs used

Transport proteins thus obtained were systematically analyzed for unusual properties using published [18] and unpublished in-house software. Among the programs described by Reddy and Saier [18], used in this report, were the GSAT, Protocol1, Protocol2, TSSearch,

SSearch and GBlast programs. Unpublished software was used to tabulate information according to TC# or other criteria such as substrate type. Unusual characteristics of the query *E. coli* sequences were identified based in part on topologies that differed from corresponding family members in TCDB as well as e-values obtained with G-BLAST. Unusual properties can result from events such as genetic deletion and fusion, sometimes resulting in the gain or loss of extra domains or the generation of multifunctional proteins. Such results can be reflective of the actual protein sequence, but they can also be artifactual, due to sequencing errors or incorrect initiation codon assignment. In the latter cases, but not the former, the protein sequences were either corrected when possible or eliminated from our study.

Orthologous relationships among homologues were estimated by measuring the percent identities. We initially used an arbitrary cutoff of 95% identity, a value appropriate in view of the similarities of the strains considered. Homologues with lower percent identities were examined manually, revealing occasional sets of orthologs that exhibited less than 95% identity (See Table S1 for orthologous assignments).

3. Results

3.1 Overview of Transporter Types

According to the transporter classification system, there are five defined classes of transport systems (classes 1-5) as well as a class of transporter auxiliary proteins (class 8) and a class of incompletely defined transporters (class 9). These will be considered in sequence.

3.1.1 Pore-forming Proteins

Eight *E. coli* genomes were analyzed for the occurrence of transport proteins using the Transporter Classification Database (TCDB; www.tcdb.org, [24]) and the G-Blast program [18].

The results are summarized according to TC subclass in Table 2 and Table S1. Examining the total number of transport proteins present in these 8 genomes, we see that *E. coli* K12 has the fewest at 1128. The most found in any genome is 1287, 159 more than in K12. However, the seven pathogenic species combined contained 838 unique transport proteins lacking in K12.

TC subclass 1.A in TCDB includes α-type channels. The eight strains have 37-42 such channel proteins. Surprisingly, however, the pathogenic organisms possess 24 non-orthologous channel proteins lacking in K12 (Table 2). It appears unlikely that α-type channels are major contributors to *E. coli* pathogenesis.

TC subclass 1.B includes outer membrane β-type porins. In this subclass, we find striking differences between the organisms, where K12 has far fewer than any of the other strains. The largest number of these porins is 108 observed in ABU, and the seven pathogens possess 151 porin proteins non-orthologous to those in K12 (Table 2). This observation suggests that porins contribute to pathogenesis as confirmed and explained below.

TC subclass 1.C includes pore-forming toxins. K12 has only nine such proteins, and E24 has just two more, but all the others have between 15-20 such toxins, and 51 toxins, non-orthologous to those in K12, were identified (Table 2). As expected, an array of toxins characterizes each of the pathogens. It should be noted that toxins that do not form transmembrane pores were not included in our study.

Small α-type channel-forming holins (TC subclass 1.E.) function in release of auto-lysins which allow phage particle release when phage-encoded, or self-destruction by a suicide-type process when chromosomally encoded [18]. The *E. coli* strains have 3-7 holins each. However, 19 of these proteins are non-orthologous to those found in K12 (Table 2). It is possible therefore that chromosomally encoded holins play important roles in pathogenicity, possibly in programmed cell death as an aid to biofilm formation and communal life ([25]; [26]; [27]).

3.1.2 Secondary Carriers

The largest number of transport systems, but not the largest number of transport proteins, includes secondary carriers belonging to TC subclass 2.A. The eight strains have anywhere from 309 to 325 such systems. K12 has 311, and 96 proteins non-orthologous to those in K12 were identified, many of which are likely to contribute to specific types of pathogenicity.

3.1.3 Primary Active Transporters

TC subclass 3.A are pyrophosphate-hydrolysis driven primary active transporters, usually multi-component systems. K12 has the fewest such systems (340), while UMN has the most (390), and 155 proteins found in pathogens appear to have no orthologs in K12. Many of these systems play essential roles in virulence.The strains examined have 3-5 decarboxylation driven sodium pumps, which probably play a housekeeping function in the maintenance of ionic homeostasis. Subclass 3.D, ion (H^+ or Na^+)-pumping electron carriers, also exhibit little variation with only seven proving to be non-orthologous to those of K12.

3.1.4 Group Translocators

TC class 4 includes group translocators that modify their substrates during transport. Subclass 4.A includes the proteins of the multi-component sugar transporting phosphotransferase system (PTS) [28]. While K12 has the fewest such systems (49), both CFT and ABU have 13 more (62). In fact, 43 PTS proteins proved to be non-orthologous to those found in K12. These systems, likely to be important virulence factors, will be analyzed below.

. Each of the eight different strains has between 7-12 TC subclass 4D group translocating glycosyl transferases (4.D; [30]; [31]). Interestingly, the pathogens possess eight sets of orthologs not found in K12, suggesting that unique glycosyl transferases may serve different functions in the different pathogens. Some of them could function in the production of capsules, known to be virulence factors in many pathogenic bacteria [32].

3.1.5 Transmembrane Electron Carriers

Electron-carriers (TC Class 5) that transfer electrons from one side of the membrane to the other, thereby influencing cellular energetics [33], do not vary in numbers appreciably between the eight strains.

3.1.7 Poorly Characterized Transporters

Tremendous variation is observed between the numbers of poorly characterized transporters found in subclass 9.A. K12 has the fewest, with only 42 such proteins while 559 has over twice this number with 87. Most of the pathogens have between 60-70 such proteins, and 94 of these proteins are lacking in K12. This shows that the pathogens possess large variable numbers of poorly characterized transporters that are likely to serve highly specific functions within the cell. It is probable that they remain poorly characterized because they are not found in *E. coli* K12 and other commonly studied model bacteria. Elucidation of their functions and mechanisms of action is likely to prove particularly interesting and important for specific aspects of *E. coli* pathogenesis. In contrast to the situation observed for subclass 9.A, the strains examined have relatively little variation in the numbers of subclass 9B members. The smallest number is found in O15 (81), and the largest number is found in CFT (91) with K12 having 90. Nevertheless, the pathogens collectively have 26 such proteins lacking in K12.

3.2 Pathogenicity-related Transport Protein Analyses

Transport proteins likely to be important in pathogenicity include (1) toxins, (2) trans-envelope protein secretion systems, (3) outer membrane protein secretion systems, and (4) outer membrane iron-siderophore receptors that function with cytoplasmic membrane ABC-type iron uptake porters. The transport proteins that fall into these four classes are summarized in Tables 3 through 6, respectively.

3.2.1 Toxins identified in E. coli strains

Table 3 summarizes the toxins identified in the eight *E. coli* strains included in this study. In addition to the pore-forming subunits that function in conjunction with type III secretion systems (IIITCP), seven families of toxins are represented. These will be discussed sequentially according to their TC numbers.

HlyE is a well-characterized toxin found in *E. coli*, *Salmonella* and *Shigella* species. Its high resolution X-ray structure is available, and models of its membrane-inserted homooligomeric pore complex have been proposed [34, 35]. Five of the eight *E. coli* strains examined possess this toxin.

Another haemolysin is the *E. coli* Haemolysin A (HlyA), part of the RTX superfamily of pore-forming proteins [36]. The general mechanism proposed for HlyA is as follows: the toxin (1) recognizes and binds to β 2-integrin receptors on host cell membranes, (2) inserts into the host membrane forming nonselective pores, and (3) transports a toxin that inhibits host protein kinase B, leading to apoptosis of the host cell [37]. This toxin was found only in two intracellular strains, both of which have HlyE as well.

Type 3 Secretion System (T3SS) pore-forming proteins (IIITCP) are typically involved in attaching/effacing mechanisms in enteropathogenic strains [16]. The EspB/D complex and other homologous pore-forming protein pairs are secreted into the host cell and oligomerize to form translocation pores at the site of contact. EspB with EspD, for example, provide translocation functions for *E. coli* effector proteins and inhibit host phagocytosis by altering host cell cytoskeletal functions [38]. IIITCP family proteins were found in two pathovars.

The prophage-encoded shiga toxin (Stx) is a heteromeric protein with a glycolipid-recognizing, pore-forming, pentameric B subunit and a single A chain with N-glycosidase activity that results in cleavage of a single adenine in the 28S rRNA, resulting in blockage of protein synthesis [40]. Two StxB pore-forming toxins appear to be encoded in the O15 genome, although no such toxin was identified in the other strains.

Clostridial cytotoxins (CCT) are tripartite proteins with N-terminal catalytic domains, C-terminal receptor regions and central channel-forming domains [41]. Upon endocytosis into the host cell, the channel-forming domain is activated by acidic pH which induces conformational changes promoting insertion into the endosomal membrane, concomitant with channel formation. The catalytic domain of CCT is translocated across the membrane, resulting in inactivation of Rho family GTPases and reorganization of the host actin cytoskeleton [42]. Two homologs of the clostridial cytotoxin were identified (see Table 3).

Serratia pore-forming toxins (S-PFT) (1.C.75) are exported through a two partner secretion system (TPS; TC # 1.B.20) [43]. Three organisms possess this type of pore-forming haemolysin, ABU, CFT and O15. The former two have huge toxins of 3216 amino acids that are nearly identical. By contrast, the O15 homolog is 1270 amino acids in length and corresponds in sequence to the N-terminal portion of the larger toxins.

Toxins of the Cytolethal Distending Toxin (CDT) family are tripartite protein complexes, CdtABC, that induce DNA cleavage, cell cycle arrest, and apoptosis in host epithelial and immune cells [45]. The catalytic subunit of the complex possesses phosphodiesterase activity that cleaves the host DNA, causing G2/M cell cycle arrest [46]. CdtA and C are dimeric subunits that deliver CdtB to the host cell cytoplasm [47]. The complete CdtA/B/C trimeric toxin system (1.C.98.1.1) was found in only one of the eight *E. coli* strains, APE.

3.2.2 Trans-envelope Protein Secretion Systems in Pathogenicity

Table 4 summarizes the various protein secretion systems present in the *E. coli* strains examined. These include (1) type I secretion systems (T1SS; ABC; TC#3.A.1), (2) type II secretion systems (T2SS; SEC-SRP complexes; TC#3.A.5) for secretion across the inner membrane, acting together with the Main Terminal Branch (MTB; TC# 3.A.15) for secretion across the outer membrane, (3) type III secretion systems (T3SS; Fla; Path; TC #3.A.6), (4) type IV secretion systems (T4SS; Conj; Vir; TC# 3.A.7), and (5) type VI secretion systems (T6SS; TC# 3.A.23) [48].

Type I secretion systems (T1SSs) identified are members of the ABC Protein Exporter-1 (TC#3.A.1.109) and Protein Exporter-2 (TC#3.A.1.110) families within the ABC functional superfamily [49]. ABC exporters consist of two transmembrane domains and two cytosolic ATP-hydrolyzing domains. T1SS efflux involves ATP hydrolysis-coupled translocation of the substrate across the two bacterial membranes in a single energy-coupled step, utilizing an outer membrane factor (OMF; TC#1.B.17) and a membrane fusion protein (MFP; TC#8.A.1) to couple cytoplasmic membrane transport with that across the periplasm and outer membrane ([50], [51]). Protein exporter families of this type were found in abundance in the pathovars.

Type III secretion systems are found in numerous Gram-negative bacterial strains and are used for secretion of flagellar and pathogenicity effector proteins. Effector proteins can be exported across both bacterial membranes as well as the host cell membrane in a single step. The type III protein secretion system includes a needle complex, the injectisome, which attaches to the host cell membrane [52, 53, 54, 55]. Several of these systems were present in *E. coli* pathogens (Table 4).

As expected, the complete general secretory pathway (TC#2.A.5.1.1) and the complete flagellar protein export complex (TC #3.A.6.2.1) were found in all strains. The UMN pathovar appears to possess six additional key components of the flagellar system (Table 4).

T4SSs vary tremendously with respect to sequence divergence and numbers of constituents required for function. An examination of potential T4SS components in the eight *E. coli* strains revealed the presence of potential subunits, suggesting that some of these organisms utilize this mechanism to promote pathogenesis.

Type VI secretion systems are found in multiple Gram-negative bacteria. Key constituents include an ATPase protein, ClpV, a phage tail-like protein that spans the outer membrane, and a “tail-spike” protein, VgrG, which penetrates the host membrane and dissociates from the complex to allow contact-dependent translocation of proteins into the host cell cytoplasm [59]. In the *E. coli* strains studied here, two sets of complete T6SS complex homologs were identified (VasA-L of 3.A.23.1.1 and EvpA-P of 3.A.23.2.1) in several strains.

3.2.3 Outer membrane protein secretion systems

Table 5 summarizes the outer membrane protein secretion systems present in the eight *E. coli* strains studied. These include members of the following families: Autotransporter-1

(TC#1.B.12), Autotransporter-2 (TC#1.B.40), outer membrane factors (OMF; TC#1.B.17), fimbrial usher proteins (FUP; TC#1.B.11), two partner secretion systems (TPS; TC#1.B.20), secretins (TC#1.B.22), outer membrane protein insertion porins (OmpIP; TC#1.B.33), curli fiber subunits (CsgA; TC#1.B.48), and putative autotransporter-3 (Invasins; TC#1.B.54).

Autotransporters are virulence factors that insert into the outer bacterial membrane to form transmembrane β-barrels that export their extracellular protein domains. An Autotransporter-1 protein consists of an N-terminal cleavable secretory signal, an exported passenger domain of variable lengths, and a C-terminal 250-300 amino acyl residue domain that inserts into the outer membrane, giving rise to a 12 TMS β-barrel structure [60].

Autotransporter adhesins (e.g., AidA; TC#1.B.12.1.1) were present in all eight *E. coli* strains examined, but virulence factor-associated autotransporters were present in only certain pathogens. For example, fibronectin binding proteins and a tracheal colonization factor autotransporter were identified only in pathovars (Table 5). Overall, the most autotransporter-1 proteins were found in ABU with sixteen homologs; fourteen were found in 559, twelve in CFT and UMN, ten in APE and E24, eight in O15, and only five in K12.

Autotransporter-2 family proteins have trimeric structures organized into three domains: an N-terminal head that adheres to the host cell membrane, a stalk, and a C-terminal anchor, rich in glycine, which forms a β-strand domain that oligomerizes to form a pore for auto-transport [63]. Haemagglutinins, a dissimilar adhesin, YadB [64], and other autotransporter-2 family members were identified in specific pathovars (Table 5). Interestingly, AT-2 family proteins are far less prevalent than AT-1 family proteins in all strains and are lacking in K12.

Invasins or intimins are also called Autotransporters-3, but a function in autotransport is not well established [65]. The N-terminal domain serves as an anchor and inserts a pore-like β-barrel in the outer membrane. The C-terminus contains folds that bind to Tir (translocated intimin receptor) and β-1 integrins on host cells, leading to pathogenesis in enterohaemorrhagic and enteropathogenic strains [66, 67]. In our study, intimin/invasin proteins were identified across all serotypes and were found in abundance in six of the seven pathogens. The UPEC strains have more intimins/invasins than the enteropathogenic strains.

Outer membrane factors (OMFs; 1.B.17) and membrane fusion proteins (MFPs; TC# 8.A.1) function with Major Facilitator Superfamily (MFS) type porters, Resistance-Nodulation Cell-Division [68] family proteins (2.A.6), ATP-Binding Cassette (ABC) porters and Aromatic Acid Exporters (AAE, TC#2.A.85) to form complexes that export various drugs, oligosaccharides, proteins, aromatic acids and siderophores across both the inner and outer membranes in a single energy-coupled step ([69], [70], [71], [72], [73]). OMF proteins form homotrimeric, 12-stranded β-barrel complexes that form holes in the outer membrane for translocation. The OMF component, TolC (TC #1.B.17.1.1), was identified in all eight strains. TolC-dependent exporters mediate translocation of hemolysins, drugs and various siderophores [74, 75]. Additional TolC-like proteins were found in the pathogens but not in K12.

The Fimbrial Usher Proteins of the FUP family function in conjunction with periplasmic chaperone proteins in fimbrial assembly [76]. The usher proteins contain central domains that span the outer membrane 24 times to form β-barrel pores. The C-terminal domains act as “plugs” that lie within the lumen of the β-barrels [77]. These plug domains, along with helical folds, regulate channel opening and export of proteins that contribute to fimbrial assembly [78]. FUPs were identified in all strains of *E. coli* but were present in greater numbers in the pathovars (Table 5).

Homologs of a single two-partner secretion (TPS) system (ShlB; TC#1.B.20.1.1) were identified. The oligomeric β-barrel channel of ShlB serves in secretion of the effector protein across the outer membrane [80]. These TPS systems were found exclusively in O15, where two paralogues were present, and in ABU, where a single protein was identified.

A Secretin (TC#1.B.22) consists of an N-terminal periplasmic domain and a C-terminal domain responsible for forming large channels via homomultimeric ring structures [81]. Secretins participate in various transport processes such as fimbrial protein export, T2SS, T3SS, and phage export [82, 83], and as expected, a number of these were identified in the pathogens (Table 5). Also as expected, outer membrane protein (OMP) insertion porins (OmpIP or BAM, TC #1.B.33), required for OMP insertion, were ubiquitously present, and all six required subunits were identified in all eight strains.

3.2.4 Iron Scavenging Outer Membrane Receptors

Table 6 lists outer membrane receptors of TC family 1.B.14, most of which are involved in the uptake of iron-siderophore complexes. This table also includes a cobalamin receptor and a copper receptor and indicates the occurrence of the TonB protein, which together with other proteins, is involved in OMR energization. TolA homologs, involved in outer membrane stabilization and colicin uptake, are also tabulated. For some of the OMRs, a single ortholog was found in all eight organisms (e.g., receptors for ferric copragen, ferrichrome, catecholate and cobalamin). Some organisms possess more than one gene encoding a specific type of iron complex uptake receptor. These include: 1.B.14.1.4 (catecholate) where four of the organisms have a single gene encoding this system, but three organisms have two, and one (CFT) has three (Table 6). A similar situation was observed for 1.B.14.7.2, an iron pesticin uptake receptor. Six additional types of outer membrane receptors specific for iron complexes were found in some of these *E. coli* strains but not others. Similarly, only four of the pathovars possess the copper receptor (TC#1.B.14.4.1). All in all, each of these organisms possesses nine to fifteen iron uptake receptors except for K12 and E24, which have only six. Interestingly, the uropathogenic strains all possess more (ten to fifteen) iron complex receptors than the other serovars.

Table 6 also includes the energizing modules of family 2.C.1, TonB, which energizes OMR-mediated uptake, and TolA, which provides outer membrane stability and mediates colicin uptake [Table S1; 85]. It can be seen that while *E. coli* K12 has just one of each of these two proteins, four of the pathogens have two TonB's, five of them have two TolA's, and one (559) has three TolA's. TonB, but not TolA, associates with ExbB-ExbD or TolQ-TolR to energize uptake of iron-siderophore complexes and other large molecules across the outer membranes of Gram-negative bacteria via outer membrane receptors (OMR; TC# 1.B.14; 17370038, 23443998). The dissimilar Tol complex includes six proteins, TolA, TolB, YbgF, Pal and the pmf-dependent energizer, TolQR. This complex is involved in the maintenance of outer membrane stability and facilitates late stages of cell division (19075020, 21285349).

3.2.5 Inner membrane Iron Uptake Systems

Table 7 summarizes inner membrane iron uptake systems identified in the eight *E. coli* strains. These systems function to transport iron from the periplasm into the cytoplasm of the bacterium, cooperating with the outer membrane iron-scavenging OMR complexes, which import iron from the surrounding extracellular environment into the periplasm. Various mechanisms are employed for inner membrane transport of iron/iron-chelate complexes. These include the CorA heavy metal ion uptake channels (1.A.35), the zinc-iron permeases (ZIP (2.A.5)), metal ion transporters (Nramp (2.A.55)), GTPase-coupled ferrous iron uptake systems (FeoB (9.A.8)), and ATP-binding Cassette (ABC (3.A.1)) transporters.

Zinc-Iron Porters (ZIP) have about of eight TMSs with histidine-rich repeats near the N- and C-termini [86]; a cation symport mechanism may be operative [89]. A single such transport protein was found in each of the eight strains examined (Table 7). Metal ion transporter (Nramp) homologues generally function by a symport mechanism in a 1:1 ratio of ferrous ion and H^+ although stoichiometrics have been reported to be variable [90]. A single Nramp protein was found in each of the eight strains of *E. coli* examined (Table 7). Another iron influx system, FeoB (TC#9.A.8), has N-terminal catalytic domains with sequences homologous to GTP-binding domains [91]. Their C-termini catalyze transport, possibly coupled to K^+-activated GTPase activity. GTP hydrolysis has been reported to be required for transport, and if there is direct energy coupling, the mechanism may resemble that of ABC transporters ([92]; [93]; [94]; [95]). Two FeoB homologues were identified in each of the eight strains of *E. coli*.

Four types of inner membrane ABC iron-uptake systems were identified: ferric porters (TC#3.A.1.10), iron chelate porters (TC#3.A.1.14), manganese/zinc/iron chelate porters (TC#3.A.1.15), and homologs of the *Brachyspira* iron transporters (TC#3.A.1.20). A complete four-subunit ferric-citrate uptake system (TC#3.A.1.14.1) was identified in five of the eight strains. Complete ferric-enterobactin and ferric-hydroxamate uptake systems were identified in all eight strains of *E. coli* examined. However, a second complete ferric-enterobactin system (TC#3.A.1.14.2) was identified in two strains.

Homologs of the *Shigella* heme uptake system (ShuTUV (3.A.1.14.18)) were present in five pathogenic strains as complete systems. Complete systems corresponding to the *Salmonella* Mn^{2+} and Fe^{2+} uptake system (3.A.1.15.7) were identified in four pathovars.

Figure 2 reveals the correlation between numbers of OMRs and the number of iron ABC uptake systems. The juxtaposition of the two data sets demonstrated that the UPEC strains, ABU and CFT, contain the greatest numbers of both OMRs and inner membrane iron-siderophore transporters. E24 and K12 contain the smallest numbers of both types of systems. A clear correlation between the numbers of iron-siderophore OMRs and inner membrane transporters is evident for the eight strains of *E. coli* (RSQ value = 0.90). The slope of the trendline (SLOPE = 1.85) confirms the positive correlation between the two sets of values.

3.2.6 Nutrient Transporters: Intracellular vs. Extracellular Pathogens

We identified numerous nutrient uptake porters that are uniquely found only in the three intracellular pathogens or only in the extracellular pathogens (Table 8). Transporters found exclusively in the intracellular pathovars include certain α-type channels (TC#1.A), β-barrel porins (1.B), holins (1.E), MFS porters (2.A.1), multidrug resistance (MDR) RND-type efflux pumps (2.A.6), ABC porters (3.A.1), PTS sugar uptake transporters (4.A), and various TC class 9.B proteins. Thus, the APE, CFT and ABU strains, all primarily intracellular pathogens, possess many transport systems that take up metabolic products produced via host intracellular metabolic processes. Examples include a phosphoglycerate:Pi antiporter (2.A.1.4.2) that takes up glycolytic intermediates, 2- and 3-phosphoglycerates as well as phosphoenolpyruvate, a pmf-dependent acetate uptake system (TC#1.A.14.2.2), an ATP-dependent ribose porter (3.A.1.2.1) and a phosphoenolpyruvate (PEP)-dependent D-tagatose/D-psicose/D-sorbose PTS uptake system (4.A.2.1.9). While ribose is a substrate of RNA biosynthesis and a product of RNA degradation, the latter 2-keto hexoses are intermediates of several intracellular metabolic pathways and of nutritional value ([96]; [97]). These intracellular pathogens also uniquely possess a citrate:H^+ symporter (2.A.1.6.1), a fumarate-malate transporter (2.A.13.1.2), a citrate:succinate antiporter (2.A.47.3.2), a tripartite tricarboxylate (citrate, isocitrate and cis-aconitate) transporter (2.A.80.1.1), and a putative C4-dicarboxylate transporter (9.B.50.1.2), all of which are specific for intermediates in the Krebs (TCA) cycle, and none of which are found in the extracellular pathovars. In addition to Krebs cycle metabolism, C4-dicarboxylates can be generated via multiple pathways including amino acid deamination and lipolysis.

Two of the intracellular pathogens, APE and CFT, possess an arginine/agmatine antiporter (2.A.3.2.7), which allows these cells to survive under acidic conditions, for example, as exist inside lysosomes [98]. These intracellular pathogens also possess a probable antimonite/arsenite resistance exporter (2.A.47.4.2). Arsenite can be passively taken up by host cells via aquaglyceroporins (TC # 1.A.8) [99]. Additionally, an ATP-dependent nucleoside group translocator (4.B.1.1.1) that synthesizes NMN, an intermediate in NAD synthesis, and a thiamin porter (4.B.1.1.4), involved in the synthesis of thiamin pyrophosphate (TPP), were found in these strains but not in the extracellular pathogens (Table 8).

Surprisingly, the intracellular pathogens possess a glucuronate/galacturonate porter (2.A.1.14.2), which is absent in the extracellular pathogens (Table 8). These metabolic products have been shown to be generated intracellularly when exogenous sugars such as lactose are metabolized by *E. coli* [100]. These compounds are present intracellularly in numerous organs of animals, and these *E. coli* strains utilize cytoplasmic UDP-glucuronyltransferases for mucopolysaccharide biosynthesis [101]. Additionally, a sialic acid uptake porter (2.A.56.1.6) is found exclusively in the intracellular pathogens. Although sialic acids are found in abundance in cell surface glycolipids and extracellular glycoproteins, *N*-acetylneuraminic acid, the main mammalian sialic acid, can be found intracellularly where it participates in glycolipid and glycoprotein biosynthesis [102]. Sialic acid-containing polysaccharide capsules are virulence factors in *E. coli* urinary tract infections and contribute to biofilm formation [103].

Intracellular *E. coli* strains lack various transporters present in extracellular pathogens that take up metabolites normally found extracellularly. For example, the latter, but not the former strains possess a rhamnose oligosaccharide porter (3.A.1.5.12), a melibiose permease (2.A.2.1.1) and a 2-O-α-mannosyl-D-glycerate porter (4.A.2.1.3). These first two oligosaccharides are constituents of glycolipid and glycoproteins found on the external surfaces of intestinal villus cells, while the last compound is a known intracellular osmolyte in some bacteria [104]. The extracellular strains, but not the intracellular strains, also have a xylose:H^+ symporter (2.A.1.1.3), a mannose PTS porter (4.A.2.1.6), a glucitol PTS transporter (4.A.4.1.2), and a galactitol PTS permease (4.A.5.1.3). The former two sugars are found in abundance in cell surface polysaccharides [105, 106] while the hexitols are common osmolytes in animals [107]. The α-glucoside-specific IICB permease of the PTS (4.A.1.1.10), which transports many glucosides is similarly found in the extracellular pathogens but lacking in intracellular strains (Table 9).

Other transporters lacking in intracellular but present in extracellular pathogens include an uptake system for the folate catabolite, p-aminobenzoyl-glutamate (2.A.68.1.1), and a cyanate/thiocyanate porter (2.A.1.17.1) [108, 109]). Thiocyanate and cyanate are found in extracellular environments, and although toxic, they can be used as a nitrogen source following destruction by cyanase, CynS [108]. *E. coli* cells lacking the *cyn* operon are more sensitive to the toxic effects of cyanate and thiocyanate than strains that possess it [110].

A putrescine uptake porter (2.A.3.1.13) was found to be present only in extracellular strains. Putrescine, like other positively charged polyamines, stabilizes the negatively charged DNA during replication, but it is also found in abundance in extracellular environments in mammals such as seminal fluid and urine, especially during episodes of protein breakdown [111, 112]. Several MDR and iron-siderophore transporters are found exclusively in intracellular pathogens, while others are present in extracellular pathogens exclusively. These facts may reflect the natural cellular substrates of MDR pumps currently not recognized.

3.3 Proteins with e-values between 0.1 and 0.0001

Several proteins were identified that gave poor scores in the G-BLAST search, but which nevertheless proved to be members of TC families. Some of these are presented here in order of their TC numbers. (1) A putative invasin with similarily to proteins in the OmpA family (TC#1.B.6) was identified and given the TC number 1.B.6.2.13. (2) A homolog of pore-forming phage coat protein A was identified and assigned TC# 1.B.53.1.4. (3) Several proteins proved to be homologous to the cytotoxic pore-forming oligomeric fimbrial subunit, MrxA. One such protein has been entered into TCDB under TC#1.C.80.1.2. (4) A holin of 108 aas was identified and entered into TCDB with TC#1.E.2.1.10. This protein was encoded by a gene within a prophage segment of the genome of UMN with two adjacent genes, a lysozyme inhibitor, and a lytic protein, probably a lysozyme. (5) An ABC porter, YnjBCD, was assigned TC#3.A.1.19.4. Although it is annotated as a sulfate/thiosulfate transporter, other members of this family transport vitamins. (6) Another protein designated YjiG proved to be a distant member of the FeoB family (TC#9.A.8). A nucleoside-recognition domain may be present in some of these homologs. YjiG was entered into TCDB with TC# 9.B.156.1.1.

3.4 Unique characteristics of enterohaemorrhagic (EHEC) strain, O15

Strain O15 exhibited a number of characteristics that distinguished it from the other six pathogenic strains of *E. coli* examined. It has two-partner secretion (TPS) systems corresponding to TC# 1.B.20.1.3 and 1.B.20.1.4. The former system plays a role in contact inhibition of growth

[68] while the latter protein is a ShlB-type protein that contains a domain critical for substrate recognition and folding [113]. It probably secretes a haemolysin-like virulence factor [114] and has been entered into the database under 1.B.20.1.7.

This strain uniquely has an AT-2 type adhesin, most closely related to TC# 1.B.40.1.3, as well as an intimin, most closely related to TC# 1.B.54.1.1. These proteins were found in no other *E. coli* strain examined. Most surprisingly, we identified 14 hits of 1.B.6.2.1 and 1.B.6.2.2, all related to OmpX of the OmpA family. These proteins are in the Ail/Lom family, which in *Yersinia* species are multifunctional virulence factors that protect against complement [115]. Equally surprising was the unique discovery of 12 putative holins corresponding to TC# 1.E.1.1.3. These holins may be related to phage-encoded shiga-toxins [116].

4. Discussion

4.1 Iron siderophore receptors and transporters contribute to E. coli *pathogenesis in a host organism.*

E. coli is a facultative anaerobe that utilizes iron primarily for electron transport and cellular respiration. Succinate dehydrogenase and various cytochromes as well as NADH and ferric oxidase activities are diminished with an iron deficiency [117]. In humans, iron sequestration plays an important role in host defense against pathogens. Certain conserved eukaryotic genes encode siderophore/iron-uptake complexes that allow the host to upregulate iron sequestration in response to inflammatory signals accompanying infection [118]. Some of these genes play pivotal roles in host defense in Crohn’s disease, for their upregulation allows the host intestinal epithelial cells to sequester more iron [119]. In our study, the pathogenic *E. coli* strains examined proved to have greater numbers of iron-siderophore receptor-encoding genes than the nonpathogenic K12 strain.

Certain iron-siderophore receptors and ABC iron uptake systems are abundant only in pathovars (Tables 6 and 7). These receptors include a Fe^{3+}-catecholate receptor (1.B.14.1.4) and the ferric-yersiniabactin uptake receptor (1.B.14.7.2). The ferric-yersiniabactin uptake receptor is known to be required for biofilm production in UPEC strains [120], possibly relevant to host inflammatory signaling. Ferri-enterobactin receptors (1.B.14.1.3) and ferrichrome receptors (1.B.14.1.15) were identified exclusively in UPEC strains (ABU and CFT). These receptors may serve specific functions in UPEC pathogenicity.

The increased numbers of iron-complex receptors in pathovars indicate targets for combating *E. coli* pathogenicity. Increases in siderophore receptor complexes may serve as compensatory mechanisms in response to host defense. Increased ferrichrome sequestration undoubtedly allows these pathovars to take up iron more readily, leading to increased survival in the host.

As shown in Figure 2, increases in numbers of iron-sequestering outer membrane receptors correlate with increases in inner membrane iron ABC transport systems. The UPEC strains (ABU, CFT and UMN) have larger numbers of both iron-siderophore OMRs and inner membrane transporters. We speculate that because UPEC strains must survive in both the gastrointestinal and the urogenital tracts, they must possess a greater number of iron-siderophore transporters for cellular respiration and survival.

It has been shown that ABC porters (3.A.1) in general possess higher affinities for their substrates than secondary carriers (TC#2.A). Secondary carriers transporting metal cations typically exhibit Km values of ~ 20-800 uM [121] while primary active transporters may exhibit Km values ≤ 1 uM [122]. Interestingly, the majority of ABC iron transporters were found either exclusively in pathogenic strains or in increased numbers (Table 7), and the same strains possess the largest numbers of iron-siderophore OMRs. TC subclass 2.A iron uptake secondary carriers appear to be present in invariant numbers in all eight *E. coli* strains although the ABC iron-specific transporters differ greatly among the different serovars (Table 7). This suggests that the low affinity secondary iron carriers serve housekeeping functions outside of the body, where iron concentrations are relatively high, while the ABC transporters function in pathogenesis in the *in vivo* environment, where competition with the host is an important factor.

4.2 Pore-forming Toxins.

EHEC and EPEC pathovars typically operate by attaching and effacing (A/E) mechanisms. This type of invasion includes utilizing a Type III secretion system to inject effector proteins into host cells. One effector, EspF, plays an important role in tight junction disruption as well as inhibition of sodium and water uptake [123]. The EspB/D complex was identified in UMN (UPEC) and O15 (EHEC) and serves to initiate pore formation in the host cell plasma membrane as well as translocation of EspF into the cell. UPEC strains typically utilize Type I Secretion Systems for adhesion and entry through manipulating the host cell cytoskeleton using effectors that stimulate Rho-family GTPases and kinases [124]. Nevertheless, a complete T3SS was identified in UMN, suggesting that an A/E mechanism of invasion may occur in this pathovar.

The identification of Haemolysin A (HlyA) exclusively in the UPEC strains supports a previous finding that these strains can utilize haemolysins to inhibit protein kinase B signaling and lead to apoptosis of host cells [37]. Similarly, the exclusive presence of shiga toxin in O15 supports previous findings of EHEC pathogenicity [125]. The Stx pathway may provide an alternative pathway by which the EHEC strain can inhibit chemical signaling and immune responses in the host cell.

Homologs of the clostridial cytotoxin (CCT) form channels and inactivate Rho-type GTPases, leading to manipulation of the host cytoskeleton [42]. Predictably, such a toxin was identified in the UPEC strain, ABU, but more surprisingly, it was also found in O15. This may suggest an alternative mechanism by which EHEC strains manipulate the host's cytoskeletal machinery since these pathovars typically utilize the mitochondrial-associated protein [78] to inhibit the host cell control protein 42 (CDC42), which provides regulatory functions in host cell actin dynamic control [126]. Since the homologs in ABU and O15 are 85% identical, the same mechanism is likely to be operative.

AIEC strains such as APE, have been cited in 36% of Crohn's disease. These pathovars operate through necrosis factors that impair host immune responses, allowing the bacteria to colonize the ileal mucosa and lamina propia [127]. We identified the active subunit of Cytolethal Distending Toxin (CdtB) only in APE. The CdtB active subunit induces DNA double-strand breakage, leading to host cell cycle arrest in the G2/M phase [128]. This is preferable in the AIEC pathotype, presumably because pauses and irregularities in host cell cycle give the bacteria time to proliferate and colonize host cells. Rapid proliferation of these AIEC cells can then induce secretion of Tumor Necrosis Factor Alpha (TNF-α) that causes inflammation in host cells.

Serratia-type pore-forming toxins (S-PFT) were identified in ABU (UPEC), CFT (UPEC) and O15 (EHEC). These toxins exhibit properties vastly different from those of RTX pore-forming haemolysins, which are exported via two-partner secretion systems and are much larger in size [43]. The presence of two-partner secretion system(s) in both ABU and O15 confirmed the possibility of a novel *Serratia*-type Pore-forming Toxin (S-PFT) in both UPEC and EHEC strains (see Table 3).

4.3 Outer Membrane Protein Secretion Systems.

Many autotransporter-1 systems were identified in the seven pathovars examined. Examples include the fibronectin binding protein (1.B.12.1.3), a tracheal colonization factor (1.B.12.2.2), a firmicute homolog (1.B.12.2.4), and a *Salmonella* BigA homolog (1.B.12.5.5) (see Table 5). Fibronectin binding protein is known to assist in host cell adhesion by *S. typhimurium* [129], providing evidence that a similar mechanism of adhesion may be utilized by UPEC, AIEC, ETEC and EAEC strains for host cell targeting. Interestingly, homologs of the *B. pertussis* tracheal colonization factor were identified in all pathovars except for O15, providing clues as to how such strains target cilia-rich epithelia in the intestines.

Several autotransporter-2 systems were found exclusively in the pathovars. Homologs of the membrane-anchored haemagglutinin, identified in UMN and O15, may play roles in bacterium-host cell adhesion [19]. Trimeric adhesins such as Cha (1.B.40.1.5) and UpaG (1.B.40.2.3) were also identified exclusively in pathovars, and they are known to function in adhesion to the host extracellular matrix [131]. YadB homologs (1.B.40.1.3) function by a similar mechanism, and one was identified in O15, suggesting that it may function specifically in EHEC strains.

EHEC and EPEC strains have been shown to use invasins/intimins to target translocated intimin receptors (Tir) and β-1 integrins on host extracellular matrices for adhesion purposes followed by stimulation of actin rearrangements via the N-Wasp pathway ([132]; [133]). UPEC strains, however, utilize type I pili to bind β-1 integrin on host cell extracellular matrices to initiate actin rearrangements [124]. The presence of invasins/intimins to target β-1 integrins reveals a potential novel mechanism of cell-adhesion and actin rearrangement utilized by these UPEC pathovars.

The MdtP outer membrane factor (OMF; TC# 1.B.17.3.9) functions with the MdtO aromatic acid/drug exporter (2.A.85.6.1) and the auxiliary MFP protein, MdtN (8.A.1.1.3). This OMF was found in all pathovars but not in K12. This may indicate a multi-drug resistance mechanism found exclusively in the pathogenic strains that contributes to their resistance to antibiotics.

Fimbrial usher proteins (FUPs) serve important functions in the assembly of fimbriae [76]. As expected, these proteins were found ubiquitously in all strains including K12. However, greater numbers of the encoding genes were observed in all pathovars compared to K12, presumably contributing to pathogenesis by promoting bacterium-host cell adhesion [79].

4.4 Multiple pathovars contain T6SS constituents

Potentially complete VasA-L T6SSs were identified in multiple pathovars. Protein products of the *icmF*, *hlc* and *clpV* genes play essential roles in biofilm assembly and general motility [134]. In recent studies, the T6SS present in *P. aeruginosa* and other bacterial cells was shown to engage in “T6SS dueling” with surrounding bacteria in competition for survival in the microbiome [135, 136].

With the discovery of T6SSs in *E. coli* pathovars, we speculate that *E. coli* cells engage in T6SS-mediated competition in the human body. It is possible that pathovars of *E. coli* can utilize T6SSs both for offense and for defense in the host microbiome. Such a mechanism may prove valuable during invasion of the colon, where microbes are densely packed with other types of facultative/obligate anaerobes competing for limited metabolic resources.

4.5 Transporters in intracellular vs. extracellular pathogens

An interesting pattern revealed by our studies was the existence of different sets of nutrient uptake transporters, depending on the organismal site of proliferation. Intracellular versus extracellular organisms were distinguishable on the basis of the nature of the substrates transported. In general, the intracellular pathovar-specific strains take up metabolites expected to be found inside host cells while the extracellular pathovars transport substrates that are normally found in abundance outside of host cells. Examples of this can be seen in transporters for glycolytic and Kreb cycle intermediates found only in intracellular pathogens as well as transporters for oligosaccharides found only in extracellular pathogens (Table 9). These facts indicate that these organisms have acquired transport systems through the frequent gain and loss of the encoding genes probably via horizontal transfer, to take advantage of nutrients available in their specific environments. Since intracellularity may be a relatively recent development, this suggests that the gain and loss of genes may have occurred with high frequency in response to immediate need. It seems probable that such characteristics (e.g., predilection for certain types of nutrient transporters) can be used for diagnostic purposes.

4.6 Unique characteristics of O15

In screening the data, we noticed that each strain examined has characteristics that distinguish it from all others. Particularly noteworthy was strain O15, which had numerous characteristics lacking in the other seven strains. One such example includes extra two-partner secretion systems as well as a unique AT-2 adhesin and an intimin. More striking was the occurance of large numbers of OmpA-like Ail/Lom family proteins that probably serve multiple virulence functions, including protection against complement as has been documented in *Yersinia* species [115]. Additionally, this strain possessed numerous holins, all homologous to 1.E.1.1.3, a unique characteristic.

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6. Tables

Table 1. Seven *E. coli* pathovars, the non-virulent *E. coli* K12 strain, and their basic traits.

Strain	Abbr.	Genome size (Mbp)	# of Proteins	Host Location	Pathological condition	Pathovar Type
55989	559	5.15	4,759	Extracellular	Diarrhoea	EAEC
ABU 83972	ABU	5.13	4,796	Intracellular	Bacteremia	UPEC
APEC O1	APE	5.50	4,853	Intracellular	Respiratory infection (avians)	AIEC
CFT073	CFT	5.23	5,369	Intracellular	Urinary tract infection & pyelonephritis	UPEC
E24377A	E24	5.25	4,991	Extracellular	Enterotoxicity	ETEC
UMN026	UMN	5.36	5,014	Extra/Intra -cellular	Urinary tract infection	UPEC
O157:H7	O15	5.70	5,477	Extracellular	Haemorrhagic colitis	EHEC
K12 MG1655	K12	4.64	4,290	Extracellular	None	Non-virulent

Table 2. Numbers of proteins (even numbered columns) and percent distribution of subclasses by TC number (odd numbered columns) for all eight strains of *E. coli* as well as numbers of transport proteins per strain (bottom) and all strains combined, with and without K12 (last four columns).

Subclass	**559**	**%**	**CFT**	**%**	**ABU**	**%**	**APE**	**%**	**E24**	**%**	**UMN**	**%**	**O15**	**%**	**K12**	**%**	**all**	**%**	**All-K12**	**%**
1.A	42	3.4	37	2.9	41	3.2	41	3.3	42	3.5	39	3.1	42	3.47	39	3.5	323	3.3	284	3.3
1.B	94	7.6	103	8.0	108	8.4	91	7.3	89	7.4	95	7.5	96	7.93	67	5.9	743	7.5	676	7.7
1.C	15	1.2	18	1.4	20	1.6	15	1.2	11	0.9	15	1.2	21	1.74	9	0.8	124	1.3	115	1.3
1.E	5	0.4	6	0.5	4	0.3	6	0.5	3	0.2	7	0.6	14	1.16	4	0.4	49	0.5	45	0.5
2.A	318	25.6	325	25.4	319	24.8	315	25.3	309	25.7	319	25.2	299	24.71	311	27.6	2515	25.5	2204	25.2
2.C	5	0.4	5	0.4	4	0.3	4	0.3	3	0.2	4	0.3	3	0.25	4	0.4	32	0.3	28	0.3
3.A	358	28.8	378	29.5	386	30.0	369	29.7	353	29.4	390	30.8	369	30.50	340	30.1	2943	29.8	2603	29.8
3.B	4	0.3	3	0.2	5	0.4	5	0.4	5	0.4	4	0.3	4	0.33	4	0.4	34	0.3	30	0.3
3.D	69	5.5	66	5.2	64	5.0	59	4.7	69	5.7	72	5.7	68	5.62	69	6.1	536	5.4	467	5.3
4.A	56	4.5	62	4.8	62	4.8	61	4.9	55	4.6	61	4.8	51	4.21	49	4.3	457	4.6	408	4.7
4.B	2	0.2	4	0.3	4	0.3	4	0.3	2	0.2	2	0.2	2	0.17	2	0.2	22	0.2	20	0.2
4.C	10	0.8	17	1.3	16	1.2	11	0.9	9	0.7	11	0.9	7	0.58	8	0.7	89	0.9	81	0.9
4.D	9	0.7	10	0.8	12	0.9	9	0.7	8	0.7	7	0.6	9	0.74	8	0.7	72	0.7	64	0.7
5.A	43	3.5	44	3.4	44	3.4	45	3.6	42	3.5	43	3.4	43	3.55	45	4.0	349	3.5	304	3.5
5.B	3	0.2	2	0.2	2	0.2	2	0.2	2	0.2	4	0.3	3	0.25	3	0.3	21	0.2	18	0.2
8.A	37	3.0	45	3.5	43	3.3	40	3.2	39	3.2	42	3.3	37	3.06	33	2.9	316	3.2	283	3.2
8.B	1	0.1	1	0.1	1	0.1	1	0.1	1	0.1	1	0.1	1	0.08	1	0.1	8	0.1	7	0.1
9.A	87	7.0	64	5.0	63	4.9	77	6.2	71	5.9	66	5.2	60	4.96	42	3.7	530	5.4	488	5.6
9.B	86	6.9	91	7.1	89	6.9	88	7.1	89	7.4	85	6.7	81	6.69	90	8.0	699	7.1	609	7.0
total	1244	100	1281	100	1287	100	1243	100	1202	100	1267	100	1210	100	1128	100	9862	100	8734	100

Table 3. Toxins identified in *E. coli* pathovars and K12.

Family	TC ID	Function	559	ABU	APE	CFT	E24	UMN	O15	K12
HlyE	1.C.10.1.1	Pore-forming haemolysin, HlyE	0	1	0	1	0	1	1	1
RTX toxin	1.C.11.1.3	Pore-forming haemolysin, HlyA	0	2	0	1	0	0	0	0
IIITCP	1.C.36.1.1	T3SS: pore-forming complex, EspBD	0		0	0	0	0	2	0
IIITCP	1.C.36.3.1 and 3.2	T3SS: pore-forming complex, SipBD	0	0	0	0	0	2	0	0
IIITCP	1.C.36.5.1	T3SS: pore-forming complex, SseBCD	0	0	0	0	0	0	1	0
Shiga toxin B	1.C.54.1.1	Shiga toxin B, St-B	0	0	0	0	0	0	2	0
Clostridial cytotoxin	1.C.57.3.2 and 3.3	Pore formation; necrosis in host, Cnf	0	1	0	0	0	0	1	0
S-PFT	1.C.75.1.1	Pore-forming haemolysin, ShlA	0	1	0	1	0	0	1	0
Cytotoxic major fimbrial subunit (Mrx-A)	1.C.80.1.1	Adhesive fimbriae (pore formation)	2	4	3	5	2	2	4	2
Cytolethal distending toxin	1.C.98.1.1	Cell cycle arrest/apoptosis, CdtABC	0	0	3	0	0	0	0	0

Table 4. Pathogenicity-related transenvelope protein secretion systems.

Family	TC ID	Function	559	ABU	APE	CFT	E24	UMN	O15	K12
T1SS	3.A.1.105.3 and 105.4	Drug Exporter 1	8	8	8	8	7	8	8	8
	3.A.1.109.4	Protein Exporter 1	0	4	0	4	0	2	2	0
	3.A.1.110.1	Protein Exporter 2	0	3	0	4	0	0	0	0
	3.A.1.113.3	Peptide 3 Exporter	1	1	1	1	1	1	1	1
	3.A.1.134.7	Peptide 7 Exporter	15	14	13	14	13	13	14	13
T2SS GSP	3.A.5.1.1	SEC-SRP complex	7	7	7	7	7	7	7	7
MTB	3.A.15.1.1	Pullulanese secretion system	8	13	14	8	8	7	0	8
	3.A.15.2.1	Pilin secretion/fimbrial assembly system	5	4	4	3	4	5	4	4
	3.A.15.3.1	LSP/ fimbrial assembly system	0	0	0	1	0	1	0	0
T3SS	3.A.6.1.1	Type III Secretion System Complex	4	1	1	1	6	8	13	1
	3.A.6.2.1	Flagellar Protein Export Complex	11	11	11	11	11	17	11	10
T4SS	3.A.7.3.1	Pertussis Toxin Exporter	0	0	0	0	0	4	0	0
	3.A.7.7.1	Trs DNA Transfer Protein Complex	2	2	2	2	2	2	2	2
	3.A.7.11.1	Type IV Beta-Proteobacterial DNA Secretion System	2	1	4	1	2	2	3	1
	3.A.7.13.2	Plasmid pLS20 Conjugation System	1	2	2	1	1	2	1	1
	3.A.7.14.2	Conjugation System Plasmid DNA IntP/TcpA-J	5	4	3	5	5	4	5	5
T6SS	3.A.23.1.1	T6SS VasA-L	19	8	18	7	17	13	13	0
	3.A.23.2.1	T6SS EvpA-P	19	5	6	5	6	2	2	1

Table 5. Outer membrane protein secretion systems.

Family	TC ID	Function	559	ABU	APE	CFT	E24	UMN	O15	K12
FUP	1.B.11.2.1 and 2.2	Type π fimbrial usher protein, PapC and YbgQ	3	3	3	4	3	3	2	1
	1.B.11.3.2, 3.3, 3.5. 3.6 and 3.9	Type γ fimbrial usher protein, MrkC, EcpC, YcbS, YraJ, and FimD	8	8	5	6	6	8	7	6
	1.B.11.4.1	Type α fimbrial usher protein, CfaC	2	1	1	1	2	1	1	1
AT-1	1.B.12.1.1	Adhesin, AidA	1	1	1	1	1	1	1	2
	1.B.12.1.2	Virulence factor, IcsA (VirG)	2	2	0	2	2	0	1	0
	1.B.12.1.3	Fibronectin binding protein, MisL	1	0	1	1	1	2	1	0
	1.B.12.2.1	Pertactin, Ptt	1	0	0	0	1	1	0	1
	1.B.12.2.2	Tracheal colonization factor, TcfA	1	1	1	1	1	1	0	0
	1.B.12.2.3	Resistance to killing proteins, BrkA	0	0	1	0	0	0	0	0
	1.B.12.2.4	Putative adhesin/protease/pertactin	2	3	1	3	0	1	0	0
	1.B.12.4.2 and 4.3	Serine proteases, EspP and Tsh	3	3	1	3	0	1	1	0
	1.B.12.5.5	Virulence factor, BigA	0	1	1	0	0	1	0	0
	1.B.12.8.2	Auto-aggregation adhesin, Flu	1	3	1	3	2	1	1	1
	1.B.12.8.3	Adhesin, TibA	2	2	2	1	2	3	3	1
OMF	1.B.17.1.1 and 1.4	Hemolysin, drug and siderophore export protein, TolC	1	1	1	1	1	2	2	1
	1.B.17.3.9	Multidrug resistance outer membrane export protein, MdtP	1	1	1	1	1	1	1	0
TPS	1.B.20.1.3 and 1.4	Two-partner secretion exporter, CdiB and OptB	0	1	0	0	0	0	2	0
Secretin	1.B.22.1.1	PulD secretin	1	2	2	1	1	1	0	1
	1.B.22.3.3	YscC secretin	0	0	0	0	0	1	2	0
	1.B.22.4.2	HofQ secretin	1	1	1	1	1	1	1	1
	1.B.22.5.1	Phage gene IV protein secretin	0	0	0	0	1	0	0	0
OMIP	1.B.33.1.3	Outer membrane insertion complex	6	6	6	6	6	6	6	6
AT-2	1.B.40.1.2	Haemagglutinin	0	0	0	0	0	1	1	0

	1.B.40.1.3	Adhesin, YadB	0	0	0	0	0	0	1	0
	1.B.40.1.5	Adhesin, Cha	0	0	1	0	0	1	0	0
	1.B.40.2.3	Adhesin, UpaG	1	1	1	1	1	0	1	0
CsgA	1.B.48.1.1	Curli fiber subunit, CsgA	1	1	1	1	1	1	1	1
AT-3	1.B.54.1.1	Intimin/Invasin (putative autotransporter-3), Eae	2	5	4	4	4	5	4	2

Table 6. Outer membrane iron-siderophore receptors.

Family	TC ID	Receptor Specificity	559	ABU	APE	CFT	E24	UMN	O15	K12
OMR	1.B.14.1.1	Ferric coprogen, FhuE	1	1	1	1	1	1	1	1
	1.B.14.1.2	Ferrichrome, FhuA	1	1	1	1	1	1	1	1
	1.B.14.1.3	Ferric enterobactin, IroN	0	1	0	1	0	0	0	0
	1.B.14.1.4	Catecholate, CirA	1	2	2	3	1	1	2	1
	1.B.14.1.9	Catecholate, Flu	1	1	1	1	1	1	1	1
	1.B.14.1.10	Ferroxamine, FoxA	0	1	1	1	0	0	1	0
	1.B.14.1.12	Ferric citrate, FecA	1	1	0	0	1	1	0	1
	1.B.14.1.13	Ferric receptor, CfrA	1	1	0	1	0	1	1	0
	1.B.14.1.15	Ferrichrome, FcuA	0	1	0	1	0	0	0	0
	1.B.14.2.2	Heme, HemA	0	2	1	2	0	1	1	0
	1.B.14.3.1	Cobalamin, BtuB	1	1	1	1	1	1	1	1
	1.B.14.4.1	Cupric ion, OprC	0	1	1	1	0	1	0	0
	1.B.14.7.2	Ferric-yersinabactin, FyuA	2	2	2	1	1	2	1	1
	1.B.14.9.3	Ferrichrome/Aerobactin, IutA	1	1	0	1	0	1	0	0
	2.C.1.1.1	TonB	1	2	2	2	1	2	1	1
	2.C.1.2.1	TolA	3	2	2	1	2	2	2	1

Table 7. Inner membrane iron uptake systems.

Family	TC ID	Function	559	ABU	APE	CFT	E24	UMN	O15	K12
CorA	1.A.35.2.1	Divalent cation transport	2	2	2	2	2	2	2	2
ZIP	2.A.5.5.1	Pmf-mediated M^{2+} uptake	1	1	1	1	1	1	1	1
Nramp	2.A.55.3.1	Divalent cation:H^+ symport	1	1	1	1	1	1	1	1
FeoB	9.A.8.1.1 and 1.9	GTPase-coupled ferrous iron uptake	2	2	2	2	2	2	2	2
FeT	3.A.1.10.3	Ferric iron uptake	1	1	1	1	1	1	1	1
FeCT	3.A.1.14.1	Ferric iron-dicitrate uptake	4	4	0	0	4	4	0	4
	3.A.1.14.2	Ferric iron-enterobactin uptake	4	8	4	8	4	4	4	4
	3.A.1.14.3	Ferric iron-hydroxamate uptake	3	3	3	3	3	3	3	3
	3.A.1.14.8	Ferric-vibrioferrin uptake	0	2	2	2	0	1	1	0
	3.A.1.14.18	Heme uptake	0	3	3	3	0	3	3	0
	3.A.1.14.21	Heme uptake	0	2	0	2	0	0	0	0
MZT	3.A.1.15.7	Mn^{2+} and Fe^{2+} uptake	0	5	4	5	0	4	0	0
BIT	3.A.1.20.1	Iron uptake complex	0	0	0	0	0	0	3	0
Total			16	32	21	30	16	24	19	16

Table 8. Metabolite transporters unique to intracellular vs. extracellular pathogens.

Family	TCID	Function	Exclusively in 2 of 3 intracellular pathovars	Exclusively in all 3 intracellular pathovars	Exclusively in extracellular pathovars
E-ClC	1.A.13.2.3	Chloride efflux		x	
TEGT	1.A.14.2.2	Acetate transport		x	
FNT	1.A.16.1.2	Formate transport			x
OMF porin	1.B.6.1.2	Solute diffusion		x	
Tsx	1.B.10.1.1	Nucleoside-specific channel		x	
FUP	1.B.11.2.1	Type π fimbrial export		x	
	1.B.11.2.2	Putative fimbrial export		x	
	1.B.11.3.3	Type γ fimbrial export		x	
	1.B.11.3.5	Type γ fimbrial export		x	
AT-1	1.B.12.1.1**	Adhesin export		x	
	1.B.12.2.1	Pertactin (adhesin) export			x
	1.B.12.2.2**	Tracheal colonization factor export		x	
	1.B.12.4.1	Protease export		x	
	1.B.12.8.2**	Adhesin export			x
	1.B.12.8.3	Adhesin/invasin export		x	
OMF	1.B.17.3.4*	Metal cation (Ag^+)			x

		export			
OMA	1.B.18.1.2	Polysaccharide export			x
Gene IV secretin (OMS)	1.B.22.5.1*	Phage export			x
OmpL porin	1.B.35.2.2	Small molecule transport			x
AT-2	1.B.40.1.2*	Haemaglutinin export			x
	1.B.40.1.3*	Adhesin (YadB) export			x
AT-3 (Int/Inv)	1.B.54.1.1*	γ-Intimin export			x
	1.B.54.1.2**	Invasin export		x	
IIITCP (EspB/D)	1.C.36.1.1	Host pore for T3SS			x
ST-B	1.C.54.1.1*	STX pore-forming virulence factor			x
Cnt2	1.C.57.3.3*	Pore-forming virulence factor			x
Lambda holin	1.E.2.1.4*	Holin; autolysis			x
OMR	1.E.14.1.9	Holin; autolysis		x	
MFS, SP	2.A.1.1.3	Monosaccharide uptake			x
MFS; DHA1	2.A.1.2.7	Drug efflux		x	
MFS; DHA1	2.A.1.2.52	Drug efflux			x
MFS; DHA2	2.A.1.3.18	Efflux of signaling molecules	x		

MFS; OPA	2.A.1.4.2	Glycolytic intermediate uptake	x		
MFS; MHS	2.A.1.6.1*	Tricarboxylate uptake		x	
	2.A.1.6.9	Metabolite uptake		x	
MFS; ACS	2.A.1.14.2	Hexuronate uptake		x	
MFS; AAHS	2.A.1.15.2	Aromatic acid uptake			x
MFS; CP	2.A.1.17.1	Cyanate uptake			x
GPH	2.A.2.1.1	Disaccharide uptake			x
	2.A.2.3.9*	Glycoside uptake			x
APC	2.A.3.1.13	Putrescine (polyamine) uptake			x
	2.A.3.2.7	Arginine uptake; acid homeostasis	x		
	2.A.3.7.2	Glutamate uptake; acid homeostasis			x
	2.A.3.8.17	Amino acid derivative uptake			x
RND	2.A.6.2.19*	Drug export		x	
	2.A.6.2.6	Drug/autoinducer efflux	x		
Betaine/carnitine/choline symporter	2.A.15.2.3	Organoamine uptake			x
CPA1	2.A.36.3.1	Na^+:H^+ antiport		x	
CNT	2.A.41.2.10	Nucleoside uptake			x
DASS	2.A.47.3.2	Citrate uptake; succinate export		x	
	2.A.47.4.2	Arsenite/antimonite		x	

		export			
SulP	2.A.53.3.8	Bicarbonate uptake			x
TRAP-T	2.A.56.1.5**	Rhamnogalacturonide uptake		x	
	2.A.56.1.6	Sialic acid uptake		x	
DcuC	2.A.61.1.2*	Dicarboxylate antiport			x
PST	2.A.66.2.10	Lipopolysaccharide precursor export	x		
AbgT	2.A.68.1.1	p-Aminobenzoyl-glutamate uptake			x
TTT	2.A.80.1.1	Tricarboxylate uptake		x	
ABC; CUT2	3.A.1.2.1**	Ribose uptake		x	
	3.A.1.2.8	Sugar uptake			x
	3.A.1.2.11**	Sugar alcohol uptake		x	
	3.A.1.2.13	Autoinducer-2 uptake		x	
ABC; PepT	3.A.1.5.12	Rhamnose oligosaccharide uptake			x
	3.A.1.5.20	Oligopeptide uptake		x	
ABC; LPT	3.A.1.125.2	Lipoprotein export			x
ArsAB	3.A.4.1.1*	Arsenite export			x
NDH	3.D.1.9.1*	H^+/K^+ exchange (Hydrogenase)			x
NFO	3.D.6.1.2	H^+ export; NADH:ferridoxin oxido-reductase			x
PTS; Glc	4.A.1.1.3	Maltose uptake		x	
	4.A.1.1.9	Glucose uptake		x	
	4.A.1.1.10	Glucose uptake			x

PTS; Fru	4.A.2.1.3*	2-O-α-Mannosyl-D glycerate uptake			x
	4.A.2.1.6*	Mannose uptake			x
	4.A.2.1.9	Keto sugar uptake		x	
PTS; Gut	4.A.4.1.2	Sugar alcohol (glucitol) uptake			x
PTS; Gat	4.A.5.1.3	Sugar alcohol (galactitol) uptake			x
PnuC	4.B.1.1.4	Coenzyme precursor (thiamin) uptake		x	
DUF318	9.B.28.1.1*	Unknown			x
YiaW; DUF3302	9.B.32.1.2*	Unknown			x
UIT3	9.B.50.1.2**	Possible dicarboxylate uptake		x	
DUF805	9.B.124.1.1*	Unknown			x
DUF805 protein	9.B.124.1.4	Unknown		x	

Table S1. Occurrence of homologues of recognized transport proteins in the eight strains of *E. coli* included in this study. Blue boxes indicate orthologous relationships for any one protein. Yellow boxes indicate comparison scores that are too low to establish substrate specificity.

NCBI Acc. #	*559*	ABU	*APEC*	CFT	E243	UMN	O157	K12	TCID #	E-Value	Acc #	# orthologs (blue)	Substrate
YP_002401928.1	+	+	+	+	+	+	+	+	**1.A.1.4.1**	e-06	Q38998	8	Unknown
YP_006108792.1	-	-	-	-	+	-	-	-	**1.A.1.4.4**	e-07	Q94A76	1	Unknown
YP_002401751.1	+	+	+	+	+	+	+	+	**1.A.12.3.1**	e-06	P0ACA3	8	Unknown
YP_002404007.1	+	+	+	+	+	+	+	+	**1.A.12.3.1**	e-06	P0ACA3	8	Unknown
YP_002404845.1	-	-	-	-	+	-	+	-	**1.A.12.3.1**	e-07	P0ACA3	2	Unknown
YP_002403089.1	-	-	-	-	-	-	+	+	**1.A.14.2.2**	e-05	P0AAC4	2	Unknown
YP_002401281.1	-	-	-	-	+	-	-	-	**1.A.14.2.2**	e-05	P0AAC4	1	Unknown
YP_002401831.1	+	-	-	-	-	-	-	-	**1.A.14.2.2**	e-06	P0AAC4	1	Unknown
YP_002403920.1	-	+	-	-	-	-	-	-	**1.A.28.2.1**	e-05	Q9S408	1	Unknown
YP_006106303.1	+	-	-	-	+	+	-	+	**1.A.30.1.5**	e-07	Q8EAG6	4	Unknown
YP_002403828.1	+	+	+	+	+	+	+	+	**1.A.34.1.1**	e-05	P71044	8	Unknown
YP_002402711.1	+	-	-	-	-	-	-	-	**1.A.34.1.1**	e-06	P71044	1	Unknown
YP_002269341.1	+	+	+	+	+	+	+	+	**1.A.34.1.1**	e-07	P71044	8	Unknown
YP_002331260.1	+	+	+	+	+	+	+	+	**1.A.78.1.1**	e-07	Q9YS30	8	Unknown
YP_002401660.1	+	+	+	+	+	+	+	+	**1.B.12.1.1**	0.0281	Q03155	8	Unknown
YP_002403605.1	+	-	-	-	-	-	-	-	**1.B.12.1.1**	e-06	Q03155	1	Unknown
YP_002401809.1	-	+	+	+	-	-	-	-	**1.B.54.1.2**	e-05	P11922	3	Unknown
YP_006105298.1	+	-	+	-	+	+	+	+	**1.C.57.3.4**	e-06	Q7MDK6	6	Unknown
YP_002402085.1	+	+	+	+	-	+	+	-	**1.C.80.1.1**	e-05	Q8KRT4	6	Unknown
YP_002403600.1	-	-	-	-	-	-	+	-	**1.C.80.1.1**	e-05	Q8KRT4	7	Unknown
YP_002403249.1	+	-	-	-	+	+	+	+	**1.C.80.1.1**	e-06	Q8KRT4	5	Unknown
YP_002404399.1	+	-	-	-	+	-	-	+	**1.C.80.1.1**	e-06	Q8KRT4	3	Unknown
YP_002405494.1	+	-	-	-	+	+	-	-	**1.C.80.1.1**	e-06	Q8KRT4	3	Unknown
YP_002401727.1	-	+	-	+	-	-	-	-	**1.C.80.1.1**	e-06	Q8KRT4	2	Unknown
YP_002404401.1	+	-	-	-	+	-	+	+	**1.C.80.1.1**	e-07	Q8KRT4	4	Unknown

YP_002402041.1	+	-	-	-	-	-	-	-	**1.C.80.1.1**	e-07	Q8KRT4	1	Unknown
YP_002405801.1	+	-	-	-	-	-	-	-	**1.C.80.1.1**	e-07	Q8KRT4	1	Unknown
YP_002403334.1	+	+	+	+	-	+	-	-	**2.A.1.25.6**	e-05	Q9HWG8	5	Unknown
YP_002331338.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e -05	Q9HV74	8	Unknown
YP_002403932.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e -05	Q9HV74	8	Unknown
YP_006108894.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-07	Q9HV74	8	Unknown
YP_001463382.1	+	+	+	+	+	+	+	+	**2.A.37.1.1**	e-05	P0A754	8	Unknown
YP_002403325.1	+	-	-	-	+	-	-	+	**2.A.37.1.1**	e-07	P0A754	3	Unknown
YP_006106351.1	+	-	-	-	+	-	-	-	**2.A.38.4.5**	e-05	P73948	2	Unknown
YP_854266.1	+	+	+	+	+	+	+	+	**2.A.38.4.5**	e-06	P73948	8	Unknown
YP_006104401.1	+	+	+	+	+	+	+	+	**2.A.53.3.4**	e-06	B9LBX9	8	Unknown
YP_006106368.1	-	+	+	+	-	-	-	-	**2.A.56.1.3**	e-07	P44543	3	Unknown
YP_002402404.1	-	-	-	-	+	-	-	-	**2.A.66.4.2**	e-06	Q65ZW3	1	Unknown
YP_002403115.1	+	-	-	-	-	-	-	-	**2.A.66.6.2**	e-05	A3RZV8	1	Unknown
YP_002403121.1	-	+	+	+	-	-	-	-	**2.A.7.21.4**	e-07	Q3SAW5	3	Unknown
YP_002401665.1	-	-	+	+	-	-	-	-	**3.A.1.10.1**	e-07	P21408	2	Unknown
YP_002404115.1	-	-	-	-	+	-	-	-	**3.A.1.105.4**	e-07	Q4VWD0	1	Unknown
YP_002413866.1	-	+	-	+	-	-	-	-	**3.A.1.13.1**	e-05	Q8ZRP7	2	Unknown
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YP_002403116.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-05	A6QEW8	8	Unknown
YP_006105557.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-05	A6QEW8	8	Unknown
YP_002401216.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-05	A6QEW9	8	Unknown
YP_002403429.1	+	-	-	-	+	+	+	+	**3.A.1.134.7**	e-05	A6QEW8	5	Unknown
YP_002405315.1	+	-	-	-	+	-	+	+	**3.A.1.134.7**	e-05	A6QEW8	4	Unknown
YP_002404100.1	-	-	-	-	-	+	-	-	**3.A.1.134.7**	e-05	A6QEW8	1	Unknown
YP_002404789.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-06	A6QEW8	8	Unknown
YP_002404441.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-07	A6QEW8	8	Unknown
YP_002413661.1	-	+	+	+	-	+	-	-	**3.A.1.14.1**	e-05	P15028	4	Unknown

YP_002413646.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-06	P02925	8	Unknown
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YP_006107717.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-06	P02925	8	Unknown
YP_006107352.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-07	P02925	8	Unknown
YP_002327703.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-07	P02925	8	Unknown
YP_854402.1	+	+	+	+	+	+	+	+	**3.A.1.21.2**	e-06	P63391	8	Unknown
YP_002414104.1	-	-	-	-	-	+	-	-	**3.A.1.5.3**	e-05	P33590	1	Unknown
YP_002404335.1	-	-	-	-	-	+	-	-	**3.A.11.1.1**	e-05	P39695	1	Unknown
YP_002403093.1	+	+	+	+	+	+	+	+	**3.A.11.1.1**	e-06	P39694	8	Unknown
YP_002401340.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-05	P15643	4	Unknown
YP_002403852.1	-	+	-	-	-	-	-	-	**3.A.15.1.1**	e-07	P15752	1	Unknown
YP_002332057.1	-	-	+	-	-	-	-	-	**3.A.15.3.1**	e-05	Q9XD69	1	Unknown
YP_002405040.1	-	-	-	-	-	+	-	-	**3.A.15.3.1**	e-07	Q9XD69	1	Unknown
YP_002401919.1	+	+	-	-	+	-	-	-	**3.A.15.3.1**	e-07	Q9XD69	3	Unknown
YP_002404236.1	+	+	+	+	+	+	+	+	**3.A.16.1.2**	e-07	P25694	8	Unknown
YP_002404537.1	+	+	+	+	+	+	+	+	**3.A.17.1.1**	e-05	P03726	8	Unknown
YP_002401851.1	+	+	+	+	+	+	+	+	**3.A.17.1.1**	e-05	P03726	8	Unknown
YP_002403929.1	+	+	+	+	+	+	+	+	**3.A.17.1.1**	e-06	P03726	8	Unknown
YP_002402202.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-05	P38919	8	Unknown
YP_002401157.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-07	P38919	8	Unknown
YP_002401194.1	+	-	-	-	+	-	-	-	**3.A.18.1.1**	e-07	P38919	2	Unknown
YP_002413874.1	+	+	+	+	+	+	+	+	**3.A.20.1.1**	0.0007	O09012	8	Unknown
YP_002413882.1	+	+	+	+	+	+	+	+	**3.A.3.2.24**	e-05	O66938	8	Unknown
YP_001464198.1	+	+	+	+	+	+	+	+	**3.A.3.2.29**	e-07	D5C355	8	Unknown
YP_001462754.1	+	+	+	+	+	+	+	+	**3.A.5.8.1**	e-05	P14906	8	Unknown
YP_001464359.1	+	+	+	+	+	+	+	+	**3.A.5.8.1**	e-06	P14906	8	Unknown
YP_002405004.1	+	+	+	+	+	+	+	+	**3.A.5.8.1**	e-06	P14906	8	Unknown
YP_002413009.1	-	-	-	-	-	+	+	-	**3.A.6.1.1**	e-05	Q93KS8	2	Unknown
YP_002328231.1	-	-	-	-	-	+	-	-	**3.A.6.1.1**	e-07	Q9ZA78	1	Unknown
YP_002330051.1	-	-	-	-	+	-	-	-	**3.A.6.1.1**	e-07	Q9ZA78	1	Unknown

YP_002273860.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-06	P0A1L5	1	Unknown
YP_002401248.1	-	-	-	-	+	-	-	-	**3.A.7.1.1**	e-05	P13464	1	Unknown
YP_002401317.1	-	-	-	-	+	-	-	-	**3.A.7.11.1**	e-05	Q5EPC7	1	Unknown
YP_002404526.1	+	+	+	+	+	+	+	+	**3.A.7.13.2**	e-05	E9RJ10	8	Unknown
YP_006105187.1	-	-	-	-	-	+	-	-	**3.A.7.3.1**	e-07	Q91UX1	1	Unknown
YP_002403846.1	-	-	-	-	-	-	+	-	**3.A.7.9.1**	e-05	Q5ZYC1	1	Unknown
YP_002405230.1	+	+	+	-	+	+	+	+	**3.B.1.1.3**	e-07	Q9ZAA7	7	Unknown
YP_002402194.1	+	+	+	+	+	+	+	+	**3.B.1.1.5**	e-05	Q9V0A4	8	Unknown
YP_002401432.1	+	+	+	+	+	+	+	+	**3.D.1.6.3**	e-05	Q9SK66	8	Unknown
YP_002403425.1	-	+	-	+	-	+	-	-	**3.D.1.6.3**	e-06	O80800	3	Unknown
YP_002401642.1	+	-	-	+	+	+	+	+	**3.D.1.6.3**	e-07	O80800	6	Unknown
YP_002403484.1	-	-	-	-	-	-	+	-	**3.D.1.9.1**	e-06	P23481	1	Unknown
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YP_002413653.1	+	+	+	+	+	+	+	+	**3.D.5.1.1**	e-06	Q56584	8	Unknown
YP_002405784.1	+	-	-	-	-	-	-	-	**3.D.6.1.1**	e-05	Q07394	1	Unknown
NP_754326.1	+	+	+	+	+	+	+	+	**3.D.7.1.1**	e-07	P96797	8	Unknown
YP_002403323.1	+	-	-	-	-	-	+	-	**3.D.8.1.1**	e-05	Q59574	2	Unknown
YP_002271280.1	+	+	+	+	+	+	-	+	**3.D.8.1.1**	e-06	O27599	7	Unknown
YP_006105183.1	+	+	+	+	+	+	+	+	**3.D.8.1.2**	e-07	Q48941	8	Unknown
YP_002403349.1	+	+	+	+	+	+	+	+	**3.D.8.1.2**	e-07	Q48943	8	Unknown
NP_754451.1	-	-	-	-	-	+	-	-	**4.A.4.1.1**	e-07	P05706	1	Unknown
YP_006107346.1	+	+	-	+	-	-	-	-	**4.A.7.1.1**	e-05	P69822	3	Unknown
YP_002271990.1	-	-	-	+	-	-	-	-	**4.C.1.1.4**	e-05	P69451	1	Unknown
YP_006105705.1	+	-	-	-	-	-	-	-	**4.D.1.1.2**	e-05	Q54066	1	Unknown
YP_006107221.1	-	-	-	-	-	-	+	-	**4.D.1.1.2**	e-05	Q54066	1	Unknown
YP_001463948.1	-	+	-	+	-	+	+	-	**4.D.1.1.3**	e-05	P75905	4	Unknown
YP_002402356.1	+	+	+	+	+	+	+	+	**4.D.1.1.3**	e-07	P75905	8	Unknown
YP_002329079.1	-	-	-	+	-	-	-	-	**4.D.1.1.3**	e-07	P75905	1	Unknown
YP_006107887.1	-	+	-	-	-	-	-	-	**4.D.1.1.3**	e-07	P75905	1	Unknown
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YP_002402552.1	-	+	+	+	-	-	-	-	**8.A.1.1.3**	e-07	B1LPP9	3	Unknown
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YP_002404392.1	-	-	-	-	+	-	-	-	**8.A.28.1.1**	e-05	Q01484	1	Unknown
YP_002401256.1	+	+	+	+	+	+	+	+	**8.A.3.2.2**	0.0052	Q93NW3	8	Unknown
YP_002404095.1	-	+	+	+	-	+	+	-	**8.A.8.1.1**	e-05	P0AA04	5	Unknown
YP_002401568.1	+	+	+	+	+	+	+	+	**8.A.9.1.1**	e-07	Q05839	8	Unknown
YP_002401569.1	+	-	-	-	+	-	-	+	**8.A.9.1.2**	e-07	Q07837	3	Unknown
YP_002404287.1	-	+	+	+	-	-	-	-	**8.A.9.1.2**	e-07	Q07837	3	Unknown
YP_002404291.1	+	+	+	+	+	+	+	+	**9.A.10.1.1**	0.0002	P38993	8	Unknown
YP_854268.1	+	+	+	+	+	+	+	+	**9.A.10.1.1**	e-06	P38993	8	Unknown
YP_002404282.1	+	+	-	+	+	+	+	+	**9.A.10.2.3**	e-05	P31545	7	Unknown
YP_851425.1	+	+	+	+	+	+	+	+	**9.A.30.1.3**	e-06	B5UIP4	8	Unknown
YP_002404542.1	+	+	+	+	+	+	+	+	**9.A.34.1.1**	e-05	Q9KN49	8	Unknown
YP_002403861.1	+	+	+	+	+	+	-	+	**9.A.34.1.1**	e-05	Q9KN49	7	Unknown
YP_002402384.1	+	-	-	-	-	-	-	-	**9.A.34.1.1**	e-05	Q9KN52	1	Unknown
YP_002404758.1	+	-	-	-	-	-	-	-	**9.A.34.1.1**	e-05	Q9KN46	1	Unknown
YP_002405096.1	-	-	+	+	-	-	-	-	**9.A.34.1.1**	e-06	Q9KN48	2	Unknown
YP_002403754.1	+	-	-	-	-	-	-	-	**9.A.34.1.1**	e-06	Q9KN44	1	Unknown
YP_002405589.1	-	-	+	-	-	+	-	-	**9.A.34.2.1**	e-06	Q6EE17	2	Unknown
YP_002401959.1	+	+	+	+	+	+	+	+	**9.A.8.1.1**	0.7176	P33650	8	Unknown
YP_002402551.1	+	+	+	+	+	+	+	+	**9.A.8.1.1**	e-07	P33650	8	Unknown
YP_006105921.1	+	+	+	+	+	+	+	+	**9.A.8.1.3**	e-06	P73182	8	Unknown
YP_002405302.1	+	+	-	+	+	+	+	+	**9.A.8.1.6**	e-06	Q7MV19	7	Unknown
YP_002403415.1	+	+	+	+	+	+	+	+	**9.A.8.1.7**	e-05	A9P5Q3	8	Unknown
YP_858924.1	+	+	+	-	+	+	+	+	**9.A.8.1.8**	e-05	O29993	7	Unknown
YP_002412045.1	+	+	+	+	+	+	+	+	**9.A.8.1.8**	e-06	O29993	8	Unknown
YP_002402432.1	+	+	+	+	+	+	+	+	**9.B.10.1.1**	e-05	C0SP99	8	Unknown
YP_002401581.1	+	+	+	+	+	+	+	+	**9.B.102.4.1**	e-05	A0LFK9	8	Unknown
YP_002404595.1	-	+	-	-	-	-	-	-	**9.B.11.1.1**	e-05	P13332	1	Unknown
YP_006106641.1	+	+	+	+	+	+	+	+	**9.B.124.1.1**	e-06	P64592	8	Unknown

YP_002402112.1	+	+	+	+	+	+	+	+	9.B.27.2.1	e-06	P0AA60	8	Unknown
YP_006104938.1	-	-	+	-	-	-	-	-	9.B.42.1.1	e-06	P45754	1	Unknown
YP_002401927.1	-	-	-	-	-	+	-	-	9.B.97.1.2	e-05	Q286Z2	1	Unknown
YP_002401926.1	+	+	+	+	+	+	+	+	1.A.1.13.1	0	P31069	8	cation
YP_002404650.1	+	+	+	+	+	+	+	+	1.A.11.1.1	0	P69681	8	amine (ammonia)
YP_002401594.1	+	+	+	+	+	+	+	+	1.A.12.3.1	e-121	P0ACA3	8	anion
YP_002405578.1	-	+	+	+	-	-	-	-	1.A.13.2.3	0	P76481	3	anion
YP_002404184.1	+	+	+	+	+	+	+	+	1.A.14.2.1	e-118	P0AAC6	8	Unknown
YP_002401949.1	-	+	+	+	-	-	-	-	1.A.14.2.2	e-09	P0AAC4	3	putative acetate
YP_002402572.1	+	-	-	-	-	-	-	-	1.A.14.2.2	e-10	P0AAC4	1	putative acetate
YP_002401684.1	+	+	+	+	+	+	+	+	1.A.14.2.2	e-118	P0AAC4	8	putative acetate
YP_002403123.1	+	+	+	+	+	+	+	+	1.A.22.1.1	e-60	P0A742	8	nonselective
YP_002403122.1	+	+	+	+	+	+	+	+	1.A.23.1.1	0	P77338	8	nonselective
YP_002401382.1	+	+	+	+	+	+	+	+	1.A.23.1.3	0	P39285	8	nonselective
YP_002411063.1	+	+	+	+	+	+	+	+	1.A.23.2.1	e-129	P0C0S1	8	nonselective
YP_002404382.1	+	+	+	+	+	+	+	+	1.A.23.3.2	0	P75783	8	putative nonselective
YP_002404381.1	+	+	+	+	+	+	+	+	1.A.23.4.3	e-179	P0AEB5	8	putative nonselective
YP_002401828.1	+	+	+	+	+	+	+	+	1.A.23.4.5	0	P0AAT4	8	putative nonselective
YP_002401829.1	+	+	+	+	+	+	+	+	1.A.30.1.1	e-163	P09348	8	M+ cation
YP_002401156.1	+	+	+	+	+	+	+	+	1.A.30.1.1	e-175	P0AF06	8	M+ cation
YP_002405200.1	+	+	+	+	+	+	+	-	1.A.30.1.1	e-26	**P0AF06**	7	M+ cation
YP_002273337.1	-	-	-	-	-	+	-	-	1.A.30.1.1	e-47	P09348	1	M+ cation
YP_002405203.1	+	+	+	+	+	+	+	+	1.A.30.2.1	e -133	P0ABU7	8	M+ cation
YP_002402584.1	+	+	+	+	+	+	+	+	1.A.30.2.1	e-77	P0ABV2	8	M+ cation
YP_002403625.1	+	+	+	+	+	+	+	+	1.A.30.2.2	e-126	P0ABU9	8	M+ cation
YP_853458.1	+	+	+	+	+	+	+	+	1.A.30.2.2	e-67	P0ABV8	8	M+ cation
YP_006104496.1	+	+	+	+	+	+	+	+	1.A.35.1.1	e -175	P0ABI4	8	M2+ cation
YP_002271841.1	+	+	+	+	+	+	+	+	1.A.35.4.1	e-165	Q9EYX5	8	M2+ cation
YP_006104497.1	-	+	-	-	-	-	-	-	1.A.45.1.1	e-43	Q01146	1	M2+ cation
YP_002271840.1	-	+	-	-	-	-	-	-	1.A.45.1.1	e-36	Q01074	1	M2+ cation

YP_853457.1	-	+	-	-	-	-	-	-	1.A.45.1.1	e-36	Q01076	1	DNA
YP_853459.1	-	-	-	-	-	-	+	-	1.A.45.1.1	e-49	Q01076	1	DNA
YP_002403626.1	+	-	-	-	-	-	-	-	1.A.45.1.1	e-106	Q01076	1	DNA
YP_002402725.1	-	-	+	-	-	-	-	-	1.A.45.1.1	e-143	Q01076	1	DNA
YP_002405034.1	-	-	-	-	-	-	+	-	1.A.45.1.1	e-39	Q01074	1	DNA
YP_002401290.1	-	-	+	-	-	-	-	-	1.A.45.1.1	e-59	Q01146	1	DNA
YP_002402621.1	-	-	+	-	-	-	-	-	1.A.45.1.1	e-60	Q01074	1	DNA
YP_002405308.1	+	-	-	-	-	-	-	-	1.A.45.1.1	e-60	Q01074	1	DNA
YP_001463339.1	+	+	+	+	+	+	+	+	**1.A.46.3.4**	e-173	B2N0W4	8	DNA
YP_002402016.1	+	+	+	+	+	+	+	+	**1.A.62.2.1**	e-21	A0M015	8	DNA
YP_002402071.1	+	+	+	+	+	+	+	+	**1.A.62.2.1**	e-24	A0M015	8	Anions
YP_002328485.1	+	+	+	+	+	+	+	+	**1.A.8.1.1**	e-150	P0AER0	8	unknown
YP_002401391.1	-	-	-	-	+	+	-	-	**1.A.8.1.1**	e-97	P0AER0	2	unknown
YP_853015.1	+	+	+	+	+	+	+	+	**1.A.8.3.1**	e-100	P60844	8	water
YP_002403495.1	+	+	+	+	+	+	+	+	**1.B.1.1.1**	0	P02931	8	polyols
YP_002329865.1	+	+	+	+	+	+	+	+	**1.B.1.1.2**	0	P02932	8	water
YP_002412976.1	-	-	+	-	-	-	-	-	**1.B.1.1.2**	e-96	P02932	1	nonselective
YP_002402589.1	+	-	+	-	+	+	+	+	**1.B.1.1.3**	0	P06996	6	nonselective
YP_006106282.1	-	-	-	-	-	+	-	-	**1.B.1.1.3**	e-116	P06996	1	anion selective
YP_006105475.1	+	+	+	+	+	+	-	+	**1.B.1.1.3**	e-130	P06996	7	nonselective
YP_002401880.1	+	-	-	-	+	+	+	-	1.B.1.1.3	e-29	P06996	4	nonselective
YP_001463266.1	-	+	-	+	-	-	-	-	**1.B.1.1.4**	e-101	P21420	2	nonselective
YP_002403908.1	-	+	+	+	-	+	-	-	**1.B.1.1.5**	0	P07238	4	nonselective
	+	+	+	+	+	-	-	-	**1.B.1.1.5**	0	P07238	4	nonselective
	-	-	-	-	+	-	-	-	**1.B.1.1.5**	e-98	P07238	1	nonselective
	+	+	-	+	+	+	+	+	**1.B.1.2.1**	e-12	P97056	7	nonselective
YP_006108391.1	-	+	+	+	-	-	-	-	**1.B.10.1.1**	e-105	P0A927	3	nucleoside
YP_002401539.1	+	+	+	+	+	+	+	+	**1.B.10.1.1**	e-176	P0A927	8	nucleoside
YP_002271749.1	-	-	-	-	-	-	+	-	**1.B.11.2.1**	0	P07110	1	protein usher (PapC pores)

YP_006108762.1	-	+	+	+	-	+	-	-	**1.B.11.2.1**	0	P07110	4	protein usher (PapC pores)
YP_002329981.1	-	-	-	-	-	+	-	-	**1.B.11.2.1**	0	P07110	1	protein usher (PapC pores)
YP_002403604.1	+	-	-	-	+	-	-	-	**1.B.11.2.1**	0	P07110	2	protein usher (PapC pores)
NP_755465.1	-	-	-	+	-	-	-	-	**1.B.11.2.1**	0	P07110	1	protein usher (PapC pores)
YP_006106705.1	-	+	+	+	-	-	-	-	**1.B.11.2.1**	e-171	P07110	3	protein usher (PapC pores)
YP_002401808.1	+	-	-	-	+	+	-	+	**1.B.11.2.2**	0	P75750	4	protein usher (PapC pores)
YP_002269340.1	-	-	-	-	-	-	+	-	**1.B.11.2.2**	0	P75750	1	unknown
YP_002404417.1	+	-	-	-	+	-	-	-	**1.B.11.2.2**	0	P75750	2	unknown
YP_006107455.1	-	+	+	+	-	-	-	-	**1.B.11.2.2**	0	P75750	3	unknown
YP_002403394.1	+	+	+	+	+	+	-	+	**1.B.11.3.2**	e-119	P21647	7	fimbrial protein usher
YP_002271391.1	-	-	-	-	-	-	+	-	**1.B.11.3.2**	e-122	P21647	1	fimbrial protein usher
YP_002401272.1	+	-	-	-	+	-	-	+	**1.B.11.3.3**	0	P33129	3	fimbrial protein usher
YP_002268748.1	-	-	-	-	-	-	+	-	**1.B.11.3.3**	0	P33129	1	fimbrial protein usher
YP_002410914.1	-	-	-	-	-	+	-	-	**1.B.11.3.3**	0	P33129	1	fimbrial protein usher
YP_006104298.1	-	+	+	+	-	-	-	-	**1.B.11.3.3**	0	P33129	3	fimbrial protein usher
YP_002410798.1	-	-	-	-	-	+	-	-	**1.B.11.3.3**	e-115	P33129	1	fimbrial protein usher
YP_006108775.1	-	+	-	-	-	-	-	-	**1.B.11.3.3**	e-133	P33129	1	fimbrial protein usher
YP_002414540.1	-	-	-	-	-	+	-	-	**1.B.11.3.5**	0	Q8CVM4	1	fimbrial protein usher
YP_006107825.1	-	+	+	+	-	-	-	-	**1.B.11.3.5**	0	Q8CVM4	3	fimbrial protein usher
YP_002404518.1	+	-	-	-	+	-	+	+	**1.B.11.3.6**	0	P42915	4	fimbrial protein usher
YP_006108861.1	-	+	+	+	+	+	+	+	**1.B.11.3.9**	0	P30130	7	fimbrial protein usher
YP_006108861.1	+	-	-	-	-	+	+	+	**1.B.11.3.9**	0	P30130	4	fimbrial protein usher
YP_002402082.1	+	-	-	-	+	-	-	+	**1.B.11.3.9**	0	P30130	3	fimbrial protein usher
YP_002402709.1	+	+	+	+	-	+	+	-	**1.B.11.3.9**	0	P30130	6	fimbrial protein usher

YP_002404928.1	+	-	-	-	-	-	-	-	**1.B.11.3.9**	0	P30130	1	fimbrial protein usher
YP_006105297.1	-	+	-	+	-	-	-	-	**1.B.11.3.9**	e-146	P30130	2	fimbrial protein usher
YP_002273255.1	-	-	-	-	-	-	+	-	**1.B.11.3.9**	e-164	P30130	1	fimbrial protein usher
YP_006105227.1	-	+	-	-	-	-	-	-	**1.B.11.3.9**	e-167	P30130	1	fimbrial protein usher
YP_002405119.1	+	-	-	-	+	+	-	-	**1.B.11.3.9**	e-173	P30130	3	fimbrial protein usher
YP_002401420.1	+	+	+	+	+	+	+	+	**1.B.11.4.1**	e-12	P25733	8	fimbrial protein usher
YP_002404466.1	+	-	-	-	+	-	-	-	**1.B.11.4.1**	e-83	P25733	2	fimbrial protein usher
YP_002271639.1	-	-	-	-	-	-	+	+	**1.B.12.1.1**	e-50	Q03155	2	protein adhesins
YP_002403506.1	+	-	-	-	+	-	-	+	**1.B.12.1.1**	e-50	Q03155	3	protein adhesins
YP_002413282.1	-	-	-	-	-	+	-	-	**1.B.12.1.1**	e-52	Q03155	1	protein adhesins
YP_006106605.1	-	+	+	+	-	-	-	-	**1.B.12.1.1**	e-58	Q03155	3	protein adhesins
YP_006106715.1	-	+	-	+	-	-	-	-	**1.B.12.1.2**	e-103	Q7BCK4	2	protein virulence factor
YP_002401441.1	+	-	-	-	+	-	+	-	**1.B.12.1.2**	e-115	Q7BCK4	3	protein virulence factor
YP_002402351.1	+	+	-	+	+	-	-	-	**1.B.12.1.2**	e-95	Q7BCK4	4	protein virulence factor
YP_002402715.1	+	-	-	-	-	+	+	-	**1.B.12.1.3**	e-105	Q9Z625	3	protein virulence factor
YP_001462797.1	-	-	-	-	+	-	-	-	**1.B.12.1.3**	e-105	Q9Z625	1	protein virulence factor
YP_852298.1	-	-	+	-	-	+	-	-	**1.B.12.1.3**	e-27	Q9Z625	2	protein virulence factor
NP_754776.1	-	-	-	+	-	-	-	-	**1.B.12.1.3**	e-85	Q9Z625	1	protein virulence factor
YP_002402383.1	+	-	-	-	+	+	-	+	**1.B.12.2.1**	e-38	P14283	4	protein virulence factor
YP_001461547.1	-	-	-	-	+	+	-	-	**1.B.12.2.2**	e-24	Q45343	2	protein virulence factor
YP_006104584.1	-	+	+	+	-	-	-	-	**1.B.12.2.2**	e-24	Q45343	3	protein virulence factor
YP_002401499.1	+	-	-	-	-	-	-	-	**1.B.12.2.2**	e-24	Q45343	1	protein virulence factor
YP_853299.1	-	-	+	-	-	-	-	-	**1.B.12.2.3**	e-09	Q45340	1	protein virulence factor
YP_006107283.1	-	+	-	+	-	+	-	-	1.B.12.4 family			3	protein virulence factor
YP_006104502.1	-	+	+	+	-	-	-	-	1.B.12.4 family			3	protein virulence factor
YP_002404249.1	+	+	-	+	-	-	-	-	**1.B.12.4 family**			3	protein virulence factor
YP_002405532.1	+	-	-	-	-	-	-	-	**1.B.12.4 family**			1	protein virulence factor

YP_002405547.1	+	-	-	-	-	-	-	-	**1.B.12.4 family**			1	protein virulence factor
YP_002412393.1	-	-	-	-	-	+	-	-	**1.B.12.5.5**	0	P25927	1	protein virulence factor
YP_852571.1	-	-	+	-	-	-	-	-	**1.B.12.5.5**	0	P25927	1	protein virulence factor
YP_006105724.1	-	+	-	-	-	-	-	-	**1.B.12.5.5**	0	P25927	1	protein virulence factor
YP_002269864.1	-	-	-	-	-	-	+	-	**1.B.12.8.2**	0	P39180	1	Fluff Protein
YP_002415461.1	-	-	-	-	-	+	-	-	**1.B.12.8.2**	0	P39180	1	Fluff Protein
YP_002404320.1	+	-	-	-	-	+	-	-	**1.B.12.8.2**	0	P39180	2	Fluff Protein
YP_001464349.1	-	-	-	-	+	-	-	-	**1.B.12.8.2**	0	P39180	1	Fluff Protein
YP_001465820.1	-	-	-	-	+	-	-	-	**1.B.12.8.2**	0	P39180	1	Fluff Protein
YP_006105327.1	-	+	-	+	-	-	-	-	**1.B.12.8.2**	**0**	**P39180**	2	Fluff Protein
YP_006107322.1	-	+	-	+	-	-	-	-	**1.B.12.8.2**	**0**	**P39180**	2	Fluff Protein
YP_002402894.1	+	+	+	+	+	+	+	+	**1.B.12.8.2**	e-28	P39180	8	Fluff Protein
YP_001463964.1	-	-	-	-	+	+	+	+	**1.B.12.8.3**	e-12	Q9XD84	4	protein virulence factor
YP_002402354.1	+	+	+	+	+	+	+	-	**1.B.12.8.3**	e-13	Q9XD84	7	protein virulence factor
YP_006104536.1	-	+	+	+	-	-	-	-	**1.B.12.8.3**	e-31	Q9XD84	3	protein virulence factor
YP_002413240.1	-	-	-	-	-	+	+	-	**1.B.12.8.3**	e-93	Q9XD84	2	protein virulence factor
YP_002402302.1	+	+	+	+	+	+	+	+	**1.B.14.1.1**	0	P16869	8	siderophore
YP_006107439.1	-	+	+	+	-	-	+	-	**1.B.14.1.10**	e-46	Q82VI7	4	siderophore (ferrioxamine)
YP_002405811.1	+	+	-	-	+	+	-	+	**1.B.14.1.12**	0	Q9HXB2	5	siderophore (ferric citrate)
YP_002405537.1	+	+	-	+	-	+	+	-	**1.B.14.1.13**	e-109	A3ZKG8	5	cation (ferric)
YP_006104400.1	-	+	-	+	-	-	-	-	**1.B.14.1.15**	e-58	Q05202	2	siderophore
YP_002401283.1	+	-	+	-	+	-	+	+	**1.B.14.1.2**	0	P06971	5	siderophore
YP_006104308.1	-	+	-	+	-	+	-	-	**1.B.14.1.2**	0	P06971	3	siderophore
YP_006105304.1	-	+	-	+	-	-	-	-	**1.B.14.1.3**	0	O54507	2	siderophore
YP_002403435.1	+	+	+	+	+	+	+	+	**1.B.14.1.4**	0	P17315	8	protein (coclin)
YP_854314.1	-	-	+	+	-	-	-	-	**1.B.14.1.4**	e-102	P17315	2	protein (coclin)
YP_006106341.1	-	+	-	+	-	-	+	-	**1.B.14.1.4**	e-33	P17315	4	protein (coclin)

YP_002401946.1	+	+	+	+	+	+	+	+	**1.B.14.1.9**	0	P75780	8	siderophore
YP_006107909.1	-	+	+	+	-	+	+	-	**1.B.14.2.2**	0	P31499	5	siderophore
YP_006105316.1	-	+	-	+	-	-	-	-	**1.B.14.2.2**	e-144	P31499	2	siderophore (heme)
YP_002405349.1	+	+	+	+	+	+	+	+	**1.B.14.3.1**	0	P06129	8	enzyme cofactor (cobalamin)
YP_006105552.1	-	+	+	+	-	+	-	-	**1.B.14.4.1**	e-13	P72121	4	cation (Cu 2+)
YP_002403258.1	+	+	+	+	-	+	-	-	**1.B.14.7.2**	0	P0C2M9	5	protein (pesticin)
YP_002402660.1	+	+	+	-	+	+	+	+	**1.B.14.7.2**	e-26	P0C2M9	7	protein (pesticin)
YP_002405516.1	+	-	-	+	-	+	-	-	**1.B.14.9.3**	0	Q7CGN6	3	siderophore
YP_006107282.1	-	+	-	-	-	-	-	-	**1.B.14.9.3**	0	Q7CGN6	1	siderophore
YP_001464382.1	-	-	-	-	+	-	-	-	**1.B.15.1.1**	0	P77076	1	sugar
YP_006108347.1	-	+	-	-	-	-	-	-	**1.B.15.1.1**	e-84	P77076	1	sugar
YP_006108348.1	-	+	+	+	-	+	+	-	**1.B.15.1.1**	e-97	P77076	5	sugar
YP_002404408.1	+	+	+	+	+	+	+	+	**1.B.17.1.1**	0	P02930	8	nonselective
YP_002411289.1	-	-	-	-	-	+	+	-	**1.B.17.1.4**	e-19	Q92Q38	2	nonselective
YP_002404851.1	+	-	-	-	-	-	-	-	**1.B.17.3.4**	0	Q9ZHD2	1	cation
YP_002401679.1	+	+	+	+	+	+	+	+	**1.B.17.3.5**	0	P77211	8	cation
YP_002405456.1	+	+	+	+	+	+	+	+	**1.B.17.3.9**	0	P32714	8	multidrug
YP_002403417.1	+	+	+	+	+	+	+	-	**1.B.17.3.9**	e-62	P32714	7	multidrug
YP_006107341.1	-	+	+	+	-	+	-	-	**1.B.18.1.2**	0	Q03961	4	polysaccharide
YP_002403352.1	+	+	+	+	+	+	+	+	**1.B.18.3.1**	0	P0A930	8	colanic exopolysaccharide
YP_002402183.1	+	-	-	-	+	-	+	+	**1.B.18.3.1**	e-145	P0A930	4	colanic exopolysaccharide
NP_754476.1	-	-	-	+	-	-	-	+	**1.B.18.3.1**	e-92	P0A930	2	colanic exopolysaccharide
YP_006104440.1	-	+	-	-	-	-	-	-	**1.B.20.1.3**	0	Q3YL97	1	protein TPS
YP_002269854.1	-	-	-	-	-	-	+	-	**1.B.20.1.3**	e-12	Q3YL97	1	protein TPS
YP_002269765.1	-	-	-	-	-	-	+	-	**1.B.20.1.4**	0	Q8XAN8	1	protein TPS
YP_002402561.1	+	+	+	+	+	-	+	+	**1.B.21.1.1**	0	P76045	7	nonselective porin
YP_002273391.1	-	-	-	-	-	-	+	-	**1.B.21.2.1**	e-123	P76773	1	polyol porin
YP_001465359.1	-	-	-	-	+	+	-	+	**1.B.21.2.1**	e-131	P76773	3	polyol porin

YP_006107718.1	-	+	+	+	-	-	-	+	**1.B.22.1.1**	0	P15644	4	protein
YP_002404340.1	+	+	+	-	+	+	-	-	**1.B.22.1.1**	e-147	P15644	5	protein
YP_002413888.1	-	-	-	-	-	+	+	-	**1.B.22.3.2**	e-151	P35672	2	protein (invasin)
YP_002331417.1	-	-	-	-	-	-	+	-	**1.B.22.3.3**	e-72	Q01244	1	protein
YP_002404738.1	+	+	+	+	+	+	+	+	**1.B.22.4.2**	0	Q1R5P6	8	DNA
YP_001462784.1	-	-	-	-	+	-	-	-	**1.B.22.5.1**	e-13	P03666	1	Protein
YP_002401776.1	+	+	+	+	+	+	-	+	**1.B.25.1.13**	0	P75733	7	chitosugar
YP_002402844.1	+	+	+	+	+	+	-	+	**1.B.25.1.5**	0	Q47706	7	chitosugar
YP_002405410.1	+	+	+	+	+	+	+	+	**1.B.3.1.1**	0	P02943	8	sugar
YP_002405110.1	+	+	+	+	+	-	-	+	**1.B.3.1.3**	0	P26218	6	sugar derivative
YP_002402738.1	+	+	+	+	+	-	-	-	**1.B.3.1.3**	e-161	P26218	5	sugar derivative
YP_002405639.1	+	+	+	+	+	+	+	+	**1.B.33.1.2**	e-10	P46024	8	protein (OMP)
YP_002401309.1	+	+	+	+	+	+	+	+	**1.B.33.1.3**	0	P0A943	8	protein (OMP)
YP_002403806.1	+	+	+	+	+	+	+	+	**1.B.33.1.3**	0	P77774	8	protein (OMP)
YP_002403887.1	+	+	+	+	+	+	+	+	**1.B.33.1.3**	e -140	P0AC02	8	protein (OMP)
YP_002403773.1	+	+	+	+	+	+	+	+	**1.B.33.1.3**	e -160	P0A903	8	protein (OMP)
YP_002403907.1	+	+	+	+	+	+	+	+	**1.B.33.1.3**	e-53	P0A937	8	protein (OMP)
YP_006108860.1	-	+	+	+	+	+	+	+	**1.B.35.2.1**	e-144	P69856	8	anion selective porin
YP_006107305.1	-	+	-	+	-	+	-	-	**1.B.35.2.1**	e-84	P69856	3	anion selective porin
YP_002402438.1	+	+	+	+	+	+	+	+	**1.B.39.1.1**	e-93	Q8ZP50	8	nonselective porin
YP_002411290.1	-	-	-	-	-	+	+	-	**1.B.40.1.2**	e-72	Q13U92	2	protein (hemagglutinin)
YP_002269145.1	-	-	-	-	-	-	+	-	**1.B.40.1.3**	e-08	Q7CHJ4	1	protein (adhesin)
YP_851662.1	-	-	+	-	-	-	-	-	**1.B.40.1.5**	e-09	B3FNS7	1	protein (adhesin)
YP_002411296.1	-	-	-	-	-	+	-	-	**1.B.40.1.5**	e-15	B3FNS7	1	protein (adhesin)
YP_002404993.1	+	-	-	-	+	-	+	-	**1.B.40.2.3**	0	A8A667	3	trimeric adhesin
YP_006108010.1	-	+	-	+	-	-	-	-	**1.B.40.2.3**	0	A8A667	2	trimeric adhesin
YP_859203.1	-	-	+	-	-	-	-	-	**1.B.40.2.3**	0	A8A667	1	trimeric adhesin
YP_002401193.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	0	P31554	8	polysaccharide (LPS)
YP_002405677.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	0	P0ADC6	8	polysaccharide (LPS)

YP_002404571.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	e-106	P0ADW0	8	polysaccharide (LPS)
YP_002404573.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	e-128	P0A9V1	8	polysaccharide (LPS)
YP_854457.1	-	-	+	-	-	-	-	-	**1.B.42.1.2**	e-35	P0ADC6	1	polysaccharide (LPS)
YP_002404355.1	+	+	-	+	+	-	-	-	**1.B.42.1.2**	e-36	P0ADC6	4	polysaccharide (LPS)
YP_002401748.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	e-84	P0ADC1	8	polysaccharide (LPS)
YP_002404572.1	+	+	+	+	+	+	+	+	**1.B.42.1.2**	e-94	P0ADV1	8	polysaccharide (LPS)
YP_002402031.1	+	+	+	+	+	+	+	+	**1.B.46.1.1**	e-104	P61316	8	protein (lipoprotein)
YP_002402390.1	+	+	+	+	+	+	+	+	**1.B.46.1.1**	e-113	P61320	8	protein (lipoprotein)
YP_002402239.1	+	+	+	+	+	+	+	+	**1.B.48.1.1**	e-151	P0A204	8	protein (amyloid fiber)
YP_002273158.1	-	-	-	-	-	-	+	-	**1.B.54.1.1**	0	P43261	1	protein (intimin/invasin)
YP_001464361.1	-	-	-	-	+	-	-	-	**1.B.54.1.2**	e-104	P11922	1	protein (intimin/invasin)
YP_002401426.1	+	-	-	-	+	+	+	-	**1.B.54.1.2**	e-107	P11922	4	protein (intimin/invasin)
YP_006104524.1	-	+	+	+	-	-	-	-	**1.B.54.1.2**	e-109	P11922	3	protein (intimin/invasin)
YP_006106304.1	-	+	+	-	-	-	-	-	**1.B.54.1.2**	e-14	P11922	2	protein (intimin/invasin)
YP_002402403.1	+	+	+	+	+	+	+	+	**1.B.54.1.2**	e-53	P11922	8	protein (intimin/invasin)
YP_853652.1	-	-	+	-	-	-	-	-	**1.B.54.1.2**	e-67	P11922	1	protein (intimin/invasin)
YP_006106838.1	-	+	-	+	-	+	-	-	**1.B.54.1.2**	e-71	P11922	3	protein (intimin/invasin)
YP_002413033.1	-	-	-	-	-	+	+	-	**1.B.54.1.2**	e-88	P11922	2	protein (intimin/invasin)
YP_001463325.1	-	-	-	-	+	-	-	+	**1.B.54.1.2**	e-89	P11922	2	protein (intimin/invasin)
YP_002414820.1	-	-	-	-	-	+	-	-	**1.B.54.1.2**	e-96	P11922	1	protein (intimin/invasin)
YP_006104455.1	-	+	-	+	-	-	-	-	**1.B.54.1.5**	e-16	Q7W286	2	putative intimin/invasin
YP_002402227.1	+	+	+	+	+	-	+	+	**1.B.55.1.1**	0	P69434	7	putative intimin/invasin
YP_002402099.1	+	+	+	+	+	+	+	+	**1.B.6.1.1**	0	P0A910	8	anion selective porin
YP_006107096.1	-	+	+	+	-	-	-	-	**1.B.6.1.2**	e-11	P13794	3	nonselective porin
YP_002401832.1	+	+	+	+	+	+	+	+	**1.B.6.1.2**	e-12	P13794	8	nonselective porin
YP_001464142.1	-	-	-	-	+	-	-	-	**1.B.6.1.2**	e-12	P13794	1	nonselective porin
YP_002404302.1	+	-	-	-	-	-	-	-	**1.B.6.1.2**	e-13	P13794	1	nonselective porin
YP_002404936.1	+	+	+	+	+	+	+	+	**1.B.6.1.3**	e -20	P65593	8	putative porin
YP_002403896.1	+	+	+	+	+	+	+	+	**1.B.6.1.4**	e-15	Q8KWW6	8	nonselective porin
YP_002402760.1	+	-	+	-	+	+	+	-	**1.B.6.2.1**	e-19	P0A917	5	nonselective porin

YP_002270304.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-19	P0A917	1	nonselective porin
YP_002271473.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-19	P0A917	1	nonselective porin
YP_002270238.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-20	P0A917	1	nonselective porin
YP_002401907.1	+	-	-	-	-	-	+	-	**1.B.6.2.1**	e-20	P0A917	2	nonselective porin
YP_002271095.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-21	P0A917	1	nonselective porin
YP_002271189.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-21	P0A917	1	nonselective porin
YP_002271413.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-21	P0A917	1	nonselective porin
YP_002273579.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-21	P0A917	1	nonselective porin
YP_002269436.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-22	P0A917	1	nonselective porin
YP_002328284.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-22	P0A917	1	nonselective porin
YP_002328598.1	-	-	-	-	-	-	+	-	**1.B.6.2.1**	e-22	P0A917	1	nonselective porin
YP_002402490.1	+	-	+	-	-	+	-	-	**1.B.6.2.1**	e-22	P0A917	3	nonselective porin
YP_002402169.1	+	+	-	+	-	-	-	-	**1.B.6.2.1**	e-22	P0A917	3	nonselective porin
YP_852551.1	-	-	+	-	-	-	-	-	**1.B.6.2.1**	e-22	P0A917	1	nonselective porin
NP_753376.1	-	-	-	+	-	-	-	-	**1.B.6.2.1**	e-23	P0A917	1	nonselective porin
YP_002401955.1	+	+	+	+	+	+	+	+	**1.B.6.2.1**	e-88	P0A917	8	nonselective porin
YP_002271766.1	-	-	-	-	-	-	+	-	**1.B.6.2.2**	e-19	Q0WCZ9	1	unknown
YP_002330699.1	-	-	-	-	-	-	+	-	**1.B.6.2.2**	e-24	Q0WCZ9	1	unknown
YP_002405688.1	+	-	-	-	-	-	-	-	**1.B.6.2.9**	e-08	G4CMU4	1	unknown
YP_002403610.1	+	-	+	-	+	+	+	+	**1.B.9.1.1**	0	P10384	6	lipids (FFA) porin
YP_006106711.1	-	+	-	+	-	-	-	-	**1.B.9.1.1**	0	P10384	2	lipids (FFA) porin
YP_006105201.1	-	+	-	+	-	-	-	-	**1.C.1.2.2**	e-23	P02978	2	cation channel (coclin)
YP_006104265.1	-	+	-	-	-	-	-	-	**1.C.1.4.1**	e-08	P04419	1	nonselective channel
YP_006104263.1	-	+	-	-	-	-	-	-	**1.C.1.4.1**	e-23	P09883	1	nonselective channel
YP_851309.1	-	-	+	-	-	-	-	-	**1.C.1.4.1**	e-27	P09883	1	nonselective channel
YP_002412216.1	-	-	-	-	-	+	+	+	**1.C.10.1.1**	e-159	P77335	3	nonselective porin
YP_006105538.1	-	+	-	+	-	-	-	-	**1.C.10.1.1**	e-45	P77335	2	nonselective porin
YP_006108795.1	-	+	-	-	-	-	-	-	**1.C.11.1.3**	0	P09983	1	cation selective porin
YP_006108796.1	-	+	-	+	-	-	-	-	**1.C.11.1.3**	e-72	P09983	2	cation selective porin
YP_002273154.1	-	-	-	-	-	-	+	-	**1.C.36.1.1**	e-168	O69413	1	protein (T3Pore)

YP_002273153.1	-	-	-	-	-	-	+	-	**1.C.36.1.1**	e-80	Q8XC86	1	protein (T3Pore)
YP_002414816.1	-	-	-	-	-	+	-	-	**1.C.36.3.1**	e-12	Q03945	1	protein (T3Pore)
YP_002414818.1	-	-	-	-	-	+	-	-	**1.C.36.3.2**	e-24	Q56026	1	protein (T3Pore)
YP_002273155.1	-	-	-	-	-	-	+	-	**1.C.36.5.1**	e-09	Q7BVH7	1	protein (T3Pore)
YP_002271220.1	-	-	-	-	-	-	+	-	**1.C.54.1.1**	e-23	P69178	1	protein (shiga toxin)
YP_002271796.1	-	-	-	-	-	-	+	-	**1.C.54.1.1**	e-24	P69178	1	protein (shiga toxin)
YP_006108791.1	-	+	-	-	-	-	-	-	**1.C.57.3.2**	0	Q8KTM3	1	putative nonselective
YP_002270020.1	-	-	-	-	-	-	+	-	**1.C.57.3.3**	e-17	Q47107	1	putative nonselective
YP_002269764.1	-	-	-	-	-	-	+	-	**1.C.75.1.1**	e-34	P15320	1	nonselective
YP_006104441.1	-	+	-	+	-	-	-	-	**1.C.75.1.1**	e-41	P15320	2	nonselective
YP_002271750.1	-	-	-	-	-	-	+	-	**1.C.80.1.1**	e-08	Q8KRT4	1	nonselective
YP_001463678.1	-	-	-	-	+	-	-	-	**1.C.80.1.1**	e-08	Q8KRT4	1	nonselective
YP_006107264.1	-	+	-	-	-	-	-	-	**1.C.80.1.1**	e-08	Q8KRT4	1	nonselective
YP_002332069.1	-	-	-	-	-	+	+	+	**1.C.80.1.1**	e-09	Q8KRT4	3	nonselective
NP_757241.1	-	-	-	+	-	-	-	-	**1.C.80.1.1**	e-10	Q8KRT4	1	nonselective
YP_002404416.1	+	-	-	-	+	-	-	+	**1.C.80.1.1**	e-11	Q8KRT4	3	nonselective
YP_002271743.1	-	-	-	-	-	-	+	-	**1.C.80.1.1**	e-11	Q8KRT4	1	nonselective
YP_859945.1	-	-	+	-	-	-	-	-	**1.C.80.1.1**	e-11	Q8KRT4	1	nonselective
NP_755467.1	-	-	-	+	-	-	-	-	**1.C.80.1.1**	e-13	Q8KRT4	1	nonselective
YP_006108764.1	-	+	-	-	-	-	-	-	**1.C.80.1.1**	e-13	Q8KRT4	1	nonselective
YP_002404930.1	+	-	-	-	-	-	-	-	**1.C.80.1.1**	e-13	Q8KRT4	1	nonselective
YP_002273032.1	-	-	-	-	-	-	+	-	**1.C.80.1.1**	e-14	Q8KRT4	1	nonselective
YP_006107454.1	-	+	+	+	-	-	-	-	**1.C.80.1.1**	e-14	Q8KRT4	3	nonselective
NP_757036.1	-	-	-	+	-	-	-	-	**1.C.80.1.1**	e-15	Q8KRT4	1	nonselective
YP_002414017.1	-	-	-	-	-	+	-	-	**1.C.80.1.1**	e-18	Q8KRT4	1	nonselective
YP_854256.1	-	-	+	-	-	-	-	-	**1.C.80.1.1**	e-18	Q8KRT4	1	nonselective
YP_006105224.1	-	+	-	+	-	-	-	-	**1.C.80.1.1**	e-20	Q8KRT4	2	nonselective
YP_002402825.1	+	+	+	+	+	+	+	+	**1.C.82.1.1**	e-52	Q9ZK21	8	nonselective
YP_002403628.1	+	-	-	-	-	-	-	-	**1.C.87.1.1**	e-41	P35837	1	DNA
YP_853461.1	-	-	+	-	-	-	-	-	**1.C.87.1.1**	e-74	P35837	1	DNA

YP_852558.1	-	-	+	-	-	-	-	-	**1.C.98.1.1**	e-18	Q46670	1	CdtB subunit
YP_852556.1	-	-	+	-	-	-	-	-	**1.C.98.1.1**	e-40	Q46668	1	CdtB subunit
YP_852557.1	-	-	+	-	-	-	-	-	**1.C.98.1.1**	e-77	Q46669	1	CdtB subunit
YP_002412159.1	-	-	-	-	-	+	-	-	**1.E.1.1.1**	e-90	P27360	1	protein holin (murein hydrolase)
YP_002402784.1	+	+	+	+	+	+	-	+	**1.E.1.1.2**	e-33	P77237	7	protein holin
YP_002401881.1	+	-	-	-	-	-	-	+	**1.E.1.1.2**	e-34	P77237	2	protein holin
NP_755064.1	-	-	-	+	+	+	-	+	**1.E.1.1.2**	e-35	P77237	4	protein holin
YP_002269671.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-12	O48430	1	protein holin
YP_002402144.1	+	+	+	+	-	+	+	-	**1.E.1.1.3**	e-20	O48430	6	protein holin
YP_002270281.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-20	O48430	1	protein holin
YP_002271496.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-20	O48430	1	protein holin
YP_002271791.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-20	O48430	1	protein holin
YP_002270568.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-21	O48430	1	protein holin
YP_002270628.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-21	O48430	1	protein holin
YP_002328258.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-21	O48430	1	protein holin
YP_002328796.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-21	O48430	1	protein holin
YP_002269991.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-22	O48430	1	protein holin
YP_002271119.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-22	O48430	1	protein holin
YP_002328577.1	-	-	-	-	-	-	+	-	**1.E.1.1.3**	e-33	O48430	1	protein holin
YP_002403419.1	+	+	+	+	+	+	+	+	**1.E.14.1.4**	e-56	F4V3T5	8	protein holin
YP_006108535.1	-	+	+	+	-	-	-	-	**1.E.14.1.9**	e-58	E7UC95	3	protein holin (autolysin)
YP_853473.1	-	-	+	-	-	-	-	-	**1.E.2.1.1**	e-55	P03705	1	protein holin
YP_002403164.1	+	-	-	-	-	-	-	-	**1.E.2.1.4**	e-08	Q9RIH4	1	protein holin
YP_002411737.1	-	-	-	-	-	+	-	-	**1.E.3.1.1**	e-15	P51773	1	protein holin
YP_852011.1	-	-	+	-	-	-	+	-	**1.E.3.1.1**	e-45	P51773	2	protein holin
NP_752886.1	-	-	-	+	-	-	-	-	**1.E.7.1.3**	e-11	Q54418	1	protein holin (nuclease)
YP_002404208.1	+	+	+	+	+	+	+	+	**2.A.1.1.1**	0	P0AEP1	8	sugar
YP_002401184.1	+	+	+	+	+	+	+	+	**2.A.1.1.114**	0	P31679	8	sugar
YP_002403001.1	+	+	+	+	+	+	+	+	**2.A.1.1.115**	0	P76230	8	sugar

YP_002404104.1	+	+	+	+	+	+	+	+	**2.A.1.1.2**	0	P0AE24	8	sugar
YP_002405405.1	+	-	-	-	+	-	+	+	**2.A.1.1.3**	0	P0AGF4	4	sugar
YP_002402995.1	+	+	+	+	+	+	+	+	**2.A.1.1.92**	0	P38055	8	sugar
YP_002404037.1	+	+	-	+	+	+	-	+	**2.A.1.1.95**	0	Q46909	6	sugar
YP_002405261.1	+	+	+	+	-	-	-	-	**2.A.1.1.95**	e-16	Q46909	4	sugar
YP_853986.1	-	-	+	-	-	-	-	-	**2.A.1.1.95**	e-166	Q46909	1	sugar
YP_002404229.1	+	+	+	+	+	+	+	+	**2.A.1.10.1**	0	P0AFF4	8	nucleoside
YP_002403708.1	+	+	+	+	-	-	-	+	**2.A.1.10.2**	0	P45562	5	nucleoside
YP_002403383.1	+	+	+	+	+	+	+	+	**2.A.1.10.4**	0	P76417	8	nucleoside
YP_002404931.1	+	+	+	+	+	+	+	+	**2.A.1.11.3**	e-177	P37662	8	di carboxylate
YP_002404590.1	+	+	+	+	+	+	+	+	**2.A.1.12.1**	0	P41036	8	sugar derivative
YP_006107307.1	-	+	-	+	-	+	-	-	**2.A.1.12.1**	0	P41036	3	sugar derivative
YP_002415427.1	-	-	-	-	-	+	-	+	**2.A.1.12.1**	e-76	P41036	2	sugar derivative
YP_002404055.1	+	+	+	+	+	+	+	+	**2.A.1.14.1**	e-171	P42237	8	di carboxylate
YP_002404499.1	+	+	+	+	+	+	+	+	**2.A.1.14.14**	0	Q8FDB7	8	di carboxylate
YP_002404464.1	+	+	+	+	+	+	+	+	**2.A.1.14.2**	0	P0AA78	8	di carboxylate
NP_756357.1	-	-	-	+	-	-	-	-	**2.A.1.14.2**	e-103	P0AA78	1	di carboxylate
YP_006108681.1	-	+	+	+	-	-	-	-	**2.A.1.14.2**	e-120	P0AA78	3	di carboxylate
YP_002411759.1	-	-	-	-	-	+	-	-	**2.A.1.14.2**	e-99	P0AA78	1	di carboxylate
YP_002405861.1	+	-	-	-	+	-	+	+	**2.A.1.14.33**	0	P39398	4	di carboxylate
YP_002405343.1	+	+	+	+	+	-	-	-	**2.A.1.14.33**	e-132	P39398	4	di carboxylate
YP_006106617.1	-	+	+	+	-	+	+	+	**2.A.1.14.35**	0	P76470	6	unknown
YP_002271658.1	-	-	-	-	-	-	+	+	**2.A.1.14.35**	e-95	P76470	2	unknown
YP_002405080.1	+	+	+	+	+	+	-	+	**2.A.1.14.7**	0	P0AA76	7	di carboxylate
YP_002415545.1	-	-	-	-	-	+	-	-	**2.A.1.14.9**	0	Q9RPV1	1	aromatic carboxylate
YP_001463490.1	-	-	-	-	+	-	+	-	**2.A.1.15.1**	e-82	Q51955	2	aromatic acid
YP_002402918.1	+	+	+	+	+	+	+	+	**2.A.1.15.12**	0	P76197	8	putative aromatic acid
YP_002402919.1	+	+	+	+	+	+	+	+	**2.A.1.15.13**	0	P76198	8	putative aromatic acid

YP_002401484.1	+	-	-	-	+	+	+	+	**2.A.1.15.2**	e-180	P77589	5	aromatic acid
YP_002401472.1	+	-	-	-	+	+	+	+	**2.A.1.17.1**	e-165	P17583	5	anion
YP_002403017.1	+	+	+	+	+	+	+	+	**2.A.1.17.3**	0	P76242	8	putative anion
YP_002401523.1	+	+	+	+	+	+	+	+	**2.A.1.2.14**	0	P23910	8	sugar
YP_002402732.1	+	+	+	+	+	+	+	+	**2.A.1.2.15**	0	P31122	8	sugar
YP_002401983.1	+	+	+	+	+	+	+	+	**2.A.1.2.19**	0	P0AEY8	8	multidrug
YP_002402255.1	+	+	+	+	+	+	-	+	**2.A.1.2.20**	0	P25744	7	multidrug
YP_002402266.1	+	+	+	+	+	+	+	+	**2.A.1.2.21**	0	P69367	8	multidrug
YP_002405100.1	+	+	+	+	+	+	+	+	**2.A.1.2.22**	0	P31462	8	specific drug
YP_002405051.1	+	+	+	+	+	+	-	+	**2.A.1.2.26**	0	P0ADL1	7	nucleoside
YP_002411081.1	-	-	-	-	-	+	+	-	**2.A.1.2.26**	e-66	P0ADL1	2	nucleoside
YP_002405849.1	+	-	-	-	+	+	+	+	**2.A.1.2.52**	0	P39386	5	multidrug
YP_002402744.1	+	+	+	+	+	+	+	+	**2.A.1.2.55**	0	P31126	8	peptide
YP_002401554.1	+	+	+	+	+	+	+	+	**2.A.1.2.60**	0	P77726	8	unknown
YP_002402890.1	+	+	+	+	+	+	+	+	**2.A.1.2.62**	0	P37597	8	unknown
YP_002402887.1	+	+	+	+	+	+	+	+	**2.A.1.2.65**	0	P77389	8	unknown
YP_002405715.1	+	-	-	-	-	-	-	-	**2.A.1.2.68**	0	P02980	1	specific drug
YP_002403464.1	+	+	+	+	+	+	+	+	**2.A.1.2.7**	0	P28246	8	multidrug
YP_002270349.1	-	-	-	-	-	-	+	-	**2.A.1.2.7**	e-34	P28246	1	multidrug
YP_006105663.1	-	+	+	+	-	-	-	-	**2.A.1.2.7**	e-35	P28246	3	multidrug
YP_002405064.1	+	+	+	+	+	+	+	+	**2.A.1.2.9**	e-163	P31442	8	multidrug
YP_002401207.1	+	-	-	-	+	-	-	+	**2.A.1.20.1**	0	P31675	3	sugar
YP_002403451.1	+	+	+	+	+	+	+	+	**2.A.1.20.2**	0	P33026	8	sugar
YP_002405047.1	+	-	-	-	+	+	-	+	**2.A.1.20.3**	0	P31436	4	sugar
YP_002415416.1	-	-	-	-	-	+	-	-	**2.A.1.21.11**	e-23	D3Q871	1	unknown
YP_002401563.1	+	+	+	+	+	+	+	+	**2.A.1.25.2**	0	P0AE16	8	cofactor substrate
YP_002402038.1	+	+	+	+	+	+	+	+	**2.A.1.26.1**	0	P21503	8	unknown
YP_002403830.1	+	+	+	+	+	+	+	+	**2.A.1.27.1**	0	Q47142	8	aromatic
YP_002403061.1	+	+	+	+	+	+	+	+	**2.A.1.3.17**	0	P76269	8	specific drug
YP_002403545.1	+	+	+	+	+	+	+	+	**2.A.1.3.17**	e-31	P76269	8	specific drug

YP_852504.1	-	-	+	+	-	-	-	-	**2.A.1.3.18**	e-70	Q9KIH3	2	multidrug
YP_002403949.1	+	+	+	+	+	+	+	+	**2.A.1.3.2**	0	P0AEJ0	8	multidrug
YP_002403366.1	+	+	+	+	+	+	+	+	**2.A.1.3.26**	0	P36554	8	multidrug
YP_002403676.1	+	+	+	+	+	+	+	+	**2.A.1.3.36**	0	C5W789	8	multidrug
YP_002403677.1	+	+	+	+	+	+	+	+	**2.A.1.3.36**	0	C5W790	8	multidrug
YP_002405147.1	+	+	+	+	+	+	+	+	**2.A.1.3.51**	0	P31474	8	unknown
YP_002401608.1	+	+	+	+	+	+	+	+	**2.A.1.35.1**	0	P52067	8	specific drug
YP_002405358.1	+	+	+	+	+	+	+	+	**2.A.1.36.1**	0	P43531	8	aromatic amine
YP_002403944.1	+	+	+	+	+	+	+	-	**2.A.1.36.3**	0	P76628	7	unknown
YP_002401699.1	+	+	+	+	+	+	+	+	**2.A.1.38.1**	e-163	P24077	8	siderophore
YP_002405055.1	+	+	+	+	+	+	+	+	**2.A.1.4.1**	0	P0AGC0	8	anion
YP_854265.1	-	-	+	+	-	-	-	-	**2.A.1.4.2**	0	P12681	2	anion
YP_002403513.1	+	+	+	+	+	+	+	+	**2.A.1.4.3**	0	P08194	8	anion
YP_002405056.1	+	+	+	+	+	+	+	+	**2.A.1.4.4**	0	P09836	8	anion
YP_002269002.1	-	-	-	-	-	-	+	-	**2.A.1.4.4**	e-96	P09836	1	anion
YP_002404098.1	+	+	+	+	+	+	+	+	**2.A.1.42.1**	0	P39196	8	lysophospholipid
YP_002404099.1	+	+	+	+	+	+	+	+	**2.A.1.42.2**	e-176	Q89SS6	8	lysophospholipid
YP_002413287.1	-	-	-	-	-	+	+	-	**2.A.1.46.5**	e-52	C2UR80	2	unknown
YP_002403588.1	+	+	+	-	-	+	+	+	**2.A.1.46.6**	0	P77549	6	unknown
YP_001463667.1	-	-	-	-	+	-	-	-	**2.A.1.46.6**	e-175	P77549	1	unknown
YP_002404823.1	+	+	+	+	+	+	+	+	**2.A.1.46.7**	0	P37621	8	unknown
YP_002401474.1	+	+	+	+	+	+	+	+	**2.A.1.5.1**	0	P02920	8	sugar
YP_001464380.1	-	-	-	-	+	-	-	-	**2.A.1.5.2**	0	P16552	1	sugar
YP_002403671.1	+	-	-	-	+	+	-	-	**2.A.1.5.3**	0	P30000	3	sugar
YP_002405843.1	+	+	+	+	+	+	-	+	**2.A.1.51.2**	e-162	D6IHN4	7	unknown
YP_002273858.1	-	-	-	-	-	-	+	-	**2.A.1.51.2**	e-174	D6IHN4	1	unknown
YP_002405255.1	+	+	-	+	+	+	+	+	**2.A.1.52.1**	0	P32135	7	unknown
YP_859960.1	-	-	+	-	-	-	-	-	**2.A.1.52.1**	e-65	P32135	1	unknown
YP_002404040.1	+	+	+	+	+	+	+	+	**2.A.1.52.2**	0	F4TJX1	8	unknown
YP_006108420.1	-	+	+	+	-	-	+	-	**2.A.1.6.1**	e-60	P16482	4	tri carboxylate

YP_002404899.1	+	+	+	+	+	+	+	+	**2.A.1.6.10**	0	P37643	8	unknown
YP_002403883.1	+	+	+	+	+	+	+	+	**2.A.1.6.2**	0	P0AEX3	8	dicarboxylate
YP_002405480.1	+	+	+	+	+	+	+	+	**2.A.1.6.4**	0	P0C0L7	8	nonspecific
YP_002403260.1	+	+	+	+	+	+	+	+	**2.A.1.6.6**	0	P76350	8	monocarboxylate
YP_002405262.1	+	+	+	+	-	-	-	-	**2.A.1.6.6**	e-85	P76350	4	monocarboxylate
YP_002402753.1	+	+	-	+	+	+	+	-	**2.A.1.6.9**	0	P77228	6	unknown
YP_006108502.1	-	+	+	+	-	-	-	-	**2.A.1.6.9**	e-60	P77228	3	unknown
YP_002401986.1	+	+	+	+	+	+	+	+	**2.A.1.60.2**	0	P75810	8	sugar derivative
YP_002404067.1	+	+	+	+	+	+	+	+	**2.A.1.7.1**	0	P11551	8	sugar
YP_002405788.1	+	+	-	+	-	-	-	-	**2.A.1.7.5**	0	Q8XEV7	3	sugar derivative
YP_002402406.1	+	+	+	+	+	+	+	+	**2.A.1.8.1**	0	P10903	8	anion (nitrate/nitrite)
YP_002402675.1	+	+	+	+	+	+	+	+	**2.A.1.8.10**	0	P37758	8	anion
YP_002405291.1	+	+	+	+	+	+	+	+	**2.A.10.1.2**	e-124	P0A712	8	monocarboxylate
YP_002273395.1	-	-	-	-	-	-	+	-	**2.A.102.2.2**	e-09	Q2BM66	1	aromatic (4-toulene sulfonate)
YP_002403593.1	+	+	+	+	+	+	+	+	**2.A.102.3.1**	e-142	P0AD30	8	unknown
YP_002401225.1	+	+	+	+	+	+	+	+	**2.A.103.1.1**	0	P0ABG4	8	polysaccharide (murein)
YP_002401741.1	+	+	+	+	+	+	+	+	**2.A.103.1.2**	e-164	P0ABG7	8	polysaccharide (murein)
YP_002403934.1	+	+	+	+	+	+	+	+	**2.A.104.1.1**	e-72	A8ANM6	8	amino acid (L alanine)
YP_002405555.1	+	+	+	+	+	+	+	+	**2.A.13.1.1**	0	P0ABN5	8	dicarboxylate
YP_002405492.1	+	+	+	+	-	+	+	+	**2.A.13.1.2**	0	P0ABN9	7	dicarboxylate
YP_002404994.1	+	+	+	+	+	+	+	+	**2.A.14.1.1**	0	P33231	8	monocarboxylate
YP_002404346.1	+	+	+	+	+	+	-	+	**2.A.14.1.2**	0	Q46839	7	monocarboxylate
YP_002401440.1	+	+	+	+	+	+	+	+	**2.A.15.1.4**	0	P0ABC9	8	amine
YP_002405797.1	+	-	-	-	+	+	-	-	**2.A.15.1.9**	e-169	Q6F754	3	amine
YP_002401179.1	+	+	+	+	+	+	+	+	**2.A.15.2.1**	0	P31553	8	amine
YP_859962.1	-	-	+	-	-	-	-	-	**2.A.15.2.2**	e-68	B4EY22	1	amine
YP_002403030.1	+	-	-	-	+	+	+	+	**2.A.15.2.3**	0	P0ABD2	5	unknown
YP_002402636.1	+	+	+	+	+	+	+	+	**2.A.16.1.1**	e-178	P25396	8	anion
YP_006107836.1	-	+	-	+	-	-	-	-	**2.A.16.2.2**	e-09	Q5EAK4	2	dicarboxylate

YP_002405210.1	+	+	+	+	+	+	+	+	**2.A.16.2.2**	e-25	Q5EAK4	8	dicarboxylate
YP_002402864.1	+	+	+	+	+	+	+	+	**2.A.17.1.2**	0	P77304	8	peptide
YP_002404869.1	+	+	+	+	+	+	+	+	**2.A.17.1.3**	0	P36837	8	peptide
YP_002401799.1	+	+	+	+	+	+	+	+	**2.A.17.1.4**	0	P75742	8	peptide
YP_002405500.1	+	+	+	+	+	+	+	+	**2.A.17.1.5**	0	P39276	8	peptide
YP_002402399.1	+	+	+	+	+	+	+	+	**2.A.19.1.1**	e-166	P31801	8	cation (Ca 2+)
YP_002404568.1	+	+	+	+	+	+	+	+	**2.A.19.5.1**	e-149	P45394	8	cation (Ca 2+)
YP_002405489.1	+	-	-	-	+	+	+	+	**2.A.2.1.1**	0	A7ZUZ0	5	sugar
YP_002402845.1	+	+	+	+	+	+	+	+	**2.A.2.3.1**	0	P0CE45	8	monocarboxylate
YP_002405045.1	+	+	+	+	+	+	+	+	**2.A.2.3.4**	0	P31435	8	sugar
YP_002414739.1	-	-	-	-	-	+	+	-	**2.A.2.3.4**	e-72	P31435	2	sugar
YP_001465361.1	-	-	-	-	+	+	+	+	**2.A.2.3.9**	0	P32137	4	unknown
YP_001465360.1	-	-	-	-	+	+	+	+	**2.A.2.3.9**	e-179	P32137	4	unknown
YP_006104421.1	-	+	-	+	-	-	-	-	**2.A.2.5.1**	e-153	Q93KC2	2	sugar derivative
YP_002404866.1	+	+	+	+	+	+	+	+	**2.A.20.1.1**	0	P0AFJ7	8	anion
YP_002404363.1	+	+	+	+	+	+	+	+	**2.A.20.1.2**	0	P43676	8	anion
YP_002404624.1	+	+	+	+	+	+	+	+	**2.A.21.1.1**	0	P16256	8	enzyme cofactor (B5)
YP_002402218.1	+	+	+	+	+	+	+	+	**2.A.21.2.1**	0	P07117	8	amino acid (proline)
YP_002405070.1	+	+	+	+	+	+	+	+	**2.A.21.3.9**	e -74	A8H019	8	sugar
YP_002405443.1	+	+	+	+	+	+	+	+	**2.A.21.7.2**	0	P32705	8	monocarboxylate
YP_002401677.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e -18	Q9HV74	8	unknown
YP_002404754.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-10	Q9HV74	8	unknown
YP_002404838.1	+	-	-	-	-	-	-	-	**2.A.21.9.1**	e-11	Q9HV74	1	unknown
YP_002403367.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-13	Q9HV74	8	unknown
YP_002405481.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-13	Q9HV74	8	unknown
YP_002405902.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-15	Q9HV74	8	unknown
YP_854267.1	-	-	+	+	-	-	-	-	**2.A.21.9.1**	e-16	Q9HV74	2	unknown
YP_002405249.1	+	+	+	+	+	+	+	+	**2.A.21.9.1**	e-19	Q9HV74	8	unknown
YP_006108520.1	-	+	+	+	-	-	-	-	**2.A.21.9.1**	e-19	Q9HV74	3	unknown
YP_002404853.1	+	-	-	-	-	-	-	-	**2.A.21.9.1**	e-21	Q9HV74	1	unknown

YP_002405378.1	+	+	+	+	+	+	+	-	**2.A.21.9.1**	e-23	Q9HV74	7	unknown
YP_002273636.1	-	-	-	-	-	-	+	-	**2.A.21.9.1**	e-23	Q9HV74	1	unknown
YP_006106592.1	-	+	+	+	-	+	-	+	**2.A.21.9.1**	e-32	Q9HV74	5	unknown
YP_002402330.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-08	Q93N33	8	unknown
YP_002403679.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-09	Q93N33	8	unknown
YP_002403240.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-11	Q93N33	8	unknown
YP_002403850.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-12	Q93N33	8	unknown
YP_002401527.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-13	Q93N33	8	unknown
YP_002405293.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-13	Q93N33	8	unknown
YP_002402838.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-15	Q93N33	8	unknown
YP_006108802.1	-	+	-	+	-	-	-	-	**2.A.21.9.2**	e-15	Q93N33	2	unknown
YP_002403498.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-16	Q93N33	8	unknown
YP_002404582.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-18	Q93N33	8	unknown
YP_002402195.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-19	Q93N33	8	unknown
YP_002404712.1	+	+	+	+	+	+	+	+	**2.A.21.9.2**	e-20	Q93N33	8	unknown
YP_006107064.1	-	+	+	+	+	+	+	+	**2.A.21.9.2**	e-21	Q93N33	7	unknown
YP_002405453.1	+	+	+	+	+	+	+	+	**2.A.23.1.1**	0	P21345	8	AA & dicarboxylate
YP_002411569.1	-	-	-	-	-	+	+	-	**2.A.23.1.2**	e-77	P24943	2	AA & dicarboxylate
YP_002402955.1	+	+	+	+	+	+	+	+	**2.A.23.1.4**	e-93	P54596	8	amino acid
YP_002404905.1	+	+	+	+	+	+	+	+	**2.A.23.1.7**	0	P0A830	8	dicarboxylate
YP_002404460.1	+	+	+	+	+	+	+	+	**2.A.23.4.1**	e-177	P0AGE4	8	amino acid
YP_002401150.1	+	+	+	+	+	+	+	+	**2.A.25.1.5**	e-96	Q45068	8	amino acid
YP_002401529.1	+	+	+	+	+	+	+	+	**2.A.26.1.2**	e-158	P25185	8	amino acid
YP_002405041.1	+	+	+	+	+	+	+	+	**2.A.27.1.1**	e-178	P0AER8	8	amino acid
YP_002405708.1	+	-	-	-	-	-	-	-	**2.A.27.1.1**	e-28	P0AER8	1	amino acid
YP_002405710.1	+	-	-	-	-	-	-	-	**2.A.27.1.1**	e-63	P0AER8	1	amino acid
YP_002401683.1	+	+	+	+	+	+	+	+	**2.A.3.1.1**	0	P24207	8	amino acid
YP_002402539.1	+	-	-	-	+	+	+	+	**2.A.3.1.13**	0	P76037	5	amine
YP_002403306.1	+	+	+	+	+	+	+	+	**2.A.3.1.14**	0	P0AA47	8	amine
YP_002405181.1	+	+	+	+	+	+	+	+	**2.A.3.1.15**	0	P27837	8	unknown

YP_002403437.1	+	+	+	+	+	+	+	+	**2.A.3.1.2**	0	P25737	8	amino acid
YP_002401245.1	+	+	+	+	+	+	+	+	**2.A.3.1.3**	0	P15993	8	amino acid
YP_002403927.1	+	+	+	+	+	+	+	+	**2.A.3.1.4**	0	P25527	8	amine
YP_002401530.1	+	+	+	+	+	+	+	+	**2.A.3.1.6**	0	P37460	8	amino acid
YP_002405628.1	+	+	+	+	+	+	+	+	**2.A.3.1.7**	0	P0AAE0	8	amino acid
YP_002402662.1	+	+	+	+	+	+	+	+	**2.A.3.1.8**	0	P40812	8	amino acid
YP_002405558.1	+	+	+	+	+	+	+	+	**2.A.3.13.1**	0	P39277	8	amino acid
YP_002401785.1	+	+	+	+	+	-	+	+	**2.A.3.2.1**	0	P0AAF1	7	amine
YP_002405502.1	+	+	+	+	+	+	+	+	**2.A.3.2.2**	0	P0AAE8	8	AA/amine antiport
YP_002405484.1	+	+	+	+	+	+	+	+	**2.A.3.2.5**	0	P60061	8	AA/amine antiport
YP_859798.1	-	-	+	+	-	-	-	-	**2.A.3.2.7**	e-117	Q9Z6M8	2	AA/amine antiport
YP_859796.1	-	-	+	+	-	-	-	-	**2.A.3.2.7**	e-128	Q9Z6M8	2	AA/amine antiport
YP_002402834.1	+	+	+	+	+	+	+	+	**2.A.3.2.8**	0	P0AAE5	8	AA/amine antiport
YP_002401615.1	+	+	+	+	+	+	+	+	**2.A.3.6.4**	0	P77400	8	unknown
YP_002402039.1	+	-	-	-	+	+	+	+	**2.A.3.7.2**	0	P75835	5	unknown
YP_002402696.1	+	+	+	+	+	+	+	+	**2.A.3.7.3**	0	C8U8G2	8	glutamate /amine (GABA)
YP_002404449.1	+	+	+	+	+	+	+	+	**2.A.3.7.4**	0	P42590	8	unknown
YP_002405575.1	+	+	+	+	+	+	+	+	**2.A.3.7.5**	0	P39282	8	unknown
YP_002404718.1	+	-	-	-	+	-	+	+	**2.A.3.8.17**	0	P45539	4	amino acid
YP_002401158.1	+	+	+	+	+	+	+	+	**2.A.33.1.1**	e-174	P13738	8	cation (Na +)
YP_002402367.1	+	+	+	+	+	+	+	+	**2.A.34.1.1**	0	P0AFA7	8	cation (Na +)
YP_859969.1	-	-	+	-	-	-	-	-	**2.A.35.1.1**	e-59	P27611	1	cation (Na +)
YP_002405441.1	+	+	+	+	+	+	+	+	**2.A.36.3.1**	0	P32703	8	unknown
YP_006108896.1	-	+	+	+	-	-	-	-	**2.A.36.3.1**	e-160	P32703	3	unknown
YP_002402372.1	+	+	+	+	+	+	+	+	**2.A.36.6.3**	e-155	Q87KV8	8	cation
YP_002401186.1	+	+	+	+	+	+	+	+	**2.A.37.1.1**	0	P03819	8	cation
YP_002401185.1	+	+	+	+	+	+	+	+	**2.A.37.1.1**	e -108	P0A754	8	cation
YP_002412502.1	-	-	-	-	-	+	-	-	**2.A.37.1.1**	e-28	P0A754	1	cation
YP_002404697.1	+	+	+	+	+	+	-	+	**2.A.37.1.2**	0	P45522	7	cation
YP_002404698.1	+	+	+	+	+	+	+	+	**2.A.37.1.2**	e-108	P0A756	8	cation

YP_002401607.1	+	+	+	+	+	+	+	+	**2.A.37.1.5**	0	P39830	8	unknown
YP_002404649.1	+	+	+	+	+	+	+	+	**2.A.38.1.1**	0	P0AGI8	8	cation
YP_002405235.1	+	+	+	+	+	+	+	+	**2.A.38.1.1**	0	P0AFZ7	8	cation
YP_852529.1	-	-	+	-	-	-	-	+	**2.A.38.1.6**	0	P23849	2	cation
NP_755569.1	-	-	-	+	-	-	-	-	**2.A.38.4.5**	e-10	P73948	1	cation
YP_002401467.1	+	+	+	+	+	+	+	+	**2.A.39.1.1**	0	P0AA82	8	nucleobase
YP_006108271.1	-	+	+	+	-	-	-	-	**2.A.39.1.1**	e-26	P0AA82	3	nucleobase
YP_002401641.1	+	+	+	+	+	+	+	+	**2.A.39.3.8**	0	P75712	8	nucleobase derivative
YP_002401836.1	+	+	+	+	+	+	+	+	**2.A.4.1.4**	e-153	P75757	8	cation
YP_002405296.1	+	+	+	+	+	+	+	+	**2.A.4.7.1**	e-160	P69380	8	cation
YP_002403791.1	+	+	+	+	+	+	+	+	**2.A.40.1.1**	0	P0AGM7	8	nucleobase
YP_002402209.1	+	+	+	+	+	+	+	+	**2.A.40.1.3**	0	P75892	8	putative nucleobase
YP_852115.1	-	-	+	-	-	-	-	+	**2.A.40.1.3**	e-96	P75892	2	putative nucleobase
YP_002404150.1	+	+	+	+	+	+	+	+	**2.A.40.3.3**	0	Q46821	8	putative nucleobase
YP_002405042.1	+	+	+	+	+	+	+	+	**2.A.40.4.2**	0	P0AGM9	8	putative nucleobase
YP_002404145.1	+	+	+	+	+	+	+	+	**2.A.40.4.3**	0	P67444	8	putative nucleobase
YP_002401643.1	+	+	+	+	+	+	+	+	**2.A.40.4.4**	0	P77328	8	putative nucleobase
YP_002405053.1	+	+	+	+	+	+	-	+	**2.A.40.7.4**	0	P31440	7	unknown
YP_002405440.1	+	+	+	+	+	+	+	+	**2.A.40.7.5**	0	P0AF52	8	unknown
YP_002404147.1	+	+	+	+	+	+	+	+	**2.A.40.7.5**	e-171	P0AF52	8	unknown
YP_002405104.1	+	+	+	+	+	+	+	+	**2.A.40.7.6**	0	P31466	8	putative nucleobase
YP_002403702.1	+	+	+	+	+	+	+	+	**2.A.41.1.1**	0	P0AFF2	8	nucleoside
YP_002403442.1	+	-	-	-	+	+	+	+	**2.A.41.2.10**	0	P33021	5	nucleoside
YP_002403445.1	+	+	+	+	+	+	+	+	**2.A.41.2.9**	0	P33024	8	putative nucleoside
YP_002403138.1	+	+	+	+	+	+	+	+	**2.A.42.1.1**	0	P0AAD4	8	amino acid
YP_002404535.1	+	+	+	+	+	+	+	+	**2.A.42.1.2**	0	P0AAD2	8	amino acid
YP_002405099.1	+	+	+	+	+	+	+	+	**2.A.42.1.3**	0	P23173	8	amino acid
YP_002404062.1	+	+	+	+	+	+	+	+	**2.A.42.2.1**	0	P0AAD6	8	amino acid
YP_002404489.1	+	+	+	+	+	+	+	+	**2.A.42.2.2**	0	P0AAD8	8	amino acid

YP_002404918.1	+	+	+	+	+	+	+	+	**2.A.42.2.3**	0	P37660	8	unknown
YP_002404484.1	+	+	+	-	+	+	+	+	**2.A.42.2.4**	0	P42628	7	unknown
YP_002404108.1	+	+	+	+	+	+	+	+	**2.A.42.2.5**	0	P63340	8	unknown
YP_002402044.1	+	+	+	+	+	+	+	+	**1.A.16.1.1**	e-157	P0AC23	8	monocarboxylate
YP_002403786.1	+	-	-	-	+	+	+	+	**1.A.16.1.2**	e-129	P77733	5	anion
YP_002404715.1	+	+	+	+	+	+	+	+	**1.A.16.1.3**	e-147	P0AC26	8	anion
YP_002403614.1	+	+	+	+	+	+	+	+	**1.A.16.4.1**	e-149	P37327	8	unknown
YP_002401958.1	+	+	+	+	+	+	+	+	**2.A.45.3.2**	0	P75788	8	unknown
YP_002402642.1	+	+	+	+	+	+	-	+	**2.A.46.1.1**	e-69	P07775	7	monocarboxylate
YP_002401855.1	+	+	+	+	+	+	+	+	**2.A.47.3.1**	e-83	Q41364	8	anion
YP_002401720.1	+	+	+	+	+	+	+	+	**2.A.47.3.2**	0	P0AE74	8	anion
YP_006108517.1	-	+	+	+	-	-	-	-	**2.A.47.3.2**	e-21	P0AE74	3	anion
YP_002404435.1	+	+	+	+	+	+	+	+	**2.A.47.3.3**	0	P39414	8	anion
YP_002403558.1	+	+	+	+	+	+	+	+	**2.A.47.4.1**	e-52	P72958	8	anion
YP_006104839.1	-	+	+	+	-	-	-	-	**2.A.47.4.2**	e-11	Q9HMC9	3	anion
YP_002401288.1	+	+	+	+	+	+	+	+	**2.A.49.5.1**	0	P37019	8	anion
YP_002402821.1	+	+	-	+	+	+	+	+	**2.A.49.5.3**	0	Q8FHC1	7	anion
YP_852691.1	-	-	+	-	-	-	-	-	**2.A.49.5.3**	e-177	Q8FHC1	1	anion
YP_002403699.1	+	+	+	+	+	+	+	+	**2.A.49.7.1**	e-175	H5KWQ5	8	anion
YP_002404412.1	+	+	+	+	+	+	+	+	**2.A.5.5.1**	e-123	P0A8H3	8	cation
YP_002415410.1	-	-	-	-	-	+	-	-	**2.A.51.1.2**	e-26	Q55027	1	anion
YP_002271388.1	-	-	-	-	-	-	+	-	**2.A.52.2.1**	e-135	P76425	1	cation
YP_002403391.1	+	+	+	+	-	+	-	+	**2.A.52.2.1**	e-136	P76425	6	cation
YP_002403392.1	+	+	+	+	+	+	+	+	**2.A.52.2.1**	e-56	P64534	8	cation
YP_002401470.1	+	-	-	-	+	+	+	+	**2.A.53.3.8**	e-19	Q8F8H7	5	putative anion
YP_002401259.1	+	+	+	+	+	+	+	+	**2.A.53.3.8**	e-43	Q8F8H7	8	putative anion
YP_002402387.1	+	+	+	+	+	+	+	+	**2.A.53.3.9**	e-171	A1JRS3	8	putative anion
YP_002403701.1	+	+	+	+	+	+	+	+	**2.A.55.3.1**	0	P0A769	8	anion
YP_002404963.1	+	+	+	+	+	+	-	+	**2.A.56.1.2**	0	P37676	7	monocarboxylate
YP_002404962.1	+	-	-	-	+	+	-	+	**2.A.56.1.2**	e-167	P37675	4	monocarboxylate

YP_006107990.1	-	+	+	+	-	-	-	-	**2.A.56.1.2**	e-178	P37675	3	monocarboxylate
YP_006107989.1	-	+	-	+	-	-	-	-	**2.A.56.1.2**	e-42	P37674	2	monocarboxylate
YP_002404961.1	+	-	-	-	+	+	-	+	**2.A.56.1.2**	e-86	P37674	4	monocarboxylate
YP_001465705.1	-	-	-	-	+	-	-	-	**2.A.56.1.5**	e-107	Q8ZKS0	1	polysaccharide (rhamnogalacturonide)
YP_002413992.1	-	-	-	-	-	+	-	-	**2.A.56.1.5**	e-110	Q8ZKS0	1	rhamnogalacturonide
YP_002413991.1	-	-	-	-	-	+	-	-	**2.A.56.1.5**	e-17	Q8ZKR9	1	rhamnogalacturonide
YP_006107419.1	-	+	+	+	-	-	-	-	**2.A.56.1.5**	e-20	Q8ZKR9	3	rhamnogalacturonide
YP_002413990.1	-	-	-	-	-	+	-	-	**2.A.56.1.5**	e-57	P43020	1	rhamnogalacturonide
YP_006107418.1	-	+	+	+	-	-	-	-	**2.A.56.1.5**	e-58	P43020	3	rhamnogalacturonide
YP_001465704.1	-	-	-	-	+	-	-	-	**2.A.56.1.5**	e-63	P43020	1	rhamnogalacturonide
YP_006107420.1	-	+	+	+	-	-	-	-	**2.A.56.1.5**	e-97	Q8ZKS0	3	rhamnogalacturonide
YP_006108895.1	-	+	+	+	-	-	-	-	**2.A.56.1.6**	e-38	Q9KR64	3	monocarboxylate
YP_006108893.1	-	+	+	+	-	-	-	-	**2.A.56.1.6**	e-59	B9TSM9	3	monocarboxylate
YP_002405389.1	+	+	+	+	+	+	+	+	**2.A.58.2.1**	0	P0AF43	8	anion
YP_002404848.1	+	-	-	-	-	-	-	-	**2.A.6.1.3**	0	Q9ZHC9	1	cation
YP_002401681.1	+	+	+	+	+	+	+	+	**2.A.6.1.4**	0	P77239	8	cation
YP_002401682.1	+	+	+	+	+	+	+	+	**2.A.6.1.4**	0	P38054	8	cation
YP_002404849.1	+	-	-	-	-	-	-	-	**2.A.6.1.4**	e-154	P77239	1	cation
YP_002404850.1	+	-	-	-	-	-	-	-	**2.A.6.1.4**	e-22	P77214	1	cation
YP_002401680.1	+	+	+	+	+	+	+	+	**2.A.6.1.4**	e-58	P77214	8	cation
YP_002404890.1	+	+	+	+	+	+	+	+	**2.A.6.2 family**	0	P37637	8	multidrug
YP_002404632.1	+	+	+	+	+	+	-	+	**2.A.6.2 family**			7	multidrug
YP_006105661.1	-	+	+	+	-	-	-	-	**2.A.6.2 family**			3	multidrug
YP_002403364.1	+	+	+	+	+	+	+	+	**2.A.6.2.12**	0	P76398	8	multidrug
YP_002403365.1	+	+	+	+	+	+	+	+	**2.A.6.2.14**	0	P76399	8	multidrug
YP_006105662.1	-	+	+	+	-	-	+	-	**2.A.6.2.19**	0	Q8GC82	4	multidrug
YP_006105660.1	-	+	+	+	-	-	+	-	**2.A.6.2.19**	e-157	Q8GC84	4	multidrug

YP_002401591.1	+	+	+	+	+	+	+	+	2.A.6.2.2	0	P31224	8	multidrug
YP_002404101.1	+	+	+	+	+	+	+	+	**2.A.6.2.28**	e-10	A4KT88	8	multidrug
YP_859756.1	-	-	+	+	-	-	-	-	**2.A.6.2.6**	e-138	P52002	2	multidrug
YP_002403763.1	+	+	+	+	+	+	+	+	**2.A.6.2.7**	0	P24177	8	multidrug
YP_006106806.1	-	+	-	-	-	-	-	+	**2.A.6.2.7**	e-27	P24177	2	multidrug
YP_002401536.1	+	+	+	+	+	+	+	+	**2.A.6.4.1**	0	P0AG90	8	protein
YP_002401537.1	+	+	+	+	+	+	+	+	**2.A.6.4.3**	e-47	Q5SKE6	8	protein
YP_006105180.1	-	+	-	+	-	+	+	-	**2.A.6.8.1**	e-10	Q9EY29	4	pigments
YP_002401729.1	+	+	+	+	+	+	+	+	**2.A.61.1.1**	0	P0ABP3	8	dicarboxylate
YP_002404593.1	+	-	-	-	+	+	-	+	**2.A.61.1.2**	0	P45428	4	dicarboxylate
YP_002401734.1	+	+	-	+	+	+	+	+	**2.A.64.1.1**	e-12	P0A843	7	amino acid
YP_002405226.1	+	+	+	+	+	+	+	+	**2.A.64.1.1**	e-129	P69423	8	amino acid
YP_002405224.1	+	+	+	+	+	+	+	+	**2.A.64.1.1**	e-39	P69428	8	amino acid
YP_002405225.1	+	+	+	+	+	+	+	+	**2.A.64.1.1**	e-84	P69425	8	amino acid
YP_002403263.1	+	+	-	+	+	+	+	+	**2.A.66.1.23**	0	P76352	7	multidrug
YP_853088.1	-	-	+	-	-	-	-	-	**2.A.66.1.23**	0	P76352	1	multidrug
YP_006106319.1	-	+	-	+	-	-	-	-	**2.A.66.1.26**	e-44	Q58119	2	unknown
YP_002402893.1	+	+	+	+	+	+	+	+	**2.A.66.1.3**	0	P37340	8	multidrug
YP_002405419.1	+	+	+	+	+	+	+	+	**2.A.66.1.4**	0	P28303	8	unknown
NP_754454.1	-	-	-	+	-	-	-	-	**2.A.66.2.10**	e-26	O26447	1	polysaccharide
YP_853146.1	-	-	+	-	-	-	-	-	**2.A.66.2.10**	e-41	O26447	1	polysaccharide
YP_002413088.1	-	-	-	-	-	+	-	-	**2.A.66.2.12**	0	Q1L811	1	polysaccharide
YP_002405177.1	+	+	+	+	+	+	+	+	**2.A.66.2.3**	0	P0AAA7	8	polysaccharide
YP_006106415.1	-	+	-	-	-	-	-	-	**2.A.66.2.4**	e-29	Q44575	1	polysaccharide
YP_002403336.1	+	+	+	+	+	+	+	+	**2.A.66.2.7**	0	P77377	8	polysaccharide (LPS)
YP_002402270.1	+	+	+	+	+	+	+	+	**2.A.66.4.3**	0	P0AF16	8	unknown

YP_002403324.1	+	-	-	-	-	-	-	-	**2.A.66.5.3**	e-20	A0YL48	1	polysaccharide
YP_002402577.1	+	-	-	-	+	+	+	+	**2.A.68.1.1**	0	P46133	5	amino acid
YP_002403681.1	+	+	+	+	+	+	+	+	**2.A.69.3.5**	e-159	P0AA50	8	unknown
YP_002415412.1	-	-	-	-	-	+	-	-	**2.A.7.1.11**	e-27	Q2FD83	1	multidrug
YP_002403208.1	+	-	-	-	-	-	+	+	**2.A.7.1.3**	e-60	P23895	3	multidrug
YP_002401872.1	+	+	+	+	+	-	+	+	**2.A.7.1.3**	e-61	P23895	7	multidrug
YP_002405567.1	+	+	+	+	+	+	+	+	**2.A.7.1.4**	e-42	P69937	8	multidrug
YP_002402828.1	+	+	+	+	+	+	+	+	**2.A.7.1.9**	e-48	P69210	8	amine
YP_002402829.1	+	+	+	+	+	-	+	+	**2.A.7.1.9**	e-63	P69213	7	amine
YP_002402678.1	+	+	+	+	+	+	+	+	**2.A.7.17.2**	e-145	P46136	8	amino acid
YP_002415472.1	-	-	-	-	-	+	-	-	**2.A.7.19.2**	e-13	Q9ZPR7	1	nucleobase
YP_002402656.1	+	+	+	+	+	+	+	+	**2.A.7.21.2**	e-79	P76111	8	unknown
YP_002403527.1	+	+	-	+	+	+	+	+	**2.A.7.22.1**	e-46	Q47377	7	multidrug
YP_002403528.1	+	+	+	+	+	+	+	+	**2.A.7.22.1**	e-51	P76474	8	multidrug
YP_002402811.1	+	+	+	+	+	+	+	+	**2.A.7.26.1**	e-61	P76169	8	unknown
YP_002405215.1	+	+	+	+	+	+	-	+	**2.A.7.3.1**	e-71	O06933	7	monocarboxylate
YP_002405048.1	+	+	+	+	+	+	+	+	**2.A.7.3.12**	e-138	P31437	8	unknown
YP_002404556.1	+	+	+	+	+	+	+	+	**2.A.7.3.18**	e-170	E1ILD8	8	unknown
YP_002405630.1	+	+	+	+	+	+	+	+	**2.A.7.3.19**	e-176	P39314	8	amino acid
YP_002402743.1	+	+	+	+	+	+	+	+	**2.A.7.3.2**	e-154	P31125	8	amino acid
YP_002403230.1	+	+	+	+	+	+	+	+	**2.A.7.3.22**	e-131	p0aa70	8	unknown
YP_002405325.1	+	+	+	+	+	+	+	+	**2.A.7.3.26**	e-153	P0ABT9	8	unknown
YP_002401954.1	+	+	+	+	+	+	+	+	**2.A.7.3.6**	e-148	P0AA67	8	unknown
YP_002405289.1	+	+	+	+	+	+	-	+	**2.A.7.6.1**	e-172	P27125	7	sugar
YP_002405207.1	+	+	+	+	+	+	+	+	**2.A.7.7.2**	e-168	P27844	8	putative specific drug
YP_002405140.1	+	+	+	+	+	+	+	+	**2.A.72.1.1**	0	P63183	8	cation
YP_006106596.1	-	+	+	+	-	+	-	+	**2.A.73.1.1**	0	P76460	5	lipid (FFA)
YP_002404183.1	+	+	+	+	+	+	+	+	**2.A.75.1.2**	e-119	P11667	8	amino acid
YP_002405212.1	+	+	+	+	+	+	+	+	**2.A.76.1.1**	e-102	P0AG34	8	amino acid
YP_002405211.1	+	+	+	+	+	+	+	+	**2.A.76.1.2**	e-100	P0AG38	8	amino acid

YP_002401459.1	+	+	+	+	+	-	+	+	**2.A.76.1.3**	e-116	P75693	7	amino acid
YP_002403873.1	+	+	+	+	+	+	+	+	**2.A.76.1.4**	e-109	P38101	8	amino acid derivative
YP_002403027.1	+	+	+	+	+	+	+	+	**2.A.76.1.5**	e-116	P76249	8	amino acid
YP_002403945.1	+	+	+	+	+	+	+	+	**2.A.78.1.3**	e-129	P76630	8	amino acid
YP_002403946.1	+	+	+	+	+	+	+	+	**2.A.78.1.3**	e-52	P43667	8	amino acid
YP_002405869.1	+	+	+	+	+	+	+	+	**2.A.79.2.1**	e-144	Q8FA71	8	unknown
YP_002415475.1	-	-	-	-	-	+	-	+	**2.A.8.1.1**	e-107	P12012	2	monocarboxylate
YP_002405680.1	+	+	+	+	-	+	-	+	**2.A.8.1.2**	0	P39344	6	monocarboxylate
YP_002405830.1	+	+	-	+	+	+	+	+	**2.A.8.1.3**	0	P0AC94	7	monocarboxylate
YP_002404765.1	+	+	+	+	+	+	+	+	**2.A.8.1.4**	0	P39835	8	monocarboxylate
YP_006106719.1	-	+	+	+	+	-	+	+	**2.A.8.1.5**	0	P08555	6	amino acid
YP_002404001.1	+	+	+	+	+	-	-	+	**2.A.8.1.7**	0	Q46892	6	unknown
YP_002404787.1	+	+	+	+	+	+	+	+	**2.A.8.1.8**	0	P0AC96	8	monocarboxylate
YP_006108282.1	-	+	+	+	-	-	-	-	**2.A.80.1.1**	e-21	Q9FA46	3	tri carboxylate
YP_006108280.1	-	+	+	+	-	-	-	-	**2.A.80.1.1**	e-72	Q9FA44	3	tri carboxylate
YP_002401988.1	+	+	+	+	+	+	+	+	**2.A.81.1.4**	0	a7zjr5	8	unknown
YP_002405074.1	+	+	+	+	+	+	+	+	**2.A.81.1.5**	0	B7L824	8	unknown
YP_002402102.1	+	+	+	+	+	+	+	+	**2.A.85.1.1**	0	P75870	8	aromatic acid
YP_002404606.1	+	+	+	+	+	+	+	+	**2.A.85.1.2**	0	P46481	8	aromatic acid
YP_002404706.1	+	+	+	+	+	+	+	+	**2.A.85.1.3**	0	P45537	8	unknown
YP_002402875.1	+	+	+	+	+	+	+	+	**2.A.85.1.6**	0	Q8X638	8	unknown
YP_002405457.1	+	+	+	+	+	+	+	+	**2.A.85.6.1**	0	P32715	8	multidrug
YP_002403300.1	+	+	+	+	+	+	+	+	**2.A.85.7.1**	0	P33011	8	aromatic (furasic acid)
YP_002403787.1	+	+	+	+	+	+	+	+	**2.A.86.1.1**	e -145	P0AFI9	8	unknown
YP_002404824.1	+	+	+	+	+	+	+	+	**2.A.86.1.2**	0	P0AGM0	8	unknown
YP_002402830.1	+	+	+	+	+	+	+	+	**2.A.86.1.4**	e-159	P0AFS5	8	protein (AI2)
YP_002403790.1	+	+	+	+	+	+	+	+	**2.A.86.1.5**	e -06	C9VRY8	8	protein (AI2)
YP_002415025.1	-	-	-	-	-	+	-	-	**2.A.86.1.6**	e-22	D3LPG3	1	sugar
YP_001465363.1	-	-	-	-	+	-	+	+	**2.A.86.1.6**	e-24	D3LPG3	3	sugar
YP_002402916.1	+	+	+	+	+	+	+	+	**2.A.86.2.1**	e-169	B1LE48	8	nucleobase

YP_002404821.1	+	+	+	+	+	+	+	+	**2.A.88.8.6**	e-125	B3WJF3	8	enzyme cofactor
YP_002405095.1	+	+	+	+	+	+	+	+	**2.A.9.3.1**	0	P25714	8	protein (cytochrome oxidase)
YP_002403712.1	+	+	+	+	+	+	+	+	**2.A.93.1.4**	0	P39836	8	putative auxin
YP_002402733.1	+	+	+	+	+	+	+	+	**2.A.95.1.1**	e-120	P0AEY1	8	unknown
YP_002402423.1	+	+	+	+	+	+	+	+	**2.A.95.1.4**	e-31	Q8J305	8	amino acid
YP_002404786.1	+	+	+	+	+	+	+	+	**2.A.95.1.5**	e-89	P67143	8	putative multidrug
YP_002401153.1	+	+	+	+	+	+	+	+	**2.A.96.1.1**	e-96	P0AC98	8	unknown
YP_002403439.1	+	+	-	+	+	+	+	+	**2.A.98.1.3**	e-160	P62723	7	unknown
YP_006105480.1	-	+	+	+	-	+	-	-	**2.C.1.1.1**	e-13	P02929	4	nonspecific
YP_002402434.1	+	+	+	+	+	+	+	+	**2.C.1.1.1**	e-79	P02929	8	nonspecific
YP_002402785.1	+	-	-	-	-	-	-	-	**2.C.1.2.1**	e-08	P19934	1	unknown
YP_002401833.1	+	+	+	+	+	+	+	+	**2.C.1.2.1**	e-108	P45955	8	unknown
YP_002402786.1	+	-	-	-	-	-	-	-	**2.C.1.2.1**	e-24	P19934	1	unknown
NP_752753.1	-	-	-	+	-	-	-	+	**2.C.1.2.1**	e-31	P45955	2	unknown
YP_002401830.1	+	+	+	+	+	+	+	+	**2.C.1.2.1**	e-55	P19934	8	unknown
YP_002405407.1	+	+	+	+	+	+	+	+	**3.A.1.1.1**	0	P02916	8	sugar
YP_002405408.1	+	+	+	+	+	+	+	+	**3.A.1.1.1**	0	P0AEX9	8	sugar
YP_002405409.1	+	+	+	+	+	+	+	+	**3.A.1.1.1**	0	P68187	8	sugar
YP_002405406.1	+	+	+	+	+	+	+	+	**3.A.1.1.1**	e-153	P68183	8	sugar
YP_002402554.1	+	+	+	+	+	-	+	+	**3.A.1.1.25**	e-32	Q72H67	7	sugar
YP_002402560.1	+	+	+	+	+	-	+	-	**3.A.1.1.26**	e-131	P94360	6	sugar
YP_002402553.1	+	+	+	+	+	-	-	+	**3.A.1.1.28**	e-13	Q00749	6	sugar
YP_002404800.1	+	+	+	+	+	+	+	+	**3.A.1.1.3**	0	P10907	8	polyol
YP_002404803.1	+	+	+	+	+	+	+	+	**3.A.1.1.3**	0	P0AG80	8	polyol
YP_002404801.1	+	+	+	+	+	+	+	+	**3.A.1.1.3**	e-151	P10906	8	polyol
YP_002404802.1	+	+	+	+	+	+	+	+	**3.A.1.1.3**	e-158	P10905	8	polyol
YP_002402555.1	+	+	+	+	+	-	+	+	**3.A.1.1.7**	e-43	O51925	7	sugar
YP_002270826.1	-	-	-	-	-	-	+	+	**3.A.1.10.3**	e-23	P44513	2	cation (ferric)
YP_002329404.1	-	-	-	-	-	+	-	-	**3.A.1.10.3**	e-24	P44513	1	cation (ferric)

YP_006106081.1	-	+	+	+	-	-	-	-	**3.A.1.10.3**	e-24	P44513	3	cation (ferric)
YP_002402981.1	+	-	-	-	+	-	-	-	**3.A.1.10.3**	e-25	P44513	2	cation (ferric)
NP_755572.1	-	-	-	+	-	-	-	-	**3.A.1.101.1**	e-102	P24586	1	polysaccharide
YP_006107350.1	-	+	-	-	-	-	-	-	**3.A.1.101.1**	e-117	P24586	1	polysaccharide
YP_006107351.1	-	+	+	+	-	+	-	-	**3.A.1.101.1**	e-137	P24584	4	polysaccharide
YP_854396.1	-	-	+	-	-	-	-	-	**3.A.1.101.1**	e-90	P24586	1	polysaccharide
YP_002414096.1	-	-	-	-	-	+	-	-	**3.A.1.101.1**	e-97	P24586	1	polysaccharide
YP_002401261.1	+	+	+	+	+	+	+	+	**3.A.1.102.1**	e-10	P50333	8	polysaccharide (LPS)
YP_002401260.1	+	+	+	+	+	+	+	+	**3.A.1.105.3**	e-43	Q70J75	8	multidrug
YP_002401935.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-136	Q4VWC9	8	specific drug
YP_002404835.1	+	+	+	+	-	+	+	+	**3.A.1.105.4**	e-18	Q4VWD0	7	specific drug
YP_002404833.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-22	Q4VWC7	8	specific drug
YP_002401936.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-46	Q4VWD0	8	specific drug
YP_002404834.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-55	Q4VWC9	8	specific drug
YP_002401934.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-67	Q4VWC8	8	specific drug
YP_002401933.1	+	+	+	+	+	+	+	+	**3.A.1.105.4**	e-72	Q4VWC7	8	specific drug
YP_002402054.1	+	+	+	+	+	+	+	+	**3.A.1.106.1**	0	P60752	8	lipid
YP_002401578.1	+	+	+	+	+	+	+	+	**3.A.1.106.5**	0	A7VN01	8	multidrug
YP_002401579.1	+	+	+	+	+	+	+	+	**3.A.1.106.5**	0	A7VN02	8	multidrug
YP_006105307.1	-	+	-	+	-	-	-	-	**3.A.1.106.7**	0	Q8RMB7	2	siderophore
YP_002403477.1	+	+	-	+	+	+	+	+	**3.A.1.107.3**	e-12	P0ABM7	7	siderophore
YP_002403479.1	+	+	+	+	+	+	+	+	**3.A.1.107.3**	e-70	P0ABM0	8	siderophore
YP_002403480.1	+	+	+	+	+	+	+	+	**3.A.1.107.3**	e-99	Q8XE58	8	siderophore
YP_006108794.1	-	+	-	+	-	-	-	-	**3.A.1.109.1**	0	P08716	2	protein

YP_006104453.1	-	+	-	+	-	-	-	-	**3.A.1.109.3**	e-119	Q88RG3	2	protein
YP_006104452.1	-	+	-	+	-	-	-	-	**3.A.1.109.4**	e-09	Q9I2M2	2	putative protein
YP_002411291.1	-	-	-	-	-	+	+	-	**3.A.1.109.4**	e-115	Q9I2M1	2	putative protein
YP_006104454.1	-	+	-	+	-	-	-	-	**3.A.1.109.4**	e-65	Q9I2M0	2	putative protein
YP_002411292.1	-	-	-	-	-	+	+	-	**3.A.1.109.4**	e-73	Q9I2M0	2	putative protein
YP_002402323.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	0	P0AFK9	8	amine
YP_002402326.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	0	P69874	8	amine
YP_002402324.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	e-135	P0AFK6	8	amine
YP_002402651.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	e-14	P0AFK6	8	amine
YP_002402325.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	e-155	P0AFK4	8	amine
YP_002402649.1	+	+	+	+	+	+	+	+	**3.A.1.11.1**	e-55	P69874	8	amine
YP_002401995.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	0	P31133	8	amine
YP_002401996.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	0	P31134	8	amine
YP_002401998.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	e-133	P0AFL1	8	amine
YP_002401997.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	e-159	P31135	8	amine
YP_002402648.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	e-16	P31133	8	amine
YP_002402650.1	+	+	+	+	+	+	+	+	**3.A.1.11.2**	e-31	P31135	8	amine
YP_006105216.1	-	+	-	+	-	-	-	-	**3.A.1.110.1**	0	Q93GK4	2	protein
YP_006105217.1	-	+	-	+	-	-	-	-	**3.A.1.110.1**	0	Q93GK5	2	protein
NP_752270.1	-	-	-	+	-	-	-	-	**3.A.1.110.1**	e-49	Q93GK6	1	protein
YP_006105219.1	-	+	-	+	-	-	-	-	**3.A.1.110.1**	e-50	Q93GK6	2	protein
YP_002403491.1	+	+	+	+	+	+	+	+	**3.A.1.113.3**	0	P33941	8	protein
YP_002403941.1	+	+	+	+	+	+	+	+	**3.A.1.12.1**	0	P14175	8	amine
YP_002403943.1	+	+	+	+	+	+	+	+	**3.A.1.12.1**	0	P0AFM2	8	amine
YP_002403942.1	+	+	+	+	+	+	+	+	**3.A.1.12.1**	e-169	P14176	8	amine
YP_002403410.1	+	+	+	+	+	+	+	+	**3.A.1.12.10**	e-31	Q87WH3	8	amine
YP_002403408.1	+	+	+	+	+	+	+	+	**3.A.1.12.4**	e-70	O34992	8	amine
YP_002403409.1	+	+	+	+	+	+	+	+	**3.A.1.12.8**	e-13	Q93A34	8	amine / amino acid
YP_002403407.1	+	+	+	+	+	+	+	+	**3.A.1.12.8**	e-28	Q93A34	8	amine / amino acid

YP_002402091.1	+	+	+	+	+	+	+	+	**3.A.1.120.6**	0	P43672	8	unknown
YP_002405894.1	+	+	+	+	+	+	+	+	**3.A.1.120.6**	e-74	P43672	8	unknown
YP_002401960.1	+	+	+	+	+	+	+	+	**3.A.1.121.4**	e-141	Q83XH1	8	multidrug
YP_002404699.1	+	+	+	+	+	+	+	+	**3.A.1.121.4**	e-74	Q83XH1	8	multidrug
YP_002402019.1	+	+	+	+	+	+	+	+	**3.A.1.122.1**	0	P75830	8	multidrug
YP_002402020.1	+	+	+	+	-	+	+	+	**3.A.1.122.1**	0	P75831	7	multidrug
YP_002405466.1	+	+	+	+	+	+	+	+	**3.A.1.122.2**	e-25	O31711	8	peptide
YP_002402316.1	+	+	+	+	+	+	+	+	**3.A.1.125.1**	0	P0ADC3	8	protein (lipoprotein)
YP_002402318.1	+	+	+	+	+	+	+	+	**3.A.1.125.1**	0	P75958	8	protein (lipoprotein)
YP_002269776.1	-	-	-	-	-	-	+	-	**3.A.1.125.1**	e-09	P75958	1	protein (lipoprotein)
YP_002402317.1	+	+	+	+	+	+	+	+	**3.A.1.125.1**	e-129	P75957	8	protein (lipoprotein)
YP_002401624.1	+	+	+	+	+	+	+	+	**3.A.1.125.1**	e-49	P75957	8	protein (lipoprotein)
YP_002269774.1	-	-	-	-	-	-	+	-	**3.A.1.125.2**	e-50	O53899	1	putative lipoprotein
YP_002402026.1	+	+	+	+	+	+	+	+	**3.A.1.129.1**	0	P23886	8	AA/ peptide (GSH)
YP_002402027.1	+	+	+	+	+	+	+	+	**3.A.1.129.1**	0	P29018	8	AA/ peptide (GSH)
YP_002401291.1	+	+	+	+	+	+	+	+	**3.A.1.13.1**	e-123	Q8ZRP7	8	enzyme cofactor (B12)
YP_002402940.1	+	+	+	+	+	+	+	+	**3.A.1.13.1**	e-136	P06609	8	enzyme cofactor (B12)
YP_002402938.1	+	+	+	+	+	+	+	+	**3.A.1.13.1**	e-140	P06611	8	enzyme cofactor (B12)
YP_002403398.1	+	+	+	+	+	+	+	+	**3.A.1.132.3**	e-53	A0L4L0	8	unknown
YP_002402197.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e -17	A6QEW8	8	peptide
YP_002402331.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e -25	A6QEW8	8	peptide
YP_002273628.1	-	-	-	-	-	-	+	-	**3.A.1.134.7**	e-10	A6QEW8	1	peptide
YP_002402837.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-15	A6QEW8	8	peptide
YP_002405294.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-16	A6QEW8	8	peptide
YP_002401787.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-17	A6QEW8	8	peptide
YP_002403368.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-18	A6QEW8	8	peptide

YP_002405482.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-18	A6QEW8	8	peptide
YP_002404398.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-19	A6QEW8	8	peptide
YP_002405904.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-19	A6QEW8	8	peptide
YP_006108801.1	-	+	-	+	-	-	-	-	**3.A.1.134.7**	e-19	A6QEW8	2	peptide
YP_002404839.1	+	-	-	-	-	-	-	-	**3.A.1.134.7**	e-19	A6QEW8	1	peptide
YP_002401678.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-20	A6QEW8	8	peptide
YP_002403241.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-20	A6QEW8	8	peptide
YP_002404852.1	+	-	-	-	-	-	-	-	**3.A.1.134.7**	e-20	A6QEW8	1	peptide
YP_002404755.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-22	A6QEW8	8	peptide
YP_002405901.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-25	A6QEW8	8	peptide
YP_002401526.1	+	+	+	+	+	+	+	+	**3.A.1.134.7**	e-27	A6QEW8	8	peptide
YP_002401620.1	+	+	+	-	+	+	+	+	**3.A.1.139.2**	e-131	P77307	7	cofactor substrate (GDP)
YP_002405808.1	+	+	-	-	+	+	-	+	**3.A.1.14.1**	e-131	P15029	5	siderophore
YP_002405806.1	+	+	-	-	+	+	-	+	**3.A.1.14.1**	e-137	P15031	5	siderophore
YP_002405809.1	+	+	-	-	+	+	-	+	**3.A.1.14.1**	e-145	P15030	5	siderophore
YP_002405810.1	+	+	-	-	+	+	-	+	**3.A.1.14.1**	e-166	P15028	5	siderophore
YP_006105556.1	-	+	+	+	-	+	-	-	**3.A.1.14.11**	e-47	Q57130	4	siderophore
YP_006107437.1	-	+	+	+	-	-	+	-	**3.A.1.14.13**	e-28	Q9RK09	4	siderophore
YP_006107916.1	-	+	+	+	-	+	+	-	**3.A.1.14.18**	e-129	Q32AY3	5	siderophore
YP_006107915.1	-	+	+	+	-	+	+	-	**3.A.1.14.18**	e-141	Q32AY2	5	siderophore
YP_006107911.1	-	+	+	+	-	+	+	-	**3.A.1.14.18**	e-164	Q32AX9	5	siderophore
YP_002401698.1	+	+	+	+	+	+	+	+	**3.A.1.14.2**	e-128	P23876	8	siderophore
YP_002401697.1	+	+	+	+	+	+	+	+	**3.A.1.14.2**	e-142	P23877	8	siderophore
YP_002401696.1	+	+	+	+	+	+	+	+	**3.A.1.14.2**	e-149	P23878	8	siderophore

YP_002401700.1	+	+	+	+	+	+	+	+	**3.A.1.14.2**	e-163	C8U2V6	8	siderophore
YP_006104403.1	-	+	-	+	-	-	-	-	**3.A.1.14.2**	e-29	P23878	2	siderophore
YP_006106366.1	-	+	-	+	-	-	-	-	**3.A.1.14.2**	e-29	P23878	2	siderophore
YP_006104402.1	-	+	-	+	-	-	-	-	**3.A.1.14.21**	e-18	O68878	2	siderophore
YP_006106367.1	-	+	-	+	-	-	-	-	**3.A.1.14.21**	e-18	O68878	2	siderophore
YP_002401286.1	+	+	+	+	+	+	+	+	**3.A.1.14.3**	0	P06972	8	siderophore
YP_002401284.1	+	+	+	+	+	+	+	+	**3.A.1.14.3**	e-151	P07821	8	siderophore
YP_002401285.1	+	+	+	+	+	+	+	+	**3.A.1.14.3**	e-162	P07822	8	siderophore
YP_006107438.1	-	+	+	+	-	-	+	-	**3.A.1.14.6**	e-72	Q9RCF3	4	siderophore
YP_006107435.1	-	+	+	+	-	-	+	-	**3.A.1.14.7**	e-08	Q93PN3	4	siderophore
YP_006107436.1	-	+	+	+	-	-	+	-	**3.A.1.14.8**	e-30	Q8GRB1	4	siderophore
YP_006105555.1	-	+	+	+	-	+	-	-	**3.A.1.14.8**	e-33	Q8GRB0	4	siderophore
YP_002404812.1	+	+	+	+	+	+	+	+	**3.A.1.140.1**	e-180	P0AC31	8	protein (FstX enzyme)
YP_002403245.1	+	+	+	+	+	+	+	+	**3.A.1.15.3**	e-45	O05703	8	cation
YP_002405434.1	+	+	+	+	+	+	+	+	**3.A.1.15.4**	e-09	Q56953	8	cation
YP_002403091.1	+	+	+	+	+	+	+	+	**3.A.1.15.5**	e -143	P0A9X1	8	cation
YP_002403092.1	+	+	+	+	+	+	+	+	**3.A.1.15.5**	e-106	P39832	8	cation
YP_002403090.1	+	+	+	+	+	+	+	+	**3.A.1.15.5**	e-150	P39172	8	cation
YP_006105507.1	-	+	+	+	-	+	-	-	**3.A.1.15.7**	e-113	Q9XCS1	4	cation
YP_006105506.1	-	+	+	+	-	+	-	-	**3.A.1.15.7**	e-115	Q9XCS0	4	cation
YP_006105508.1	-	+	+	+	-	+	-	-	**3.A.1.15.7**	e-134	Q9XCS2	4	cation
YP_006105714.1	-	+	-	+	-	-	-	-	**3.A.1.15.7**	e-35	Q9XCR9	2	cation
YP_006105505.1	-	+	+	+	-	+	-	-	**3.A.1.15.7**	e-91	Q9XCR9	4	cation
YP_002401496.1	+	+	+	+	+	+	+	+	**3.A.1.17.1**	e-137	Q47539	8	amine
YP_002401495.1	+	+	+	+	-	+	+	+	**3.A.1.17.1**	e-142	Q47538	7	amine
YP_002401494.1	+	+	+	+	+	+	+	+	**3.A.1.17.1**	e-171	Q47537	8	amine
YP_002402078.1	+	+	+	+	+	+	+	+	**3.A.1.17.2**	e-72	O85763	8	amine
YP_002402075.1	+	+	+	+	+	+	+	+	**3.A.1.17.2**	e-84	Q8KZQ6	8	amine
YP_002402076.1	+	+	+	+	+	+	+	+	**3.A.1.17.2**	e-98	O85765	8	amine

YP_002401204.1	+	+	+	+	+	+	+	+	**3.A.1.19.1**	0	P31549	8	enzyme cofactor (thiamin)
YP_002401203.1	+	+	+	+	+	+	+	+	**3.A.1.19.1**	e -117	P31548	8	enzyme cofactor
YP_002401205.1	+	+	+	+	+	+	+	+	**3.A.1.19.1**	e-174	P31550	8	enzyme cofactor
YP_002405142.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	0	P04983	8	sugar
YP_002402196.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e -07	P02925	8	sugar
YP_002401476.1	+	+	+	-	+	+	+	+	**3.A.1.2.1**	e-10	P02925	7	sugar
YP_002402888.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-11	P02925	8	sugar
YP_006107652.1	-	+	+	+	-	-	-	-	**3.A.1.2.1**	e-111	P04983	3	sugar
YP_002273634.1	-	-	-	-	-	-	+	-	**3.A.1.2.1**	e-113	P04983	1	sugar
YP_002405143.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-122	P0AGI1	8	sugar
YP_002405144.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-152	P02925	8	sugar
YP_002405146.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-16	P02925	8	sugar
YP_002273632.1	-	-	-	-	-	-	+	-	**3.A.1.2.1**	e-25	P02925	1	sugar
YP_006107653.1	-	+	+	+	-	-	-	-	**3.A.1.2.1**	e-29	P02925	3	sugar
YP_002403840.1	+	+	+	+	+	+	+	+	**3.A.1.2.1**	e-34	P0AGI1	8	sugar
YP_002273633.1	-	-	-	-	-	-	+	-	**3.A.1.2.1**	e-37	P0AGI1	1	sugar
YP_002401455.1	+	-	+	-	+	+	+	-	**3.A.1.2.1**	e-38	P0AGI1	5	sugar
YP_002405679.1	+	+	+	+	-	+	-	+	**3.A.1.2.11**	e-09	Q92WK4	6	polyol
YP_006108505.1	-	+	+	+	-	-	-	-	**3.A.1.2.11**	e-09	Q92WK4	3	polyol
YP_006107651.1	-	+	+	+	-	-	-	-	**3.A.1.2.13**	e-53	A6VKS9	3	unknown
YP_002403972.1	+	-	+	-	+	+	+	+	**3.A.1.2.14**	e-10	Q0HIQ8	6	sugar
YP_002405646.1	+	+	+	+	+	+	-	+	**3.A.1.2.14**	e-137	Q0HIQ7	7	sugar
YP_002405647.1	+	+	+	+	+	+	+	+	**3.A.1.2.14**	e-59	Q0HIQ6	8	sugar
YP_002405648.1	+	+	+	+	+	+	+	+	**3.A.1.2.14**	e-75	Q0HIQ5	8	sugar
YP_002405645.1	+	+	+	+	+	+	+	+	**3.A.1.2.14**	e-98	Q0HIQ8	8	sugar
YP_002401454.1	+	-	+	-	+	+	+	-	**3.A.1.2.15**	e-22	A8H4W6	5	polyol
YP_002403130.1	+	+	+	+	+	+	+	+	**3.A.1.2.2**	0	P0AAF3	8	polyol
YP_002403131.1	+	+	+	+	+	+	+	+	**3.A.1.2.2**	0	P02924	8	polyol
YP_002403129.1	+	+	+	+	+	+	+	+	**3.A.1.2.2**	e-168	P0AE26	8	polyol

YP_002403427.1	+	+	+	+	+	+	+	+	**3.A.1.2.3**	0	P0AAG8	8	sugar
YP_002403842.1	+	+	+	+	+	+	+	+	**3.A.1.2.3**	e-13	P0AEE5	8	sugar
YP_002403426.1	+	+	+	+	+	+	+	+	**3.A.1.2.3**	e-153	P23200	8	sugar
YP_002403428.1	+	+	+	+	+	+	+	+	**3.A.1.2.3**	e-178	P0AEE5	8	sugar
YP_002403841.1	+	+	+	+	+	+	+	+	**3.A.1.2.3**	e-93	P0AAG8	8	sugar
YP_002404950.1	+	+	+	+	+	+	+	+	**3.A.1.2.4**	0	P37388	8	sugar
YP_002404951.1	+	+	+	+	+	+	+	+	**3.A.1.2.4**	e -172	P0AGI4	8	sugar
YP_002404949.1	+	+	+	+	+	+	+	+	**3.A.1.2.4**	e-178	P37387	8	sugar
YP_006108564.1	-	+	+	+	-	-	-	+	**3.A.1.2.6**	0	P32721	4	sugar
YP_006108563.1	-	+	+	+	-	-	-	+	**3.A.1.2.6**	e-157	P32720	4	sugar
YP_006108565.1	-	+	+	+	-	-	-	+	**3.A.1.2.6**	e-162	P39265	4	sugar
YP_002402718.1	+	-	-	-	+	+	+	+	**3.A.1.2.8**	0	P77257	5	unknown
YP_002402720.1	+	-	-	-	+	+	+	+	**3.A.1.2.8**	e-133	P0AFS1	5	unknown
YP_002402719.1	+	-	-	-	-	+	+	+	**3.A.1.2.8**	e-156	P77672	4	unknown
YP_002402721.1	+	-	-	-	+	+	+	+	**3.A.1.2.8**	e-174	P76142	5	unknown
YP_002401453.1	+	-	+	-	+	+	+	-	**3.A.1.2.9**	e--87	Q7BSH4	5	sugar
YP_002401452.1	+	-	+	-	+	+	+	-	**3.A.1.2.9**	e-25	Q7BSH5	5	sugar
YP_002269001.1	-	-	-	-	-	-	+	-	**3.A.1.20.1**	e-26	Q9Z4R9	1	siderophore
YP_002269000.1	-	-	-	-	-	-	+	-	**3.A.1.20.1**	e-28	O54372	1	siderophore
YP_002268999.1	-	-	-	-	-	-	+	-	**3.A.1.20.1**	e-70	O54370	1	siderophore
YP_002402910.1	+	+	+	+	+	+	+	+	**3.A.1.201.10**	e-17	B0Y3B6	8	multidrug
YP_002402700.1	+	+	+	+	+	+	+	+	**3.A.1.203.4**	e-55	Q50614	8	multidrug
YP_002403250.1	+	+	+	+	-	+	-	-	**3.A.1.21.1**	0	Q9Z375	5	siderophore
YP_002403251.1	+	+	+	+	-	+	-	-	**3.A.1.21.1**	0	Q9R7V3	5	siderophore
YP_002401332.1	+	+	+	+	+	+	+	+	**3.A.1.24.1**	0	P30750	8	amino acid
YP_002401330.1	+	+	+	+	+	+	+	+	**3.A.1.24.1**	e-144	P28635	8	amino acid
YP_002404813.1	+	+	+	+	+	+	+	+	**3.A.1.24.1**	e-44	P30750	8	amino acid
YP_002405049.1	+	+	+	+	+	+	+	+	**3.A.1.24.1**	e-78	P28635	8	amino acid
YP_002401331.1	+	+	+	+	+	+	+	+	**3.A.1.24.1**	e-91	P31547	8	amino acid
YP_002401844.1	+	+	+	+	+	+	+	+	**3.A.1.26.5**	e-27	A7NRG0	8	putative amino acid

YP_002404564.1	+	+	+	+	+	+	+	+	**3.A.1.27.3**	e-119	P0ADV7	8	nontransport
YP_002404566.1	+	+	+	+	+	+	+	+	**3.A.1.27.3**	e-143	P64606	8	lipid (phospholipid)
YP_002404567.1	+	+	+	+	+	+	+	+	**3.A.1.27.3**	e-145	P63386	8	nontransport
YP_002403612.1	+	+	+	+	+	+	+	+	**3.A.1.27.3**	e-149	P76506	8	nontransport
YP_002404563.1	+	+	-	+	+	+	+	+	**3.A.1.27.3**	e-44	P64602	7	nontransport
YP_002404565.1	+	+	+	+	+	+	+	+	**3.A.1.27.3**	e-91	P64604	8	nontransport
YP_002404190.1	+	+	+	+	+	+	+	-	**3.A.1.28.1**	e-105	Q8Z3V9	7	nucleoside derivative
NP_755384.1	-	-	-	+	-	-	-	-	**3.A.1.28.1**	e-64	Q8Z3V8	1	nucleoside derivative
YP_002404189.1	+	+	+	+	+	+	+	-	**3.A.1.28.1**	e-74	Q8XGV9	7	nucleoside derivative
YP_002404192.1	+	+	+	+	+	+	+	-	**3.A.1.28.1**	e-80	Q8Z3V7	7	nucleoside derivative
YP_002404191.1	+	+	+	-	+	+	+	-	**3.A.1.28.1**	e-88	Q8Z3V8	6	nucleoside derivative
YP_002403574.1	+	+	+	+	+	+	+	+	**3.A.1.3.1**	e-105	P0A2I9	8	amino acid
YP_002403573.1	+	+	+	+	+	+	+	+	**3.A.1.3.1**	e-106	P0A2I7	8	amino acid
YP_002403572.1	+	+	+	+	+	+	+	+	**3.A.1.3.1**	e-131	P02915	8	amino acid
YP_002403575.1	+	+	+	+	+	+	+	+	**3.A.1.3.1**	e-132	P02910	8	amino acid
YP_002403576.1	+	+	+	-	+	+	+	+	**3.A.1.3.1**	e-133	P09551	7	amino acid
YP_002403192.1	+	+	+	+	+	+	+	+	**3.A.1.3.10**	e-101	P0AFT2	8	amino acid
YP_002403191.1	+	+	+	+	+	+	+	+	**3.A.1.3.10**	e-121	P37774	8	amino acid
YP_002403194.1	+	+	+	+	+	+	+	+	**3.A.1.3.10**	e-130	P0AEM9	8	amino acid
YP_002401951.1	+	+	+	+	+	+	+	+	**3.A.1.3.2**	e-103	P0AEQ6	8	amino acid
YP_002401950.1	+	+	+	+	+	+	+	+	**3.A.1.3.2**	e-124	P10346	8	amino acid
YP_002401952.1	+	+	+	+	+	+	+	+	**3.A.1.3.2**	e-140	P0AEQ3	8	amino acid
YP_002402002.1	+	+	+	+	+	+	+	+	**3.A.1.3.3**	e-110	P0AE30	8	amino acid
YP_002402003.1	+	+	+	+	+	+	+	+	**3.A.1.3.3**	e-125	P0AE34	8	amino acid
YP_002402005.1	+	+	+	+	+	+	+	+	**3.A.1.3.3**	e-127	P0AAF6	8	amino acid
YP_002402001.1	+	+	+	+	+	+	+	+	**3.A.1.3.3**	e-128	P30860	8	amino acid
YP_002402004.1	+	+	+	+	+	+	+	+	**3.A.1.3.3**	e-139	P30859	8	amino acid
YP_002401760.1	+	+	+	+	+	+	+	+	**3.A.1.3.4**	e -122	P0AER5	8	amino acid
YP_002401759.1	+	+	+	+	+	+	+	+	**3.A.1.3.4**	e -126	P0AAG3	8	amino acid
YP_002401761.1	+	+	+	+	+	+	+	+	**3.A.1.3.4**	e-140	P0AER3	8	amino acid

YP_002401762.1	+	+	+	+	+	+	+	+	**3.A.1.3.4**	e-156	P37902	8	amino acid
YP_002404637.1	+	+	+	+	+	+	+	+	**3.A.1.3.8**	e-102	Q52814	8	amino acid
YP_002404638.1	+	+	+	+	+	+	+	+	**3.A.1.3.8**	e-107	Q52815	8	amino acid
YP_002404635.1	+	+	+	+	+	+	+	-	**3.A.1.3.8**	e-109	Q52812	7	amino acid
YP_002404636.1	+	+	+	+	+	+	+	+	**3.A.1.3.8**	e-93	Q52813	8	amino acid
YP_002404806.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	0	P22729	8	amino acid
YP_002404808.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	0	P04816	8	amino acid
YP_002404810.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	0	P0AD96	8	amino acid
YP_002404804.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	e-132	P22731	8	amino acid
YP_002404807.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	e-143	P0AEX7	8	amino acid
YP_002404805.1	+	+	+	+	+	+	+	+	**3.A.1.4.1**	e-144	P0A9S7	8	amino acid
YP_002402424.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	0	P06202	8	peptide
YP_002402428.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	0	P08007	8	peptide
YP_002402571.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	0	P77348	8	peptide
YP_002402426.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	e -128	P08006	8	peptide
YP_006107424.1	-	+	+	+	-	+	+	+	**3.A.1.5.1**	e-133	P06202	6	peptide
YP_002402425.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	e-166	P08005	8	peptide
YP_002402427.1	+	+	+	+	+	+	+	+	**3.A.1.5.1**	e-177	P04285	8	peptide
YP_002402688.1	+	-	-	-	+	+	+	+	**3.A.1.5.1**	e-76	P04285	5	peptide
YP_002401970.1	+	+	+	+	+	+	+	+	**3.A.1.5.11**	0	P75796	8	peptide
YP_002401971.1	+	+	+	+	+	+	+	+	**3.A.1.5.11**	0	P75797	8	peptide
YP_851922.1	-	-	+	-	-	-	-	+	**3.A.1.5.11**	e-129	P75797	2	peptide
YP_002401972.1	+	+	+	+	+	+	+	+	**3.A.1.5.11**	e-150	P75798	8	peptide
YP_002401973.1	+	+	+	+	+	+	+	+	**3.A.1.5.11**	e-157	P75799	8	peptide
YP_006108554.1	-	+	+	+	-	-	-	-	**3.A.1.5.11**	e-22	P75797	3	peptide
YP_002402689.1	+	-	-	-	+	+	+	+	**3.A.1.5.11**	e-49	P75799	5	peptide
YP_002402687.1	+	-	-	-	+	+	+	+	**3.A.1.5.12**	e-69	Q9X0F3	5	sugar
YP_006108550.1	-	+	+	+	-	-	-	-	**3.A.1.5.20**	e-43	P42065	3	peptide
YP_002403459.1	+	+	+	+	+	+	+	+	**3.A.1.5.21**	0	P33913	8	peptide (microcin)
YP_002403460.1	+	+	+	+	+	+	+	+	**3.A.1.5.21**	0	P0AFU1	8	peptide (microcin)

YP_002403461.1	+	+	+	+	+	+	+	+	**3.A.1.5.21**	0	P33915	8	peptide (microcin)
YP_002403462.1	+	+	+	+	+	+	+	+	**3.A.1.5.21**	0	Q8ZNJ8	8	peptide (microcin)
YP_002404922.1	+	+	+	+	+	+	+	+	**3.A.1.5.27**	e-114	P45096	8	peptide
YP_002404920.1	+	+	+	+	+	+	+	+	**3.A.1.5.27**	e-117	P45095	8	peptide
YP_002404919.1	+	+	+	+	+	+	+	+	**3.A.1.5.27**	e-143	P45094	8	peptide
YP_002404924.1	+	+	+	+	+	+	+	+	**3.A.1.5.27**	e-168	P33950	8	peptide
YP_002402691.1	+	-	-	-	-	+	+	+	**3.A.1.5.27**	e-40	P33950	4	peptide
YP_006108551.1	-	+	+	+	-	-	-	-	**3.A.1.5.27**	e-47	P45095	3	peptide
YP_006108553.1	-	+	+	+	-	-	-	-	**3.A.1.5.27**	e-56	P45096	3	peptide
YP_002402690.1	+	-	-	-	+	+	+	+	**3.A.1.5.27**	e-59	P45096	5	peptide
YP_002404921.1	+	+	+	+	+	+	+	+	**3.A.1.5.27**	e-92	P51000	8	peptide
YP_002401206.1	+	+	+	+	+	+	+	+	**3.A.1.5.28**	e-09	Q0P844	8	cation
YP_002401575.1	+	+	+	+	+	+	+	+	**3.A.1.5.28**	e-09	Q0P844	8	cation
YP_002401619.1	+	+	+	+	+	+	+	+	**3.A.1.5.28**	e-25	Q0P848	8	cation
YP_002404826.1	+	+	+	+	+	+	+	+	**3.A.1.5.3**	0	P33590	8	cation
YP_002404829.1	+	+	+	+	+	+	+	+	**3.A.1.5.3**	e-140	P33593	8	cation
YP_002404828.1	+	+	+	+	+	+	+	+	**3.A.1.5.3**	e-141	P0AFA9	8	cation
YP_002404830.1	+	+	+	+	+	+	+	+	**3.A.1.5.3**	e-148	P33594	8	cation
YP_002404827.1	+	+	+	+	+	+	+	+	**3.A.1.5.3**	e-180	P33591	8	cation
YP_006108552.1	-	+	+	+	-	-	-	-	**3.A.1.5.3**	e-33	P0AFA9	3	cation
YP_002402534.1	+	+	+	+	+	+	+	+	**3.A.1.5.5**	0	P36636	8	peptide
YP_002402537.1	+	+	+	+	+	+	+	+	**3.A.1.5.5**	0	P36634	8	peptide
YP_002402533.1	+	+	+	+	+	+	+	+	**3.A.1.5.5**	e-148	P36638	8	peptide
YP_002402535.1	+	+	+	+	+	+	+	+	**3.A.1.5.5**	e-152	P0A2J5	8	peptide
YP_002402536.1	+	+	+	+	+	+	+	+	**3.A.1.5.5**	e-152	P0A2J3	8	peptide
YP_002405467.1	+	+	+	+	+	+	+	+	**3.A.1.5.8**	e-34	Q97UG5	8	sugar
YP_002403724.1	+	+	+	+	+	+	+	+	**3.A.1.6.1**	0	P16676	8	anion
YP_002405298.1	+	+	+	+	+	+	+	+	**3.A.1.6.1**	0	P0AG78	8	anion
YP_002403726.1	+	+	+	+	+	+	+	+	**3.A.1.6.1**	e-125	P16701	8	anion
YP_002403725.1	+	+	+	+	+	+	+	+	**3.A.1.6.1**	e-155	P0AEB0	8	anion

YP_002403727.1	+	+	+	+	+	+	+	+	**3.A.1.6.1**	e-175	P16700	8	anion
YP_006108366.1	-	+	-	-	-	-	-	+	**3.A.1.6.1**	e-46	P0AG78	2	anion
YP_002405117.1	+	+	+	+	+	+	+	+	**3.A.1.7.1**	0	P0AG82	8	anion
YP_002405114.1	+	+	+	+	+	+	+	+	**3.A.1.7.1**	e-139	P0AAH0	8	anion
YP_002405115.1	+	+	+	+	+	+	+	+	**3.A.1.7.1**	e-153	P07654	8	anion
YP_002405116.1	+	+	+	+	+	+	+	+	**3.A.1.7.1**	e-153	P0AGH8	8	anion
YP_002401850.1	+	+	+	+	+	+	+	+	**3.A.1.8.1**	0	P09833	8	anion
YP_002401848.1	+	+	+	+	+	+	+	+	**3.A.1.8.1**	e-141	P37329	8	anion
YP_002401849.1	+	+	+	+	+	+	+	+	**3.A.1.8.1**	e-85	P0AF01	8	anion
YP_002405474.1	+	+	+	+	+	+	+	+	**3.A.1.9.1**	0	P16682	8	anion
YP_002405473.1	+	+	+	+	+	+	+	-	**3.A.1.9.1**	e-119	P16683	7	anion
YP_002405475.1	+	+	+	+	+	+	+	+	**3.A.1.9.1**	e-146	P16677	8	anion
YP_006107835.1	-	+	-	+	-	-	+	-	**3.A.11.1.3**	e-09	Q8VRK4	3	DNA
YP_853201.1	-	-	+	-	-	-	-	-	**3.A.11.1.3**	e-14	Q8VRK4	1	DNA
YP_002404645.1	+	+	+	+	+	+	+	+	**3.A.11.1.3**	e-33	Q8VRK4	8	DNA
YP_002402053.1	+	+	+	+	+	+	+	+	**3.A.11.2.2**	e-81	P44408	8	DNA
YP_002401572.1	+	+	+	+	+	+	+	+	**3.A.11.2.3**	e-14	A1EMW4	8	DNA
YP_002405316.1	+	+	+	+	+	+	+	+	**3.A.11.3.1**	e -68	Q9ZKE4	8	DNA
YP_002402314.1	+	+	+	+	+	+	+	+	**3.A.11.3.1**	e-08	Q9ZKE4	8	DNA
YP_002402030.1	+	+	+	+	+	+	+	+	**3.A.12.1.2**	0	P46889	8	putative DNA translocator
YP_001462785.1	-	-	-	-	+	-	-	-	**3.A.13.1.1**	e-23	P03657	1	filamentous phage
YP_002404339.1	+	+	+	-	+	+	-	-	**3.A.15.1.1**	0	P15645	5	protein
YP_006107724.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-08	P15749	4	protein
YP_006107726.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-09	P15751	4	protein
NP_755965.1	-	-	-	+	-	-	-	+	**3.A.15.1.1**	e-09	P15748	2	protein
YP_858931.1	-	-	+	-	-	-	-	-	**3.A.15.1.1**	e-09	P15748	1	protein
YP_002404331.1	+	-	-	-	+	-	-	-	**3.A.15.1.1**	e-11	P15752	2	protein
YP_854398.1	-	-	+	-	-	-	-	+	**3.A.15.1.1**	e-12	P15752	2	protein
YP_002404332.1	+	+	-	-	+	-	-	-	**3.A.15.1.1**	e-13	P15751	3	protein
YP_002414101.1	-	-	-	-	-	+	-	-	**3.A.15.1.1**	e-14	P15751	1	protein

YP_006107719.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-148	P15645	4	protein
YP_002404341.1	+	-	-	-	+	+	-	-	**3.A.15.1.1**	e-17	P15643	3	protein
YP_006107362.1	-	+	+	-	-	-	-	-	**3.A.15.1.1**	e-17	P15643	2	protein
YP_002404334.1	+	+	+	-	+	+	-	-	**3.A.15.1.1**	e-26	P15749	5	protein
YP_006107725.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-31	P15750	4	protein
YP_002404333.1	+	+	+	+	+	+	-	-	**3.A.15.1.1**	e-38	P15750	6	protein
YP_002404337.1	+	+	+	-	+	+	-	-	**3.A.15.1.1**	e-50	P15746	5	protein
YP_006107721.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-54	P15746	4	protein
YP_006107720.1	-	+	+	+	-	-	-	+	**3.A.15.1.1**	e-71	P15745	4	protein
YP_002404338.1	+	+	+	-	+	+	-	-	**3.A.15.1.1**	e-90	P15745	5	protein
YP_006107728.1	-	+	+	+	-	-	-	+	**3.A.15.2.1**	e-21	P22610	4	protein
YP_002272778.1	-	-	-	-	-	-	+	-	**3.A.15.2.1**	e-24	P22610	1	protein
YP_002404682.1	+	-	-	-	+	+	-	-	**3.A.15.2.1**	e-24	P22610	3	protein
YP_002401239.1	+	+	+	+	-	+	+	+	**3.A.15.2.1**	e-30	P22609	7	protein
YP_002404343.1	+	+	+	-	+	+	-	+	**3.A.15.2.1**	e-35	P22610	6	protein
YP_002404215.1	+	+	+	+	+	+	+	+	**3.A.15.2.1**	e-74	P24559	8	protein
YP_002401240.1	+	+	+	+	+	+	+	+	**3.A.15.2.1**	e-90	P22608	8	protein
NP_755574.1	-	-	-	+	-	+	-	-	**3.A.15.3.1**	e-11	Q5ZUC9	2	protein
YP_002404237.1	+	-	-	-	+	-	-	-	**3.A.16.1.2**	e-25	P25694	2	protein
YP_002404550.1	+	+	+	-	+	+	+	+	**3.A.16.1.2**	e-51	P25694	7	protein
YP_859985.1	-	-	+	-	-	+	-	+	**3.A.17.1.1**	0	P08956	3	DNA
YP_002403466.1	+	+	+	+	+	+	+	+	**3.A.17.1.1**	e-11	P08956	8	DNA
YP_002405855.1	+	+	-	+	-	-	+	-	**3.A.17.1.1**	e-40	P08956	4	DNA
YP_002404536.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e -60	P38919	8	mRNA
YP_002403871.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-47	P38919	8	mRNA
YP_002405164.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-51	P38919	8	mRNA
YP_002402586.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-56	P38919	8	mRNA
YP_002401938.1	+	+	+	+	+	+	+	+	**3.A.18.1.1**	e-60	P38919	8	mRNA
YP_002405125.1	+	+	+	+	+	+	+	+	**3.A.2.1.1**	0	P0ABB4	8	cation
YP_002405127.1	+	+	-	+	+	+	+	+	**3.A.2.1.1**	0	P0ABB0	7	cation

YP_002405131.1	+	+	+	+	+	+	+	+	**3.A.2.1.1**	e-143	P0AB98	8	cation
YP_002405126.1	+	+	+	+	+	+	+	+	**3.A.2.1.1**	e-152	P0ABA6	8	cation
YP_002405130.1	+	+	-	+	+	+	+	+	**3.A.2.1.1**	e-21	P68699	7	cation
YP_002405124.1	+	+	-	+	+	+	+	+	**3.A.2.1.1**	e-65	P0A6E6	7	cation
YP_002405129.1	+	+	-	+	+	+	+	+	**3.A.2.1.1**	e-66	P0ABA0	7	cation
YP_002405128.1	+	+	-	+	+	+	+	+	**3.A.2.1.1**	e-93	P0ABA4	7	cation
YP_002405659.1	+	+	+	+	+	+	+	+	**3.A.3.4.1**	0	P36640	8	cation
YP_002404846.1	+	-	-	-	-	-	-	-	**3.A.3.5.4**	0	Q9ZHC7	1	cation
YP_002401613.1	+	+	+	+	+	+	+	+	**3.A.3.5.5**	0	Q59385	8	cation
YP_002404819.1	+	+	+	+	+	+	+	+	**3.A.3.6.2**	0	P37617	8	cation
YP_002401790.1	+	+	+	+	+	+	+	+	**3.A.3.7.1**	0	P03960	8	cation
YP_002401791.1	+	+	+	+	+	+	+	+	**3.A.3.7.1**	0	P03959	8	cation
YP_002401789.1	+	+	+	+	+	+	+	+	**3.A.3.7.1**	e-98	P03961	8	cation
YP_002404877.1	+	-	-	-	+	+	+	+	**3.A.4.1.1**	0	P0AB93	5	anion
YP_002414640.1	-	-	-	-	-	+	-	-	**3.A.4.1.1**	0	P08690	1	anion
YP_002401234.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	0	P10408	8	protein
YP_002403901.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	0	P0AGD7	8	protein
YP_002404659.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	0	P0AGA2	8	protein
YP_002404814.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	0	P10121	8	protein
YP_002405355.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	e-48	P0AG96	8	protein
YP_002404547.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	e-57	P0AG99	8	protein
YP_002401585.1	+	+	+	+	+	+	+	+	**3.A.5.1.1**	e-65	P0AAQ6	8	protein
YP_002331410.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-108	P40290	1	protein
YP_002413886.1	-	-	-	-	-	+	+	-	**3.A.6.1.1**	e-126	P0C2V3	2	protein
YP_002331411.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-133	P0C2V3	1	protein
YP_001464196.1	-	-	-	-	+	+	+	-	**3.A.6.1.1**	e-14	Q7BFA7	3	protein
YP_002405167.1	+	+	+	+	+	+	+	+	**3.A.6.1.1**	e-15	P40290	8	protein
YP_002404120.1	+	-	-	-	+	-	+	-	**3.A.6.1.1**	e-22	Q7BFA4	3	protein
YP_002404125.1	+	-	-	-	+	+	-	-	**3.A.6.1.1**	e-23	Q93KT5	3	protein
YP_002413872.1	-	-	-	-	-	+	-	-	**3.A.6.1.1**	e-23	Q7BFA4	1	protein

YP_002331423.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-24	Q93KT5	1	protein
YP_001464194.1	-	-	-	-	+	+	+	-	**3.A.6.1.1**	e-26	Q93KT4	3	protein
YP_002331415.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-29	Q7BFA4	1	protein
YP_002404126.1	+	-	-	-	+	+	+	-	**3.A.6.1.1**	e-32	Q9ZA77	4	protein
YP_002331425.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-47	Q9ZA77	1	protein
YP_002331422.1	-	-	-	-	-	-	+	-	**3.A.6.1.1**	e-57	Q93KT4	1	protein
YP_002413885.1	-	-	-	-	-	+	+	-	**3.A.6.1.1**	e-99	P40290	2	protein
YP_002403112.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	0	P40729	8	protein
YP_002403210.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	0	P15928	8	protein
YP_002403213.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	0	P26465	8	protein
YP_002403212.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e -89	P15934	8	protein
YP_002403222.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-115	P54702	8	protein
YP_002411033.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-118	P26465	1	protein
YP_002403220.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-122	P54700	8	protein
YP_002411026.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-13	P26419	1	protein
YP_002411023.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-17	P54702	1	protein
YP_002403113.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-174	P40727	8	protein
YP_002403219.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-19	P0A1L1	8	protein
YP_002403221.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-25	P0A1L5	8	protein
YP_002411030.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-50	P15928	1	protein
YP_002411022.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-53	P40727	1	protein
YP_002411025.1	-	-	-	-	-	+	-	-	**3.A.6.2.1**	e-54	P54700	1	protein
YP_002403218.1	+	+	+	+	+	+	+	+	**3.A.6.2.1**	e-67	P26419	8	protein
YP_002401381.1	+	+	+	+	+	+	+	-	**3.A.6.2.1**	e-99	P40729	7	protein
YP_852012.1	-	-	+	-	-	-	+	-	**3.A.7.11.1**	e-14	O30554	2	DNA
YP_002411637.1	-	-	-	-	-	+	-	-	**3.A.7.11.1**	e-18	O30554	1	DNA
YP_853472.1	-	-	+	-	-	-	-	-	**3.A.7.11.1**	e-18	O30554	1	DNA
YP_002405757.1	+	-	-	-	-	-	-	-	**3.A.7.11.1**	e-18	Q5EPC7	1	DNA
YP_002404155.1	+	+	+	+	+	+	+	+	**3.A.7.11.1**	e-19	Q5K698	8	DNA
YP_002270067.1	-	-	-	-	-	-	+	-	**3.A.7.11.1**	e-19	O30554	1	DNA

YP_853783.1	-	-	+	-	-	-	-	-	**3.A.7.11.1**	e-20	O30554	1	DNA
YP_001464376.1	-	-	-	-	+	-	-	-	**3.A.7.11.1**	e-31	Q5EP68	1	DNA
YP_006104466.1	-	+	+	-	-	+	-	-	**3.A.7.13.2**	e-11	E9RJ18	3	DNA
YP_002403457.1	+	+	+	+	+	+	+	+	**3.A.7.13.2**	e-13	E9RJ18	8	DNA
NP_754289.1	-	-	-	+	-	-	-	-	**3.A.7.14.1**	e-25	Q52001	1	DNA
YP_002402937.1	+	+	+	+	+	+	+	+	**3.A.7.14.2**	e-09	Q15HU6	8	DNA
YP_002401378.1	+	-	-	+	+	-	+	+	**3.A.7.14.2**	e-11	Q15HU6	5	DNA
YP_002402954.1	+	+	+	+	+	+	+	+	**3.A.7.14.2**	e-12	Q15HU4	8	DNA
YP_002402885.1	+	+	-	+	+	+	+	+	**3.A.7.14.2**	e-16	Q15HU6	7	DNA
YP_002402282.1	+	+	+	+	+	+	+	+	**3.A.7.14.2**	e-20	Q15HU6	8	DNA
YP_002413012.1	-	-	-	-	-	+	-	-	**3.A.7.2.1**	e-40	O50337	1	DNA
YP_002413004.1	-	-	-	-	-	+	-	-	**3.A.7.3.1**	e-130	Q7VSX9	1	protein
YP_002413010.1	-	-	-	-	-	+	-	-	**3.A.7.3.1**	e-18	Q91UR4	1	protein
YP_002413011.1	-	-	-	-	-	+	-	-	**3.A.7.3.1**	e-39	Q9RPX6	1	protein
YP_002413013.1	-	-	-	-	-	+	-	-	**3.A.7.3.1**	e-60	Q91UW6	1	protein
YP_002402513.1	+	+	+	+	+	+	+	+	**3.A.7.7.1**	e -27	Q07711	8	DNA
YP_002402987.1	+	+	+	+	+	+	+	+	**3.A.7.7.1**	e-66	Q07711	8	DNA
YP_002403904.1	+	+	-	+	+	+	+	+	**3.A.8.1.1**	e-22	P38523	7	protein
YP_852649.1	-	-	+	+	-	-	-	-	**3.A.9.1.1**	e-08	Q8SKU2	2	protein
YP_002403359.1	+	+	+	+	+	+	+	+	**3.A.9.1.1**	e-14	Q02028	8	protein
YP_001461820.1	-	-	-	-	+	+	+	+	**3.A.9.1.1**	e-80	Q02028	4	protein
YP_006106088.1	-	+	-	+	-	-	-	-	**3.A.9.1.1**	e-85	Q02028	2	protein
YP_002404621.1	+	+	+	+	+	+	+	+	**3.B.1.1.5**	e-09	Q9V0A6	8	cation (Na +)
YP_002403582.1	+	+	+	+	+	+	+	+	**3.B.1.1.5**	e-11	Q9V0A4	8	cation (Na +)
YP_002403542.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P0AFF0	8	Cation (H+)
YP_002403543.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P0AFE8	8	Cation (H+)
YP_002403544.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P33607	8	Cation (H+)
YP_002403549.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P33602	8	Cation (H+)
YP_002403550.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P31979	8	Cation (H+)
YP_002403552.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	0	P33599	8	Cation (H+)

YP_002403547.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-107	P0AFD6	8	Cation (H+)
YP_002403553.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-129	P0AFC7	8	Cation (H+)
YP_002403548.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-179	P0AFD4	8	Cation (H+)
YP_002401788.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-31	P0AFE4	8	Cation (H+)
YP_002403554.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-81	P0AFC3	8	Cation (H+)
YP_002403546.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-84	P0AFE0	8	Cation (H+)
YP_002403551.1	+	+	+	+	+	+	+	+	**3.D.1.1.1**	e-97	P0AFD1	8	Cation (H+)
YP_006107377.1	-	+	+	+	+	-	-	-	**3.D.1.6.3**	e-10	Q9SK66	4	Cation (H+)
YP_002403856.1	+	+	+	+	+	+	+	+	**3.D.1.6.4**	e -06	Q6V9B1	8	Cation (H+)
YP_002404711.1	+	+	+	+	+	+	+	+	**3.D.1.8.1**	e-09	F4K2G0	8	Cation (H+)
YP_002401655.1	+	-	-	+	+	+	+	+	**3.D.1.8.1**	e-13	F4K2G0	6	Cation (H+)
YP_002403781.1	+	-	-	-	+	+	+	+	**3.D.1.9.1**	0	P77329	5	Cation (H+)
YP_002413502.1	-	-	-	-	-	+	+	+	**3.D.1.9.1**	0	P77416	3	Cation (H+)
YP_002403778.1	+	-	-	-	-	+	+	+	**3.D.1.9.1**	0	P23482	4	Cation (H+)
YP_002403780.1	+	-	-	-	-	+	+	+	**3.D.1.9.1**	0	P77437	4	Cation (H+)
YP_859767.1	-	-	+	+	-	-	-	-	**3.D.1.9.1**	e-09	P77423	2	Cation (H+)
YP_001463808.1	-	-	-	-	+	+	-	+	**3.D.1.9.1**	e-104	P0AEW1	3	Cation (H+)
YP_002403777.1	+	-	-	-	+	+	+	+	**3.D.1.9.1**	e-118	P23481	5	Cation (H+)
YP_001463807.1	-	-	-	-	+	+	+	+	**3.D.1.9.1**	e-124	P77858	4	Cation (H+)
YP_002403783.1	+	-	-	-	+	+	+	+	**3.D.1.9.1**	e-140	P77668	5	Cation (H+)
YP_002404148.1	+	+	+	+	+	+	-	+	**3.D.1.9.1**	e-30	P23481	7	Cation (H+)
YP_002403782.1	+	-	-	-	+	+	+	+	**3.D.1.9.1**	e-91	P77423	5	Cation (H+)
YP_002403982.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	0	P16431	8	Cation (H+)
YP_002403984.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	0	P16429	8	Cation (H+)
YP_002403981.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-105	P16432	8	Cation (H+)
YP_002403985.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-107	P0AAK3	8	Cation (H+)
YP_002403980.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-148	P16433	8	Cation (H+)
YP_002403983.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-148	P16430	8	Cation (H+)
YP_002404149.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-30	P0AAK3	8	Cation (H+)
YP_002403971.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-32	P0AAK3	8	Cation (H+)

YP_002403761.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-33	P0AAK3	8	Cation (H+)
YP_002404957.1	+	+	+	+	+	+	+	+	**3.D.1.9.2**	e-34	P0AAK3	8	Cation (H+)
YP_002402831.1	+	+	+	+	+	+	+	+	**3.D.2.1.1**	0	P0AB67	8	Cation (H+)
YP_002402832.1	+	+	+	+	+	+	+	+	**3.D.2.1.1**	0	P07001	8	Cation (H+)
YP_002401824.1	+	+	+	+	+	+	+	+	**3.D.4.3.2**	0	P0ABJ9	8	Cation (H+)
YP_002402178.1	+	+	+	+	+	+	+	+	**3.D.4.3.2**	0	P0ABJ9	8	Cation (H+)
YP_002401825.1	+	+	-	+	+	+	+	+	**3.D.4.3.2**	0	P0ABK2	7	Cation (H+)
YP_002402179.1	+	+	+	+	+	+	+	+	**3.D.4.3.2**	e-118	P0ABK2	8	Cation (H+)
YP_002401561.1	+	+	+	+	+	+	+	+	**3.D.4.5.1**	0	P0ABI8	8	Cation (H+)
YP_002401562.1	+	+	+	+	+	+	+	+	**3.D.4.5.1**	0	P0ABJ1	8	Cation (H+)
YP_002401560.1	+	+	+	+	+	+	+	+	**3.D.4.5.1**	e-103	P0ABJ3	8	Cation (H+)
YP_002401559.1	+	+	+	+	+	+	+	+	**3.D.4.5.1**	e-60	P0ABJ6	8	Cation (H+)
YP_002402858.1	+	+	+	+	+	+	+	+	**3.D.6.1.1**	e -41	Q07394	8	putative cation
YP_002402857.1	+	+	+	+	+	+	+	+	**3.D.6.1.1**	e -53	Q07396	8	putative cation
YP_002402861.1	+	+	+	+	+	+	+	+	**3.D.6.1.1**	e-36	P97054	8	putative cation
YP_002402862.1	+	+	+	+	+	+	+	+	**3.D.6.1.1**	e-37	P97055	8	putative cation
YP_002402860.1	+	+	+	+	+	+	+	+	**3.D.6.1.1**	e-42	Q52715	8	putative cation
YP_006105958.1	-	+	-	+	-	+	-	+	**3.D.6.1.1**	e-79	Q52716	4	putative cation
YP_002402859.1	+	-	+	-	+	-	+	+	**3.D.6.1.1**	e-82	Q52716	5	putative cation
YP_001463354.1	-	-	-	-	+	+	-	-	**3.D.6.1.2**	e-29	C4N8U0	2	putative cation
YP_002403516.1	+	+	+	+	+	+	+	+	**3.D.7.1.1**	e-14	P96797	8	Cation (H+)
YP_002404349.1	+	+	-	-	+	+	-	+	**3.D.7.1.1**	e-14	P96797	5	Cation (H+)
YP_002404371.1	+	+	+	+	+	+	+	+	**3.D.7.2.1**	e-139	O67092	8	Cation (H+)
YP_002402173.1	+	+	+	+	+	+	+	+	**3.D.7.2.1**	e-161	O67092	8	Cation (H+)
YP_002402172.1	+	+	+	+	+	+	+	+	**3.D.7.2.1**	e-92	O67095	8	Cation (H+)
YP_002402174.1	+	+	+	+	+	+	+	+	**3.D.7.2.2**	e-15	P31875	8	Cation (H+)
YP_002404374.1	+	+	+	+	+	+	+	+	**3.D.7.2.2**	e-68	P31884	8	Cation (H+)
YP_002403487.1	+	+	+	+	+	+	+	+	**3.D.8.1.2**	e-08	Q48941	8	Cation (H+)
YP_002402301.1	+	+	+	+	+	+	+	+	**4.A.1.1.1**	0	P69786	8	sugar
YP_002403720.1	+	+	+	+	+	+	+	+	**4.A.1.1.1**	e-82	P69783	8	sugar

YP_002405072.1	+	-	-	-	+	+	+	-	**4.A.1.1.10**	0	Q9AGA7	4	sugars and polyols
YP_002413660.1	-	-	-	-	-	+	-	-	**4.A.1.1.13**	e-141	Q57071	1	sugar
YP_002401774.1	+	+	+	+	+	+	+	+	**4.A.1.1.2**	0	P09323	8	amine
YP_002402850.1	+	+	+	+	+	+	+	+	**4.A.1.1.3**	0	P19642	8	sugar
YP_006107114.1	-	+	+	+	-	-	-	-	**4.A.1.1.3**	e-93	P19642	3	sugar
YP_006108267.1	-	+	+	+	-	-	-	-	**4.A.1.1.9**	e-116	P20166	3	sugar
YP_002405774.1	+	-	-	-	-	-	-	-	**4.A.1.1.9**	e-98	P20166	1	sugar
YP_002405112.1	+	+	+	+	+	-	-	+	**4.A.1.2.2**	0	P08722	6	sugar
YP_002403973.1	+	-	+	-	+	+	+	+	**4.A.1.2.3**	0	P24241	6	sugar
YP_002405657.1	+	+	+	+	+	+	+	+	**4.A.1.2.4**	0	P36672	8	sugar
YP_002403731.1	+	+	+	+	+	+	+	+	**4.A.1.2.7**	0	P77272	8	monocarboxylate (Acetylmuramic acid)
YP_002403448.1	+	+	+	+	+	+	+	+	**4.A.2.1.1**	0	P20966	8	sugar
YP_002404578.1	+	+	+	+	+	+	+	+	**4.A.2.1.1**	e -6	P69811	8	sugar
YP_002403450.1	+	+	+	+	+	+	+	+	**4.A.2.1.1**	e-180	P69811	8	sugar
YP_002405329.1	+	+	+	+	+	+	+	+	**4.A.2.1.10**	0	P32670	8	unknown
YP_002405330.1	+	+	+	+	+	+	+	+	**4.A.2.1.10**	e-173	P32672	8	unknown
YP_002405331.1	+	+	-	+	+	+	+	+	**4.A.2.1.10**	e-46	P69816	7	unknown
YP_002405334.1	+	+	+	+	+	+	+	+	**4.A.2.1.10**	e-59	P32676	8	unknown
YP_002403693.1	+	+	+	+	+	+	+	+	**4.A.2.1.11**	0	P77439	8	unknown
YP_002403696.1	+	+	+	+	+	+	+	+	**4.A.2.1.11**	0	P77579	8	unknown
YP_002403697.1	+	+	+	+	+	+	+	+	**4.A.2.1.11**	e-48	P69808	8	unknown
YP_002404576.1	+	+	+	+	+	+	+	+	**4.A.2.1.14**	e-15	D2RXA7	8	putative sugar transport
YP_002273416.1	-	-	-	-	-	-	+	+	**4.A.2.1.14**	e-16	D2RXA7	2	putative sugar transport
YP_002405282.1	+	-	-	-	+	-	-	-	**4.A.2.1.14**	e-16	D2RXA7	2	putative sugar transport
YP_002404987.1	+	+	+	+	+	+	+	+	**4.A.2.1.2**	0	P00550	8	polyol
YP_002401821.1	+	-	-	-	+	-	-	+	**4.A.2.1.3**	0	P54745	3	monocarboxylate
YP_002404197.1	+	+	+	+	+	+	+	+	**4.A.2.1.5**	e-118	P42956	8	polyol
YP_002405281.1	+	-	-	-	+	-	+	+	**4.A.2.1.6**	e-66	O31645	4	sugar
YP_006108084.1	-	+	+	+	-	-	-	-	**4.A.2.1.9**	0	Q1R4T1	3	putative sugar transport

YP_006108085.1	-	+	+	+	-	-	-	-	**4.A.2.1.9**	e-53	Q8FC73	3	putative sugar transport
YP_006108086.1	-	+	+	+	-	-	-	-	**4.A.2.1.9**	e-84	Q1R4S9	3	putative sugar transport
YP_002402962.1	+	+	+	+	+	+	+	+	**4.A.3.2.1**	0	P17334	8	N,N'-diacetylchitobiose
YP_002402739.1	+	+	+	+	+	-	-	-	**4.A.3.2.1**	e-21	P69791	5	sugar (N,N'-diacetylchitobiose)
YP_002402963.1	+	+	+	+	+	+	+	+	**4.A.3.2.1**	e-48	P69795	8	sugar
YP_002402961.1	+	+	+	+	+	+	+	+	**4.A.3.2.1**	e-59	P69791	8	sugar
YP_002402740.1	+	+	+	+	+	-	-	-	**4.A.3.2.1**	e-72	P17334	5	sugar
YP_002402741.1	+	+	+	+	+	-	-	-	**4.A.3.2.3**	e-16	O50982	5	sugar
YP_002403961.1	+	+	+	+	+	+	-	+	**4.A.4.1.1**	e-169	P56580	7	polyol
YP_002413652.1	-	-	-	-	-	+	-	-	**4.A.4.1.1**	e-31	P56579	1	polyol
YP_002403962.1	+	+	+	+	+	+	+	+	**4.A.4.1.1**	e-67	P05706	8	polyol
YP_002403960.1	+	+	+	+	+	+	-	+	**4.A.4.1.1**	e-92	P56579	7	polyol
YP_002413654.1	-	-	-	-	-	+	-	-	**4.A.4.1.2**	e-69	O32333	1	polyol
YP_002403378.1	+	+	+	+	+	+	+	+	**4.A.5.1.1**	0	P69831	8	polyol
YP_002403379.1	+	+	+	+	+	+	+	+	**4.A.5.1.1**	e-50	P37188	8	polyol
YP_002403380.1	+	+	+	+	+	+	+	+	**4.A.5.1.1**	e-82	P69828	8	polyol
YP_002415483.1	-	-	-	-	-	+	-	+	**4.A.5.1.3**	0	P39365	2	putative sugar
YP_002415484.1	-	-	-	-	-	+	-	+	**4.A.5.1.3**	e-48	P58035	2	putative sugar
YP_002415481.1	-	-	-	-	-	+	-	+	**4.A.5.1.3**	e-81	P39363	2	putative sugar
YP_006107885.1	-	+	+	+	-	+	+	-	**4.A.5.1.4**	0	Q8FCM4	5	putative sugar
YP_006107884.1	-	+	+	+	-	+	+	-	**4.A.5.1.4**	e-47	Q8FCM5	5	putative sugar
YP_859083.1	-	-	+	-	-	-	-	-	**4.A.5.1.4**	e-82	Q8FCM6	1	putative sugar
YP_002272943.1	-	-	-	-	-	-	+	-	**4.A.5.1.4**	e-85	Q8FCM6	1	putative sugar
YP_006107883.1	-	+	-	+	-	+	-	-	**4.A.5.1.4**	e-88	Q8FCM6	3	putative sugar
YP_001464286.1	-	-	-	-	+	-	-	-	**4.A.6.1.1**	e-08	P69797	1	sugar
YP_002403047.1	+	+	+	+	+	+	+	+	**4.A.6.1.1**	e-135	P69801	8	sugar
YP_002403048.1	+	+	+	+	+	+	+	+	**4.A.6.1.1**	e-149	P69805	8	sugar
YP_002403046.1	+	+	+	+	+	+	+	+	**4.A.6.1.1**	e-162	P69797	8	sugar

YP_001464283.1	-	-	-	-	+	-	-	-	**4.A.6.1.1**	e-46	P69805	1	sugar
YP_002401262.1	+	+	+	+	+	-	+	+	**4.A.6.1.12**	e-08	Q1CY66	7	putative sugar
YP_002410905.1	-	-	-	-	-	+	-	+	**4.A.6.1.12**	e-08	Q1CY66	2	putative sugar
YP_859056.1	-	-	+	-	-	-	-	-	**4.A.6.1.12**	e-08	Q1CY66	1	putative sugar
YP_006108469.1	-	+	+	+	-	+	+	-	**4.A.6.1.3**	e-115	P37082	5	polyol
YP_006108468.1	-	+	+	+	-	+	+	-	**4.A.6.1.3**	e-127	P37083	5	polyol
YP_002273538.1	-	-	-	-	-	-	+	-	**4.A.6.1.3**	e-52	P37080	1	polyol
YP_006108471.1	-	+	+	+	-	+	-	-	**4.A.6.1.3**	e-52	P37080	4	polyol
YP_006108470.1	-	+	+	+	-	+	-	-	**4.A.6.1.3**	e-77	P37081	4	polyol
YP_002404507.1	+	+	+	+	+	+	+	-	**4.A.6.1.4**	e-158	Q9KIQ2	7	amine
YP_002404505.1	+	+	+	+	+	+	+	+	**4.A.6.1.4**	e-86	Q9KIQ4	8	amine
YP_002404506.1	+	+	+	+	+	+	+	-	**4.A.6.1.4**	e-94	Q9KIQ3	7	amine
YP_002404514.1	+	+	+	+	+	+	+	+	**4.A.6.1.5**	e -140	P42911	8	amine
YP_002404513.1	+	+	+	+	+	+	-	+	**4.A.6.1.5**	e-150	Q9KIP7	7	amine
YP_002404512.1	+	+	+	+	+	+	+	+	**4.A.6.1.5**	e-76	P42909	8	amine
YP_002404508.1	+	+	+	+	+	+	+	-	**4.A.6.1.6**	e-16	Q2QKM4	7	sugar
YP_001464285.1	-	-	-	-	+	-	-	-	**4.A.6.1.7**	e-22	Q5M5W6	1	sugar
YP_859057.1	-	-	+	-	-	-	-	-	**4.A.6.1.7**	e-22	Q5M5W6	1	sugar
YP_001464284.1	-	-	-	-	+	-	-	-	**4.A.6.1.8**	e-27	Q82ZC5	1	monocarboxylate
YP_859058.1	-	-	+	-	-	-	-	-	**4.A.6.1.8**	e-33	Q82ZC5	1	monocarboxylate
YP_859059.1	-	-	+	-	-	-	-	-	**4.A.6.1.8**	e-33	Q82ZC6	1	monocarboxylate
YP_002405610.1	+	+	+	+	+	+	+	+	**4.A.7.1.1**	0	P39301	8	monocarboxylate (ascorbate)
YP_002411804.1	-	-	-	-	-	+	-	-	**4.A.7.1.1**	e-08	P69822	1	ascorbate
YP_002404198.1	+	-	-	+	+	+	+	+	**4.A.7.1.1**	e-19	P69820	6	ascorbate
YP_006107219.1	-	+	+	-	-	-	-	-	**4.A.7.1.1**	e-19	P69820	2	ascorbate
YP_002405783.1	+	+	-	+	-	-	-	-	**4.A.7.1.1**	e-27	P69820	3	ascorbate
YP_002405785.1	+	+	-	+	-	-	-	-	**4.A.7.1.1**	e-39	P39301	3	ascorbate
YP_002405611.1	+	+	-	+	-	+	+	+	**4.A.7.1.1**	e-54	P69822	6	ascorbate
YP_002405612.1	+	+	-	+	+	+	+	+	**4.A.7.1.1**	e-82	P69820	7	ascorbate

YP_002411803.1	-	-	-	-	-	+	+	-	**4.A.7.1.1**	e-89	P39301	2	ascorbate
YP_002405893.1	+	+	+	+	+	+	+	+	**4.B.1.1.1**	0	P24518	8	enzyme cofactor (nicotinamide ribonucleoside)
YP_002401835.1	+	+	+	+	+	+	+	+	**4.B.1.1.1**	e-123	P24520	8	enzyme cofactor
YP_006108510.1	-	+	+	+	-	-	-	-	**4.B.1.1.1**	e-13	P24518	3	enzyme cofactor
YP_006108509.1	-	+	+	+	-	-	-	-	**4.B.1.1.4**	e-18	Q8EDN0	3	enzyme cofactor
YP_002403034.1	+	+	+	+	+	+	+	+	**4.C.1.1.4**	0	P69451	8	lipids
YP_006106330.1	-	+	-	+	-	-	-	-	**4.C.1.1.4**	e-13	P69451	2	lipids
YP_002403253.1	+	+	+	+	-	+	-	-	**4.C.1.1.4**	e-15	P69451	5	lipids
YP_006107376.1	-	+	+	+	+	+	-	-	**4.C.1.1.4**	e-16	P69451	5	lipids
YP_002401694.1	+	+	+	+	+	+	+	+	**4.C.1.1.4**	e-19	P69451	8	lipids
YP_006106322.1	-	+	-	+	-	-	-	-	**4.C.1.1.4**	e-22	P69451	2	lipids
YP_002403257.1	+	+	+	+	-	+	-	-	**4.C.1.1.4**	e-27	P69451	5	lipids
YP_002402930.1	+	+	+	+	+	+	-	+	**4.C.1.1.4**	e-46	P69451	7	lipids
YP_002401176.1	+	+	+	+	+	+	+	+	**4.C.1.1.6**	0	P31552	8	amine (carnitine/crotonobetaine)
YP_006106321.1	-	+	-	+	-	-	-	-	**4.C.1.1.6**	e-13	P31552	2	amine
YP_002405445.1	+	+	+	+	+	+	+	+	**4.C.1.1.6**	e-30	P31552	8	amine
YP_002401702.1	+	+	+	+	+	+	+	+	**4.C.1.1.6**	e-35	P31552	8	amine
YP_002403530.1	+	+	+	+	+	+	+	+	**4.C.1.1.7**	e-12	Q42524	8	putative lipids transport
YP_006106318.1	-	+	-	+	-	-	-	-	**4.C.1.1.7**	e-14	Q42524	2	putative lipids transport
YP_006106324.1	-	+	-	+	-	-	-	-	**4.C.1.1.7**	e-19	Q42524	2	putative lipids transport
YP_002401465.1	+	+	+	+	+	+	+	+	**4.C.1.1.7**	e-28	Q42524	8	putative lipids transport
YP_002271282.1	-	-	-	-	-	-	+	-	**4.D.1.1.2**	e-09	Q54066	1	polysaccharide (hyaluronan)
YP_006108030.1	-	+	+	+	+	-	-	-	**4.D.1.1.2**	e-13	Q54066	4	polysaccharide
YP_002401492.1	+	+	+	+	+	+	-	+	**4.D.1.1.2**	e-15	Q54066	7	polysaccharide
YP_006106345.1	-	+	-	-	-	-	-	+	**4.D.1.1.2**	e-16	Q54066	2	polysaccharide

YP_002402225.1	+	+	+	+	+	-	+	+	**4.D.1.1.3**	0	P75905	7	unknown
YP_002411667.1	-	-	-	-	-	+	-	-	**4.D.1.1.3**	e-08	P75905	1	unknown
YP_002404910.1	+	+	+	+	+	-	+	+	**4.D.1.1.3**	e-09	P75905	7	unknown
YP_002405006.1	+	+	+	+	+	+	-	+	**4.D.1.1.3**	e-10	P75905	7	unknown
YP_002403523.1	+	+	+	+	+	+	+	+	**4.D.2.1.6**	e-16	F2KQZ0	8	unknown
YP_002401929.1	+	+	+	+	+	+	+	+	**4.D.2.4.2**	e-52	E6V6R4	8	unknown
YP_002405553.1	+	+	+	+	+	+	+	+	**5.A.1.1.1**	0	P36655	8	electrons
YP_006107450.1	-	+	+	+	-	+	-	-	**5.A.2.1.1**	e-09	P0A6M2	4	electrons
YP_002402366.1	+	+	+	+	+	+	+	+	**5.A.2.1.1**	e-75	P0A6M2	8	electrons
YP_002402407.1	+	+	+	+	+	+	+	+	**5.A.3.1.1**	0	P09152	8	electrons
YP_002402408.1	+	+	+	+	+	+	+	+	**5.A.3.1.1**	0	P11349	8	electrons
YP_002402410.1	+	+	+	+	+	+	+	+	**5.A.3.1.1**	e-122	P11350	8	electrons
YP_002402673.1	+	+	+	+	+	+	+	+	**5.A.3.1.2**	0	P19318	8	electrons
YP_002402674.1	+	+	+	+	+	+	+	+	**5.A.3.1.2**	0	P19319	8	electrons
YP_002402671.1	+	-	-	-	+	+	+	+	**5.A.3.1.2**	e-120	P0AF32	5	electrons
YP_006105786.1	-	+	+	+	-	-	-	-	**5.A.3.1.2**	e-98	P0AF32	3	electrons
YP_002402679.1	+	+	+	+	+	+	-	+	**5.A.3.2.1**	0	P24183	7	electrons
YP_002405276.1	+	+	+	+	-	+	-	+	**5.A.3.2.1**	0	P24183	6	electrons
YP_002402681.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e -107	P0AEK7	8	electrons
YP_002405275.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e-135	P0AAJ3	8	electrons
YP_002402705.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e-16	P24183	8	electrons
YP_002403485.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e-17	P24183	8	electrons
YP_002402680.1	+	+	-	+	+	+	+	+	**5.A.3.2.1**	e-172	P0AAJ3	7	electrons
YP_002404373.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e-25	P0AAJ3	8	electrons
YP_002405455.1	+	+	+	+	+	+	-	+	**5.A.3.2.1**	e-42	P24183	7	electrons
YP_002405274.1	+	+	+	+	+	+	+	+	**5.A.3.2.1**	e-61	P0AEK7	8	electrons
YP_859488.1	-	-	+	-	-	-	-	+	**5.A.3.2.1**	e-85	P24183	2	electrons
YP_002402816.1	+	+	+	+	+	+	+	+	**5.A.3.3.1**	0	P77374	8	electrons
YP_002402817.1	+	+	+	+	+	+	+	+	**5.A.3.3.1**	0	P77783	8	electrons
YP_002402818.1	+	+	+	+	+	+	+	+	**5.A.3.3.1**	e-128	P0AAJ1	8	electrons

YP_002402819.1	+	+	+	+	+	+	+	+	**5.A.3.3.1**	e-145	P76173	8	electrons
YP_002402034.1	+	+	+	+	+	+	+	+	**5.A.3.3.2**	0	P18775	8	electrons
YP_002402035.1	+	+	+	+	+	+	+	+	**5.A.3.3.2**	e-128	P18776	8	electrons
YP_002402036.1	+	+	+	+	+	+	+	+	**5.A.3.3.2**	e-146	P18777	8	electrons
YP_002271992.1	-	-	-	-	-	-	+	-	**5.A.3.3.2**	e-180	P18775	1	electrons
YP_002271991.1	-	-	-	-	-	-	+	-	**5.A.3.3.2**	e-62	P18776	1	electrons
YP_002402198.1	+	+	+	+	+	+	+	+	**5.A.3.4.1**	0	P33226	8	electrons
YP_002402199.1	+	+	+	+	+	+	+	+	**5.A.3.4.1**	0	P33225	8	electrons
YP_006105129.1	-	+	+	+	-	-	-	+	**5.A.3.4.1**	e-105	P36662	4	electrons
YP_002402200.1	+	-	-	-	+	+	+	+	**5.A.3.4.1**	e-109	P36662	5	electrons
YP_002403481.1	+	+	+	+	+	+	+	+	**5.A.3.4.1**	e-44	P33226	8	electrons
YP_002403105.1	+	+	+	+	+	+	+	+	**5.A.3.4.2**	0	P58362	8	electrons
YP_002403106.1	+	+	+	+	+	+	+	+	**5.A.3.4.2**	0	P52005	8	electrons
YP_002404935.1	+	+	+	+	+	+	+	+	**5.A.3.4.3**	0	P20099	8	electrons
YP_002402902.1	+	+	+	+	+	+	+	+	**5.A.3.5.1**	e-17	P0A1I1	8	electrons
YP_002402898.1	+	+	+	+	+	+	+	+	**5.A.3.5.1**	e-52	P37602	8	electrons
YP_002402899.1	+	+	+	+	+	+	+	+	**5.A.3.5.1**	e-56	P0A1I1	8	electrons
YP_859689.1	-	-	+	-	-	-	-	+	**5.A.3.5.2**	e-11	P31075	2	electrons
YP_002405449.1	+	+	+	+	+	+	+	+	**5.A.3.5.2**	e-39	P31077	8	electrons
YP_002405448.1	+	+	+	+	+	+	+	+	**5.A.3.5.2**	e-58	P31076	8	electrons
YP_002401814.1	+	+	+	+	+	+	+	+	**3.D.10.1.1**	0	Q65GF4	8	Cation (H+)
YP_002401815.1	+	+	+	+	+	+	+	+	**3.D.10.1.1**	e-17	Q65GF5	8	Cation (H+)
YP_002405572.1	+	+	+	+	+	+	+	+	**3.D.10.1.1**	e-24	Q65GF5	8	Cation (H+)
YP_002403869.1	+	+	+	+	+	-	+	+	**3.D.10.1.1**	e-41	Q65GF4	7	Cation (H+)
YP_002405573.1	+	+	+	+	+	+	+	+	**3.D.10.1.1**	e-74	Q65GF4	8	Cation (H+)
YP_002413941.1	-	-	-	-	-	+	-	-	**5.B.1.6.1**	e-58	Q9KN15	1	putative electron
YP_002404894.1	+	+	+	+	-	+	+	+	**5.B.3.1.1**	e-59	Q74FY6	7	electrons
YP_002405447.1	+	+	+	+	+	+	+	+	**5.B.5.1.1**	e-14	Q8EG35	8	electrons
YP_002403948.1	+	+	-	+	+	+	+	+	**8.A.1.1.1**	0	P27303	7	nontransport auxiliary
YP_002405458.1	+	+	+	+	+	+	+	+	**8.A.1.1.3**	e-149	B1LPP9	8	nontransport auxiliary

YP_002404985.1	+	+	+	+	+	+	+	+	**8.A.1.1.3**	e-19	B1LPP9	8	nontransport auxiliary
YP_002404970.1	+	-	-	-	+	-	+	+	**8.A.1.1.3**	e-22	B1LPP9	4	nontransport auxiliary
YP_006108793.1	-	+	-	+	-	-	-	-	**8.A.1.3.1**	0	P06739	2	nontransport auxiliary
YP_002401592.1	+	+	+	+	+	+	+	+	**8.A.1.6.1**	0	P0AE06	8	nontransport auxiliary
YP_002404631.1	+	+	+	+	+	+	+	+	**8.A.1.6.1**	e-128	P0AE06	8	nontransport auxiliary
YP_002403363.1	+	+	+	+	+	+	+	+	**8.A.1.6.2**	0	P76397	8	nontransport auxiliary
YP_002404889.1	+	+	+	+	+	+	+	+	**8.A.1.6.3**	0	P37636	8	nontransport auxiliary
YP_002404607.1	+	+	+	+	+	+	+	+	**8.A.1.7.1**	e-167	P46482	8	nontransport auxiliary
YP_852742.1	-	-	+	-	-	-	-	-	**8.A.1.7.1**	e-28	P46482	1	nontransport auxiliary
YP_002402874.1	+	+	-	+	+	+	+	+	**8.A.1.7.1**	e-53	P46482	7	nontransport auxiliary
YP_002401255.1	+	+	+	+	+	+	+	+	**8.A.2.1.3**	e-62	P0AA95	8	nontransport auxiliary
YP_002405591.1	+	+	+	+	+	+	+	+	**8.A.21.2.1**	e-08	O59180	8	nontransport auxiliary
YP_002405590.1	+	+	+	+	+	+	+	+	**8.A.21.2.1**	e-09	O59180	8	nontransport auxiliary
YP_002405393.1	+	-	-	-	+	-	-	-	**8.A.21.2.1**	e-22	O59180	2	nontransport auxiliary
YP_002401618.1	+	+	+	+	+	+	+	+	**8.A.21.2.1**	e-37	O59180	8	nontransport auxiliary
YP_002401445.1	+	+	+	+	+	+	+	+	**8.A.28.1.1**	e-14	Q01484	8	nontransport auxiliary
YP_002268839.1	-	-	-	-	-	-	+	-	**8.A.28.1.1**	e-14	Q01484	1	nontransport auxiliary
YP_002402181.1	+	-	-	-	+	-	+	+	**8.A.3.3.1**	0	P38134	4	nontransport auxiliary
YP_002403350.1	+	+	+	+	+	+	+	+	**8.A.3.3.2**	0	P76387	8	nontransport auxiliary
YP_006107340.1	-	+	+	+	-	+	-	-	**8.A.4.1.1**	0	P42501	4	nontransport auxiliary
YP_002401546.1	+	+	+	+	+	+	+	+	**8.A.5.1.3**	e-39	P63144	8	nontransport subunit
YP_002404378.1	+	+	+	+	+	+	+	+	**8.A.5.1.3**	e-43	P63144	8	nontransport subunit
YP_006104526.1	-	+	+	+	+	+	+	-	**8.A.5.1.4**	e-09	P80874	6	nontransport subunit
YP_002415593.1	-	-	-	-	-	+	-	-	**8.A.5.1.4**	e-11	P80874	1	nontransport subunit
YP_002404388.1	+	+	+	+	+	+	+	+	**8.A.5.1.4**	e-15	P80874	8	nontransport subunit
YP_002401335.1	+	+	+	+	+	+	+	+	**8.A.5.1.4**	e-16	P80874	8	nontransport subunit
YP_006104523.1	-	+	+	+	-	+	+	-	**8.A.5.1.4**	e-17	P80874	5	putative auxiliary (nontransport)
YP_002402877.1	+	+	+	+	+	+	-	+	**8.A.5.1.4**	e-18	P80874	7	putative auxiliary
YP_002412506.1	-	-	-	-	-	+	-	-	**8.A.5.1.4**	e-21	P80874	1	putative auxiliary

YP_002403007.1	+	+	+	+	+	+	+	+	**8.A.5.1.4**	e-23	P80874	8	putative auxiliary
YP_002404097.1	+	+	+	+	+	+	+	+	**8.A.5.1.4**	e-27	P80874	8	putative auxiliary
YP_002412501.1	-	-	-	-	-	+	-	-	**8.A.5.1.4**	e-28	P80874	1	putative auxiliary
YP_006104522.1	-	+	+	+	-	+	-	-	**8.A.5.1.4**	e-37	P80874	4	putative auxiliary
YP_002402997.1	+	+	+	+	+	+	+	+	**8.A.5.1.4**	e-47	P80874	8	putative auxiliary
YP_002403719.1	+	+	+	+	+	+	+	+	**8.A.7.1.1**	0	P08839	8	putative auxiliary
YP_002402379.1	+	+	+	+	+	+	-	+	**8.A.7.1.3**	e-12	D2RXA5	7	putative auxiliary
YP_002404092.1	+	+	+	+	+	+	+	+	**8.A.7.1.3**	e-84	D2RXA5	8	putative auxiliary
YP_006108870.1	-	+	+	+	-	-	-	-	**8.A.7.1.4**	e-26	D4GYE2	3	putative auxiliary
YP_002402931.1	+	+	+	+	+	+	+	+	**8.A.7.1.4**	e-36	D4GYE2	8	putative auxiliary
YP_002403718.1	+	+	-	+	+	+	+	+	**8.A.8.1.1**	e-42	P0AA04	7	putative auxiliary
YP_002401531.1	+	+	+	+	+	+	+	+	**8.A.9.1.1**	e-15	Q05839	8	nontransport auxiliary
YP_002405656.1	+	+	+	+	+	+	+	+	**8.A.9.1.1**	e-69	Q05839	8	nontransport auxiliary
YP_002401691.1	+	+	+	+	+	+	+	+	**8.B.14.1.2**	0	P05825	8	putative auxiliary
YP_002404843.1	+	-	-	-	-	-	-	-	**9.A.10.1.5**	e-26	Q09920	1	cation (ferric)
YP_002402220.1	+	+	+	+	+	+	+	+	**9.A.10.2.3**	0	P0AB24	8	cation (lead)
YP_002402221.1	+	+	+	+	+	+	+	+	**9.A.10.2.3**	0	P31545	8	cation (lead)
YP_002402219.1	+	+	+	+	+	+	+	-	**9.A.10.2.3**	e-132	P75901	7	cation (lead)
YP_002271817.1	-	-	-	-	-	-	+	-	**9.A.15.1.1**	e-11	P53104	1	nontransport
YP_002401503.1	+	+	+	+	+	+	+	+	**9.A.18.1.1**	0	P0AFY6	8	peptide (microcin)
YP_002403745.1	+	+	+	+	+	+	+	+	**9.A.28.1.1**	0	P41796	8	amine
YP_002269831.1	-	-	-	-	-	-	+	-	**9.A.30.1.1**	0	Q7B1W8	1	anion
YP_002404459.1	+	+	+	+	+	+	+	+	**9.A.30.1.2**	e-90	F0N2E7	8	putative anion transport
YP_001463282.1	-	-	-	-	+	-	-	-	**9.A.33.1.1**	e-13	Q9KW03	1	nontransport
YP_852021.1	-	-	+	-	-	-	-	-	**9.A.33.1.1**	e-26	Q9KW03	1	nontransport
NP_752898.1	-	-	-	+	-	-	-	-	**9.A.33.1.1**	e-31	Q9KW03	1	nontransport
YP_002271335.1	-	-	-	-	-	-	+	-	**9.A.33.1.1**	e-33	Q9KW03	1	nontransport
YP_002401352.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	0	Q9KN49	3	protein
YP_851415.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	0	Q9KN45	2	protein

YP_002410990.1	-	-	-	-	-	+	-	-	**3.A.23.1.1**	0	Q9KN49	1	protein
YP_002401349.1	+	-	-	-	+	-	-	-	**3.A.23.1.1**	0	Q9KN45	2	protein
YP_851418.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	0	Q9KN49	1	protein
YP_006107110.1	-	+	+	+	+	-	-	-	**3.A.23.1.1**	e-08	Q9KN44	4	protein
YP_002401348.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-09	Q9KN44	3	protein
YP_006107095.1	-	+	+	+	+	-	-	-	**3.A.23.1.1**	e-10	Q9KN50	4	protein
YP_851420.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-101	Q9KN51	2	protein
YP_002401365.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-104	B2D7K2	3	protein
YP_002401354.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-106	Q9KN51	3	protein
YP_002402664.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-107	B2D7K2	3	protein
YP_002410986.1	-	-	-	-	-	+	-	-	**3.A.23.1.1**	e-11	Q9KN44	1	protein
YP_006107107.1	-	+	+	-	-	-	-	-	**3.A.23.1.1**	e-11	Q9KN54	2	protein
YP_851414.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	e-11	Q9KN44	1	protein
YP_002404292.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-11	Q9KN45	1	protein
YP_002401676.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-110	B2D7K2	3	protein
YP_851429.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	e-115	B2D7K2	1	protein
YP_854041.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	e-12	Q9KN45	1	protein
YP_006105771.1	-	+	-	+	-	+	-	-	**3.A.23.1.1**	e-123	B2D7K2	3	protein
YP_852610.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-123	B2D7K2	2	protein
YP_006105776.1	-	+	-	+	-	-	-	-	**3.A.23.1.1**	e-125	B2D7K2	2	protein
YP_851424.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-128	Q9KN55	2	protein
YP_006107104.1	-	+	-	+	-	-	-	-	**3.A.23.1.1**	e-13	Q9KN45	2	protein
YP_002401358.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-135	Q9KN55	3	protein
YP_001461389.1	-	-	-	-	+	-	+	-	**3.A.23.1.1**	e-14	Q9KN47	2	protein
YP_002410989.1	-	-	-	-	-	+	-	-	**3.A.23.1.1**	e-14	Q9KN47	1	protein
YP_851417.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	e-14	Q9KN47	1	protein
YP_859967.1	-	-	+	-	-	-	-	-	**3.A.23.1.1**	e-15	Q9KN48	1	protein
YP_002401351.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-15	Q9KN47	1	protein
YP_002401355.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-19	Q9KN52	3	protein
YP_851421.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-19	Q9KN52	2	protein

YP_002404288.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-19	Q9KN54	1	protein
YP_001464287.1	-	-	-	-	+	-	-	-	**3.A.23.1.1**	e-20	Q9KN48	1	protein
YP_002402382.1	+	+	+	+	+	+	-	+	**3.A.23.1.1**	e-23	Q9KN48	7	protein
YP_002404298.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-27	B2D7K2	1	protein
YP_006107094.1	-	+	+	+	+	-	-	-	**3.A.23.1.1**	e-32	Q9KN51	4	protein
YP_002404771.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-33	Q9KN48	8	protein
YP_002404304.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-37	Q9KN51	1	protein
YP_002402565.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-41	Q9KN48	8	protein
YP_851422.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-41	Q9KN53	2	protein
YP_002402546.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-44	Q9KN48	8	protein
YP_002401353.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-45	Q9KN50	3	protein
YP_002401356.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-45	Q9KN53	3	protein
YP_851419.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-47	Q9KN50	2	protein
YP_006108519.1	-	+	+	+	-	-	-	-	**3.A.23.1.1**	e-47	Q9KN48	3	protein
YP_002405248.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-48	Q9KN48	8	protein
YP_002403967.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-49	Q9KN48	8	protein
YP_002401461.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-50	Q9KN48	8	protein
YP_851416.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-50	Q9KN46	2	protein
YP_002403992.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-51	Q9KN48	8	protein
YP_002403785.1	+	-	-	-	+	+	+	+	**3.A.23.1.1**	e-52	Q9KN48	5	protein
YP_002411028.1	-	-	-	-	-	+	-	-	**3.A.23.1.1**	e-53	Q9KN48	1	protein
YP_002405379.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-56	Q9KN48	8	protein
YP_002401350.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-56	Q9KN46	1	protein
YP_002268822.1	-	-	-	-	-	-	+	-	**3.A.23.1.1**	e-57	Q9KN46	1	protein
YP_006106593.1	-	+	+	+	-	+	-	+	**3.A.23.1.1**	e-58	Q9KN48	5	protein
YP_002403848.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-59	Q9KN48	8	protein
YP_001461388.1	-	-	-	-	+	-	-	-	**3.A.23.1.1**	e-60	Q9KN46	1	protein
YP_002404132.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-61	Q9KN48	8	protein
YP_002401357.1	+	-	-	-	+	-	+	-	**3.A.23.1.1**	e-64	Q9KN54	3	protein
YP_851423.1	-	-	+	-	-	+	-	-	**3.A.23.1.1**	e-64	Q9KN54	2	protein

YP_002402023.1	+	+	+	+	+	+	+	+	**3.A.23.1.1**	e-69	Q9KN49	8	protein
YP_006107106.1	-	+	+	+	-	-	-	-	**3.A.23.1.1**	e-76	Q9KN55	3	protein
YP_002404289.1	+	-	-	-	-	-	-	-	**3.A.23.1.1**	e-78	Q9KN55	1	protein
YP_006107098.1	-	+	+	+	+	-	-	-	**3.A.23.2.1**	0	Q6EE14	4	protein
YP_002404252.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	0	Q6EE14	1	protein
YP_002404300.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	0	Q6EE14	1	protein
YP_002404303.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-10	A8YQS0	1	protein
YP_851426.1	-	-	+	-	-	+	-	-	**3.A.23.2.1**	e-101	Q6EE20	2	protein
YP_002401360.1	+	-	-	-	+	-	-	-	**3.A.23.2.1**	e-106	Q6EE20	2	protein
YP_006107093.1	-	+	+	+	+	-	-	-	**3.A.23.2.1**	e-107	Q6EE20	4	protein
YP_002404305.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-107	Q6EE20	1	protein
YP_002404254.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-12	A8YQS0	1	protein
YP_002404257.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-13	A8YQR8	1	protein
YP_002403884.1	+	+	+	+	+	+	+	+	**3.A.23.2.1**	e-144	Q6EE14	8	protein
YP_002401362.1	+	-	-	-	+	-	+	-	**3.A.23.2.1**	e-15	Q6EE21	3	protein
YP_002404266.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-166	Q6EE20	1	protein
YP_002404259.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-17	A8YQR6	1	protein
YP_006107092.1	-	+	+	+	+	-	-	-	**3.A.23.2.1**	e-20	Q6EE21	4	protein
YP_002404253.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-20	A8YQS1	1	protein
YP_002404262.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-22	Q6EE15	1	protein
YP_002404306.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-23	Q6EE21	1	protein
YP_002404267.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-32	Q6EE21	1	protein
YP_001464145.1	-	-	-	-	+	-	-	-	**3.A.23.2.1**	e-34	A8YQR5	1	protein
YP_006107099.1	-	+	-	+	-	-	-	-	**3.A.23.2.1**	e-35	A8YQR5	2	protein
YP_002404256.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-35	A8YQR9	1	protein
YP_854036.1	-	-	+	-	-	-	-	-	**3.A.23.2.1**	e-36	A8YQR5	1	protein
YP_002404258.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-36	A8YQR7	1	protein
YP_002404263.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-61	Q6EE16	1	protein
YP_002404261.1	+	-	-	-	-	-	-	-	**3.A.23.2.1**	e-69	A8YQR5	1	protein
YP_002404217.1	+	+	+	+	+	+	+	+	**9.A.4.1.2**	e-86	P64564	8	unknown

YP_002403353.1	+	+	+	+	+	+	+	+	**9.A.40.1.1**	e-30	Q54318	8	putative transporter
YP_002401764.1	+	+	+	+	+	+	+	+	**9.A.40.1.2**	e-153	P0A2L3	8	putative transporter
YP_002403045.1	+	+	+	+	+	+	+	+	**9.A.40.1.2**	e-22	P0A2L3	8	putative transporter
YP_002403903.1	+	+	+	+	+	+	-	+	**9.A.40.2.1**	e-29	P54428	7	putative transporter
YP_002405637.1	+	+	+	+	+	+	+	+	**9.A.40.2.1**	e-32	P54428	8	putative transporter
YP_002403820.1	+	+	+	+	+	+	+	+	**9.A.41.1.1**	0	P44669	8	polysaccharide
YP_002404617.1	+	+	+	+	+	+	+	+	**9.A.41.1.1**	e-10	P44669	8	polysaccharide
YP_006107343.1	-	+	+	+	-	+	-	-	**9.A.41.1.2**	0	P42217	4	polysaccharide
YP_006107344.1	-	+	+	+	-	+	-	-	**9.A.41.1.3**	0	P42218	4	polysaccharide
YP_002405841.1	+	+	+	+	+	+	+	+	**9.A.5.4.1**	e-48	D2YRH2	8	unknown
YP_002404759.1	+	+	+	+	+	+	+	+	**9.A.8.1.1**	0	P33650	8	cation (ferrous)
YP_002403805.1	+	+	+	+	+	+	+	+	**9.A.8.1.9**	e -08	Q57986	8	cation (ferrous)
YP_002403455.1	+	+	+	+	+	+	+	+	**9.B.10.1.1**	e-10	P94400	8	cation (zinc)
YP_002405857.1	+	+	+	+	+	+	+	+	**9.B.10.1.1**	e-20	P94400	8	cation (zinc)
YP_006105318.1	-	+	-	+	-	-	-	-	**9.B.10.1.1**	e-26	P94400	2	cation (zinc)
YP_002403203.1	+	+	+	+	+	+	+	+	**9.B.102.1.1**	0	P31064	8	putative transporter
YP_002403305.1	+	-	+	-	+	-	+	+	**9.B.102.1.2**	0	P33015	5	putative transporter
YP_002402982.1	+	+	+	+	+	+	+	+	**9.B.102.4.1**	e -12	A0LFK9	8	putative transporter
YP_002403815.1	+	+	+	+	+	+	+	+	**9.B.102.4.1**	e-17	A0LFK9	8	putative transporter
YP_002404773.1	+	+	+	+	+	+	+	+	**9.B.104.1.1**	e-162	P09391	8	putative protein cleavage
YP_002401165.1	+	+	+	+	+	+	+	+	**9.B.105.1.1**	e-22	Q58AJ7	8	cation (Pb)
YP_002401982.1	+	+	+	+	+	+	+	+	**9.B.105.1.3**	e-12	P94571	8	unknown
YP_002403422.1	+	+	+	+	+	+	+	+	**9.B.114.1.1**	e -126	P0AFY2	8	unknown
YP_002404457.1	+	+	+	+	+	+	-	+	**9.B.114.1.1**	e-31	P0AFY2	7	unknown
YP_002272559.1	-	-	-	-	-	-	+	-	**9.B.114.1.1**	e-32	P0AFY2	1	unknown
YP_002403420.1	+	+	+	+	+	+	+	+	**9.B.117.1.1**	e-116	C6EAH0	8	auxiliary
YP_006108536.1	-	+	+	+	-	-	-	-	**9.B.117.1.1**	e-12	C6EAH0	3	auxiliary
YP_002404724.1	+	+	+	+	+	+	-	+	**9.B.118.1.1**	0	P45546	7	unknown
YP_002403930.1	+	+	-	+	+	+	+	+	**9.B.12.2.1**	e-26	P0AE42	7	unknown

YP_002404231.1	+	+	+	+	+	+	+	+	**9.B.120.1.1**	e -114	Q46831	8	unknown
YP_002404900.1	+	+	+	+	+	+	+	+	**9.B.121.1.1**	0	P37645	8	unknown
YP_002402322.1	+	-	-	-	+	-	-	-	**9.B.122.1.1**	e-63	P75962	2	unknown
YP_006105429.1	-	+	+	+	-	+	-	+	**9.B.122.1.1**	e-65	P75962	5	unknown
YP_002272577.1	-	-	-	-	-	-	+	+	**9.B.124.1.1**	e-48	P64592	2	unknown
YP_002404479.1	+	-	-	-	+	+	-	-	**9.B.124.1.1**	e-49	P64592	3	unknown
YP_002404478.1	+	+	+	+	+	+	+	+	**9.B.124.1.2**	e-71	P64591	8	unknown
YP_006104179.1	-	+	+	+	-	-	-	-	**9.B.124.1.4**	e-10	G2GUD4	3	unknown
YP_002401244.1	+	+	+	+	+	+	+	+	**9.B.125.1.1**	e-158	P0AE14	8	unknown
YP_002404898.1	+	+	+	+	+	+	+	+	**9.B.126.1.1**	0	P37642	8	lipids
YP_002405265.1	+	+	+	+	+	+	+	+	**9.B.126.2.1**	e -136	P0A8K8	8	putative lipids transport
YP_002403735.1	+	+	+	+	+	+	+	+	**9.B.127.1.1**	e-66	P76538	8	unknown
YP_002405179.1	+	+	+	+	+	+	+	+	**9.B.128.1.1**	0	B6I4D1	8	putative transporter
YP_002403475.1	+	+	+	+	+	+	+	+	**9.B.14.1.3**	0	P33927	8	putative transporter
YP_002405450.1	+	+	+	+	+	+	+	+	**9.B.14.1.3**	e-56	P33927	8	putative transporter
YP_002403478.1	+	+	+	+	+	+	+	+	**9.B.14.2.3**	e-145	P0ABM1	8	siderophore
YP_002401932.1	+	+	+	+	+	+	+	+	**9.B.15.1.1**	e-61	P0AAW6	8	unknown
YP_002401535.1	+	+	+	+	+	+	+	+	**9.B.18.1.1**	e-57	P0ADZ7	8	unknown
YP_002404884.1	+	+	+	+	+	+	+	+	**9.B.20.2.1**	e-20	Q55026	8	cation (Mg 2+)
YP_002405188.1	+	+	+	+	+	+	+	+	**9.B.21.2.1**	e-61	P27838	8	unknown
YP_002405640.1	+	+	+	+	+	+	+	+	**9.B.22.1.1**	0	Q4JI69	8	protein (leukotoxin)
YP_002402975.1	+	+	+	+	+	+	+	+	**9.B.27.1.1**	e-101	P76219	8	putative anion transport
YP_002402977.1	+	+	+	+	+	+	+	+	**9.B.27.1.2**	e -120	P76221	8	putative anion transport
YP_002404385.1	+	+	+	+	+	+	+	+	**9.B.27.2.1**	e -102	P0AA60	8	unknown
YP_002401202.1	+	+	+	+	+	+	+	+	**9.B.27.2.2**	e -12	P0AA63	8	unknown
YP_002404470.1	+	+	+	+	+	+	+	+	**9.B.27.2.2**	e-118	P0AA63	8	unknown
YP_002271726.1	-	-	-	-	-	-	+	+	**9.B.27.2.3**	e-107	P0ABP6	2	unknown
YP_002403583.1	+	+	+	+	+	+	-	-	**9.B.27.2.3**	e-113	P0ABP6	6	putative anion

YP_002414644.1	-	-	-	-	-	+	-	-	**9.B.28.1.1**	e-45	B5LWZ8	1	putative transporter
YP_002404880.1	+	-	-	-	+	-	-	-	**9.B.28.1.1**	e-47	B5LWZ8	2	putative transporter
YP_002404525.1	+	+	+	+	-	+	+	+	**9.B.28.1.2**	e-09	A8VTI4	7	putative transporter
YP_002403051.1	+	+	+	+	+	+	+	+	**2.A.207.1.1**	e-95	P76264	8	cation (Mg 2+)
YP_002404162.1	+	+	+	+	+	+	+	+	9.B.30.1.1	e-44	P54176	8	unknown
YP_002404431.1	+	+	+	+	+	+	+	+	**9.B.31.1.1**	e -108	P60782	8	unknown
YP_002404986.1	+	+	+	+	+	+	+	+	**9.B.32.1.1**	e-68	P32108	8	unknown
YP_002404971.1	+	-	-	-	+	-	+	+	**9.B.32.1.2**	e-59	P0ADK5	4	unknown
YP_859761.1	-	-	+	+	-	-	-	-	**9.B.33.1.1**	e-18	Q81JL2	2	unknown
YP_002403404.1	+	+	+	+	+	+	+	+	**9.B.33.1.1**	e-72	Q81JL2	8	unknown
YP_002403690.1	+	+	+	+	+	+	+	+	**9.B.33.1.1**	e-77	Q81JL2	8	unknown
YP_002403895.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-11	Q1J0W6	8	unknown
YP_002403357.1	+	+	+	+	+	+	-	+	**9.B.34.1.1**	e-11	Q1J0W6	7	unknown
YP_002403012.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-12	Q1J0W6	8	unknown
YP_002403020.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-12	Q1J0W6	8	unknown
YP_002402528.1	+	+	+	+	+	+	-	+	**9.B.34.1.1**	e-14	Q1J0W6	7	unknown
YP_002403011.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-15	Q1J0W6	8	unknown
YP_002402727.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-16	Q1J0W6	8	unknown
YP_002401975.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-17	Q1J0W6	8	unknown
YP_006106274.1	-	+	+	+	+	+	+	+	**9.B.34.1.1**	e-18	Q1J0W6	7	unknown
YP_002401513.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-18	Q1J0W6	8	unknown
YP_002402583.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-19	Q1J0W6	8	unknown
YP_002402745.1	+	+	+	+	+	+	+	+	**9.B.34.1.1**	e-19	Q1J0W6	8	unknown
YP_006105155.1	-	+	+	+	+	-	+	+	**9.B.34.1.1**	e-20	Q1J0W6	7	unknown
YP_002402694.1	+	-	-	-	+	+	+	+	**9.B.34.1.1**	e-21	Q1J0W6	5	unknown
YP_002401910.1	+	-	-	-	+	-	-	-	**9.B.34.1.1**	e-21	Q1J0W6	2	unknown
YP_002403242.1	+	+	+	+	+	+	+	+	**9.B.35.2.1**	e-15	O32142	8	putative amine (thyroxine)
YP_002404887.1	+	+	+	+	+	+	+	+	**9.B.36.1.1**	e-85	P0AET5	8	unknown
YP_002404867.1	+	+	+	+	+	+	+	+	**9.B.4.1.1**	e-63	P0A8S5	8	unknown

YP_006105896.1	-	+	-	-	-	-	-	-	**9.B.42.1.1**	e-10	P45754	1	unknown
YP_858923.1	-	-	+	-	-	-	-	-	**9.B.42.1.1**	e-15	P45754	1	unknown
YP_006107716.1	-	+	-	+	-	-	-	+	**9.B.42.1.1**	e-25	P45754	3	unknown
YP_002403244.1	+	+	+	+	+	+	+	+	**9.B.43.1.1**	e-97	Q8XB73	8	unknown
YP_002404946.1	+	+	+	+	+	+	+	+	**9.B.44.1.1**	e -59	P11286	8	unknown
YP_002404945.1	+	+	+	+	+	+	+	+	**9.B.44.1.1**	e-79	P0ADJ8	8	unknown
YP_001462755.1	-	-	-	-	+	-	-	-	**9.B.49.1.2**	e-131	Q81E21	1	monocarboxylate
YP_006108725.1	-	+	+	+	-	-	-	-	**9.B.50.1.2**	e-147	Q11G42	3	dicarboxylate
YP_002403564.1	+	+	+	+	+	+	+	+	**9.B.50.1.2**	e-64	Q11G42	8	dicarboxylate
YP_002401706.1	+	+	+	+	+	+	+	+	**9.B.59.1.1**	0	P15078	8	putative peptide
YP_002405859.1	+	+	+	+	+	+	+	+	**9.B.59.1.1**	0	P15078	8	putative peptide
YP_002328941.1	-	-	-	-	-	-	-	+	**9.B.6.1.1**	e-15	P0ACG4	1	unknown
YP_002328942.1	-	-	-	-	-	-	-	+	**9.B.6.1.1**	e-18	P0ACG4	1	unknown
YP_002327608.1	-	-	-	-	-	-	+	+	**9.B.6.1.1**	e-22	P0ACG4	2	unknown
YP_002327609.1	-	-	-	-	-	-	-	+	**9.B.6.1.1**	e-22	P0ACG4	1	unknown
YP_002404840.1	+	-	-	-	-	-	-	-	**9.B.62.1.1**	e-154	Q47455	1	putative copper
YP_002403073.1	+	+	+	+	+	+	+	+	**9.B.62.1.2**	e-19	P12377	8	putative copper
YP_858992.1	-	-	+	-	-	-	+	+	**9.B.65.1.1**	0	P45804	3	putative transporter
YP_002414511.1	-	-	-	-	-	+	-	+	**9.B.65.1.1**	0	P45804	2	putative transporter
YP_002404749.1	+	-	-	-	+	-	-	+	**9.B.65.1.1**	0	P45804	3	putative transporter
YP_006107791.1	-	+	-	+	-	-	-	-	**9.B.65.1.1**	0	P45804	2	putative transporter
NP_754452.1	-	-	-	+	-	-	-	-	**9.B.67.3.2**	e-10	A7V2W2	1	unknown
YP_006108029.1	-	+	+	+	+	-	-	-	**9.B.67.5.1**	e-37	P27243	4	unknown
YP_002403716.1	+	+	+	+	+	+	+	+	**9.B.7.1.1**	e-151	P0A6J3	8	putative anion transport
YP_002401732.1	+	+	+	+	+	+	+	+	**9.B.71.1.1**	e-69	P37002	8	unknown
YP_002402836.1	+	+	+	+	+	+	+	+	**9.B.72.1.1**	e-25	P52112	8	putative monocarboxylate
YP_002403753.1	+	+	+	+	+	+	+	+	**9.B.75.2.1**	e-131	P76555	8	amino acid
YP_002405676.1	+	+	+	+	+	+	+	+	**9.B.93.1.1**	e-174	P0AF98	8	putative transporter
YP_002404356.1	+	+	+	+	+	+	-	-	**9.B.93.1.2**	e-169	E1IMB6	6	putative transporter
YP_002404944.1	+	+	+	+	+	+	+	+	**9.B.97.1.1**	e-177	P37669	8	cofactor substrate

NP_752900.1	-	-	-	+	-	-	-	-	9.B.97.1.3	e-16	Q2NEN2	1	putative transporter

7. Figure Legends

Figure 1. Distribution of transport proteins according to TC class (top) & TC subclass (bottom) for *E. coli* K12 str. MG1655 (top) and the seven pathogenic strains combined (bottom). Similar distributions for the eight *E. coli* strains individually and combined are presented in supplementary figures S1A-S1I.

Figure 2. Total number of proteins associated with iron transport in the eight *E. coli* strains in which (A) shows the relationship between the serovars (x-axis) and number of iron-siderophore transporters (y-axis). The OMR-type transporters are represented in dark gray while the ABC iron-siderophore uptake porters are presented in light gray. (B) Correlation between iron-sequestering OMRs (x-axis) and ABC iron-uptake transporters (y-axis) for the eight strains of *E. coli* examined. The best-fit line has a slope of 1.85 and a R^2 value is 0.90.

Figure 3. Schematic view of an *E. coli* cell showing transport proteins of particular importance for pathogenesis. All *E. coli* cells have the same secondary carriers for iron uptake which therefore do not play a specific role in pathogenesis (center left). Systems preferentially present in pathogens (top) often lacking in *E. coli* K12, include pro-toxins, ABC-type iron uptake systems which are proposed to function with their iron-specific outer membrane receptors (OMRs), transenvelope protein secretion systems types 1-6 and autotransporters of the types AT1-3 transporters specifically found in extracellular versus intracellular pathogens are illustrated in the bottom right and left, respectively. See text for details.

Figure S1. Distribution of transport proteins organized according to TC class (left) & TC subclass (right) for each strain examined: (A) *E. coli* 559, (B) ABU, (C) APE, (D) CFT, (E) E24, (F) UMN, (G) O15, (H) K12 and (I) all eight strains.

***Detailed Response to Reviewers**

Dear Dr. Gorvel,

Thank you for the second editorial review of our manuscript. We were pleased that reviewer #1 was happy with the revisions made, but are particularly grateful to reviewer #2 for the further useful suggestions for improvement. We have attempted to satisfy all of the criticisms cited in the letter, and we will go through these point by point to mention how we have modified the manuscript in accordance with these suggestions.

Major revisions (Reviewer #2):

(1) A complete legend describing Figure 3 has now been provided. Additionally, in the previous revised manuscript, Table 1 had been modified to alter the APEC O1 designation from ExPEC to AIEC, and this convention has been used throughout the paper. In Table 6, we have now deleted the statement “energy-transducing systems” for both TonB and TolA. In the previous revision of the manuscript, we did remove Table 8 and combined Figures 2 and 3, as stated in our covering letter. Complete descriptions of all figures can be found on the figure legends page. We apologize for not having previously corrected reference to Table S2 (which is no longer referred to in the text), and we have referred to Table S1 both at the end of the methods section and the beginning of the results section.

(2) The reviewer’s second major concern deals with our treatment of OMR energizers. We have corrected the text to state that TonB and not TolA play a role in OMR function. We have further clarified the occurrences of Tol complexes, mentioning not only the number of TolA homologs in the different strains, but also referring to all of the constituents of this complex (See section 3.2.4). We have also provided the relevant references suggested by Reviewer #2.

(3) The colors presented in Tables S1 and 8 are now explained.

(4) The reference cited (Reddy and Saier, 2012) provides detailed information about the programs used, but in the methods section, we have also described how these programs have been used for the current studies. As mentioned, orthologous relationships are defined by a cutoff of 95% identity except in rare instances when sequence divergence was more extensive.

(5) Reviewer #2 is absolutely correct; the number of unique transport proteins present in the pathogenic strains but lacking in K12 is not 718, but 838. We have corrected this mistake in section 3.1.1.

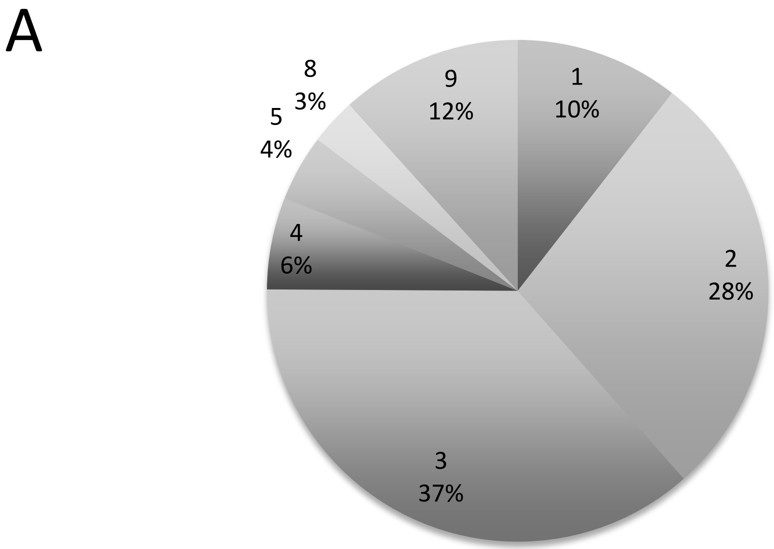
We thank you and the reviewers for the careful review of our revised manuscript. In fact, we are so grateful that we would like to acknowledge his or her contribution in the acknowledgement section. We hope these revisions render our paper suitable for publication in *Microbial Pathogenesis*. If further improvements are desired, we will be happy to modify the manuscript further.

Yours sincerely,

Fengyi (Andy) Tang and Milton H. Saier, Jr.

Figure

Distribution of transport proteins in E. coli K12 organized by class



Distribution of Transport Proteins in E. Coli K 12 Organized by Subclass

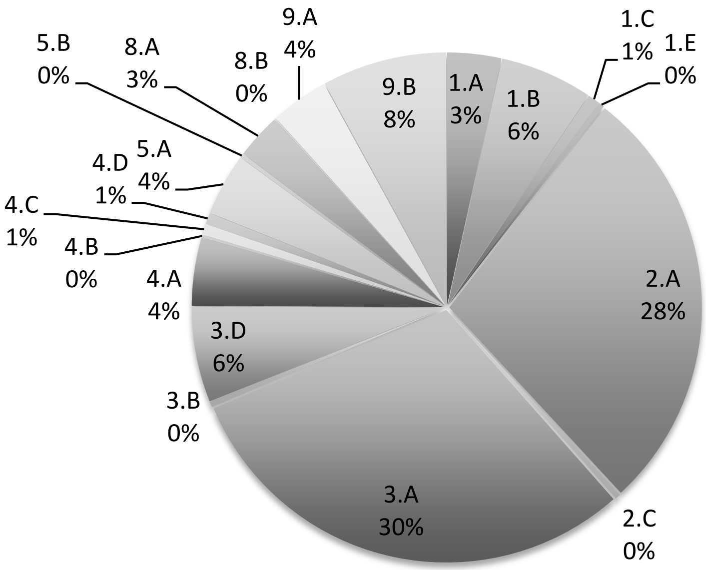
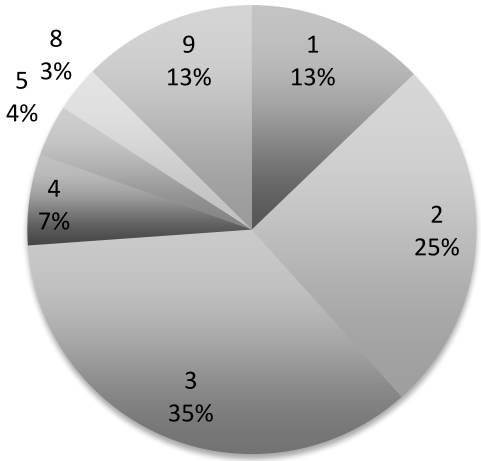


Figure 1

Distribution of combined transport proteins exclusively in seven pathogenic strains organized by TC class

B



Distribution of combined transport proteins exclusively in seven pathogenic strains organized by TC subclass

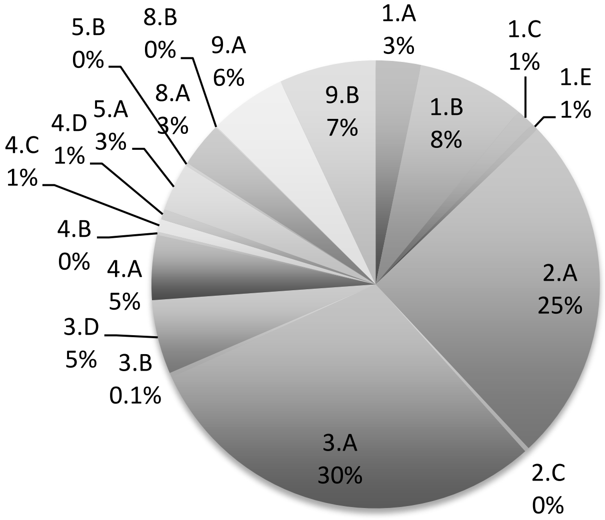
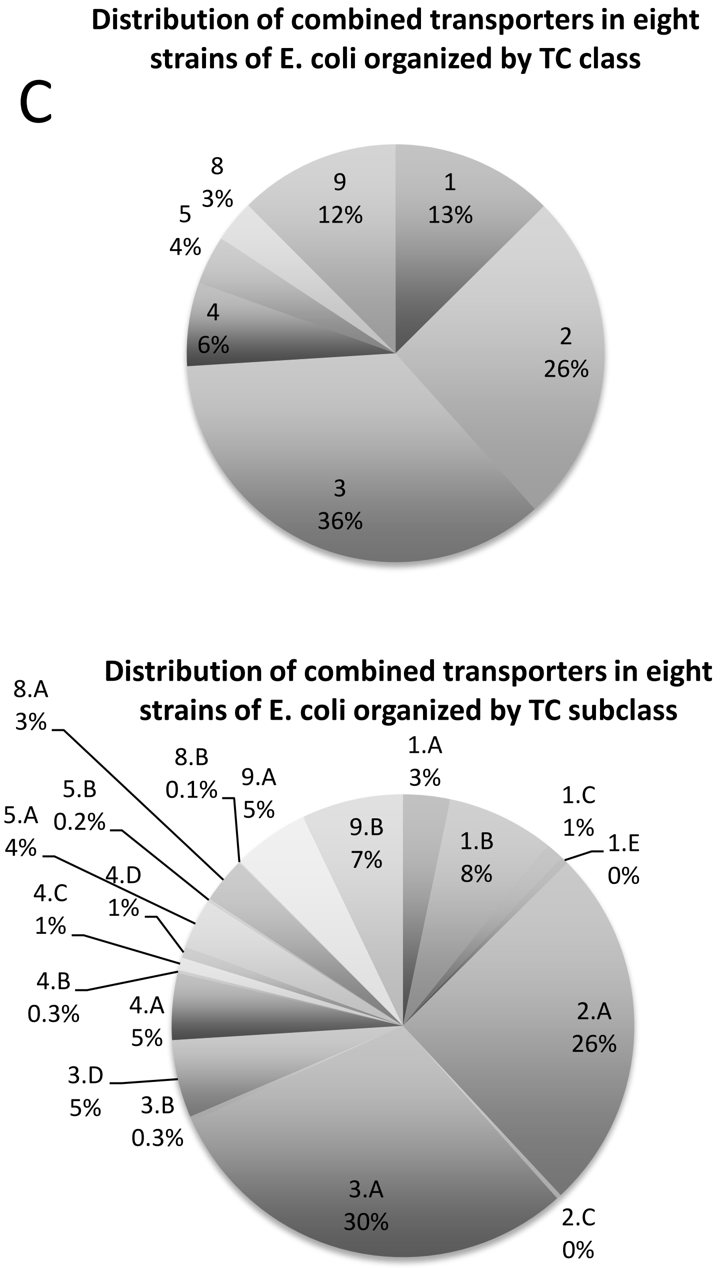


Figure 1



C

Distribution of combined transporters in eight strains of E. coli organized by TC class

Distribution of combined transporters in eight strains of E. coli organized by TC subclass

Figure 1

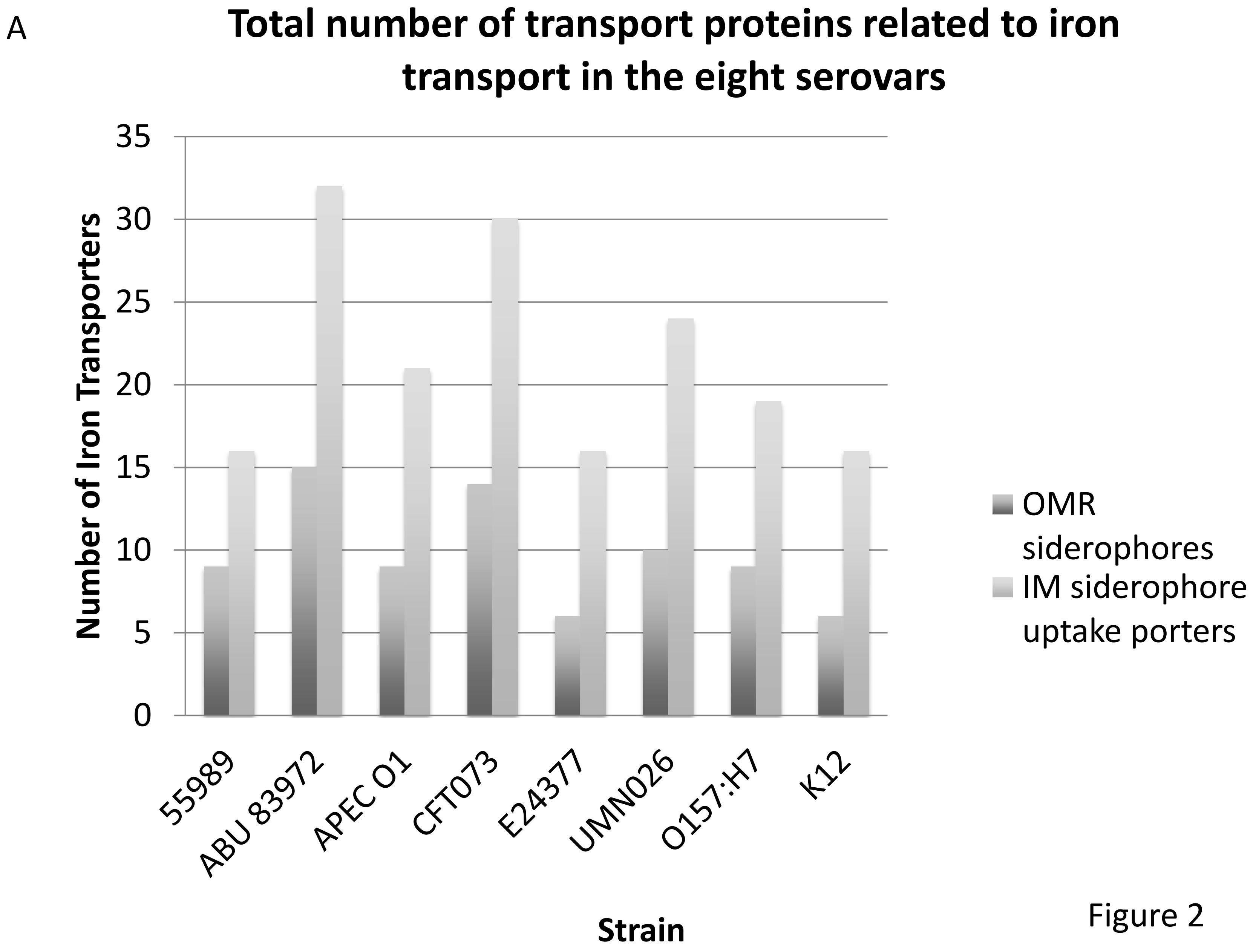

A
Total number of transport proteins related to iron transport in the eight serovars
Number of Iron Transporters
35
30
25
20
15
10
5
0
55989
ABU 83972
APEC O1
CFT073
E24377
UMN026
O157:H7
K12
Strain
OMR siderophores
IM siderophore uptake porters

Figure 2

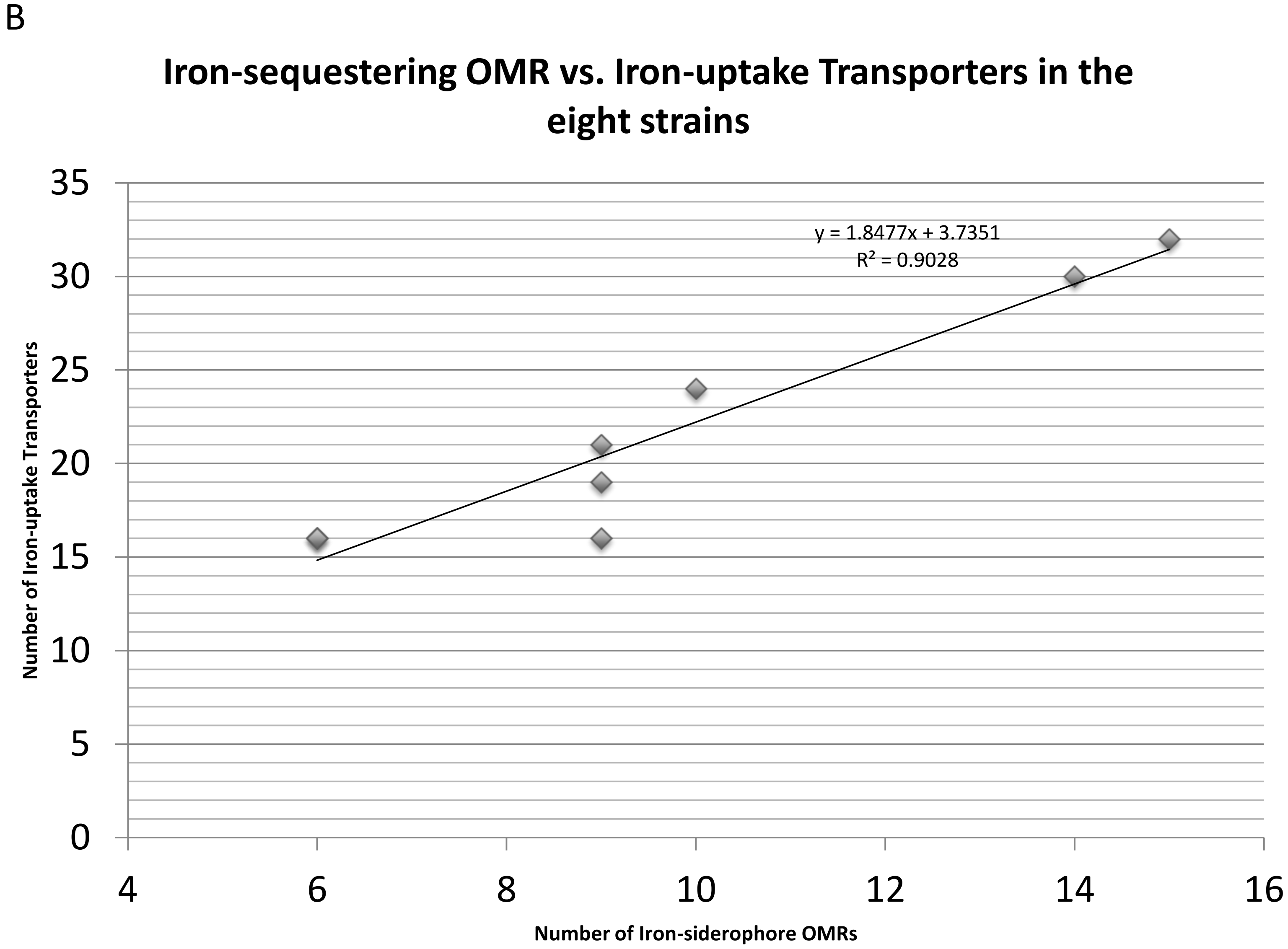
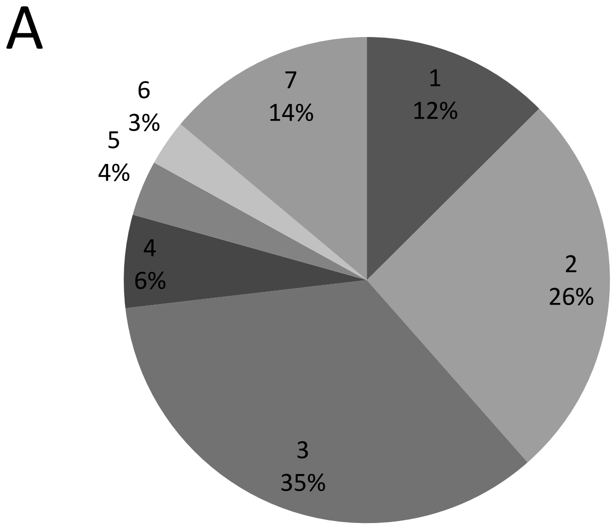
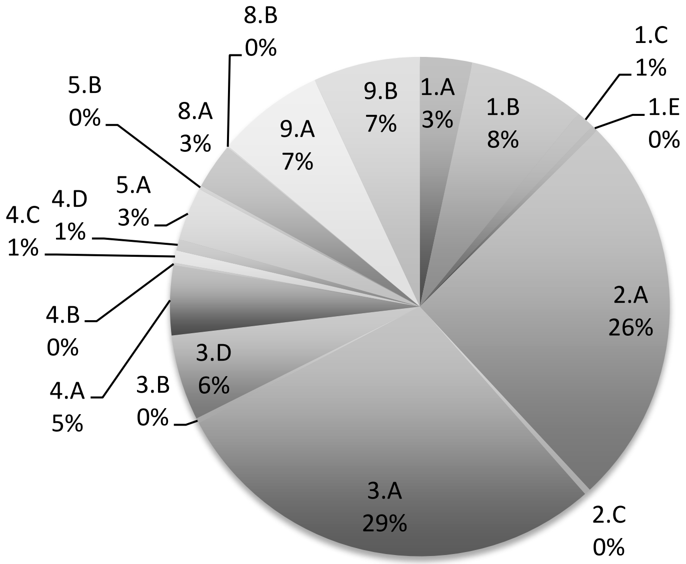

B
Iron-sequestering OMR vs. Iron-uptake Transporters in the eight strains
y = 1.8477x + 3.7351
R² = 0.9028
Number of Iron-uptake Transporters
0
5
10
15
20
25
30
35
4
6
8
10
12
14
16
Number of Iron-siderophore OMRs

Figure 2



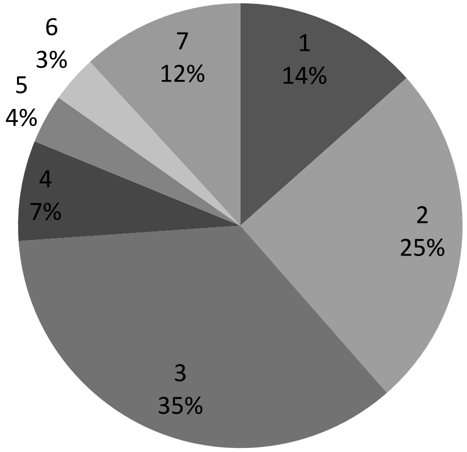
Distribution of transport proteins in E. coli 55989 organized by TC class



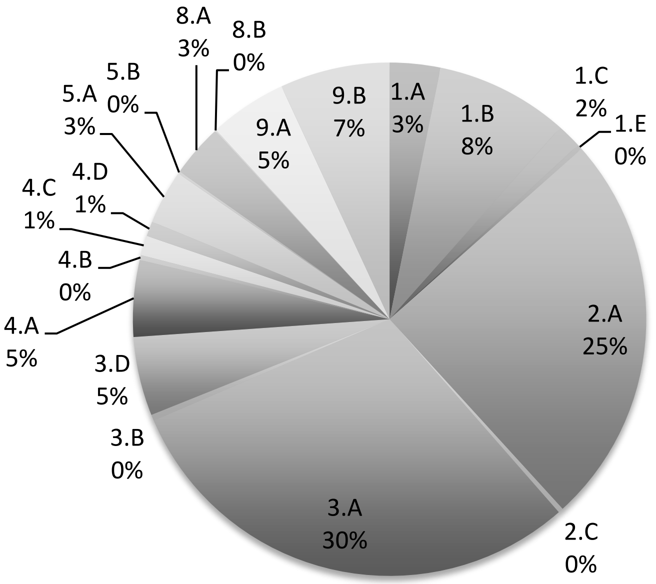
Distribution of Transport proteins in E. coli 55989 organized by TC subclass

Figure S1

B

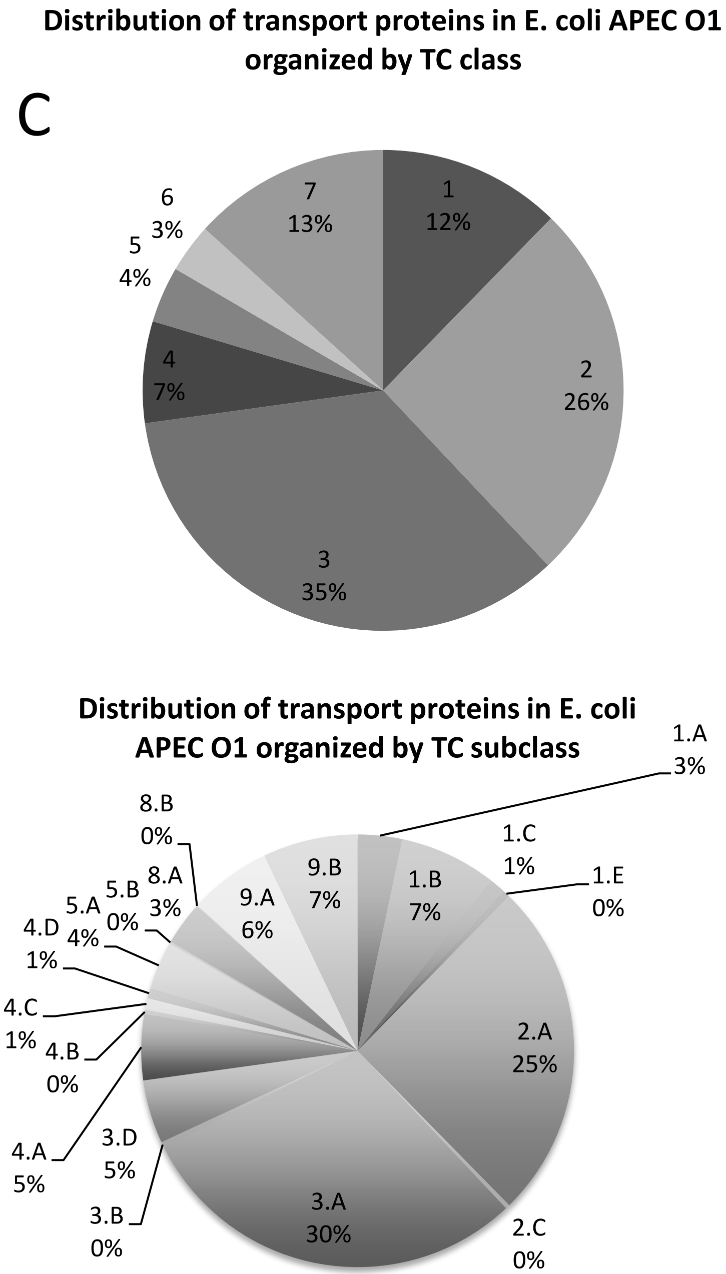


Distribution of transport proteins in E. coli ABU 83972 organized by TC class



Distribution of transport proteins in E. coli ABU 83972 organized by TC subclass

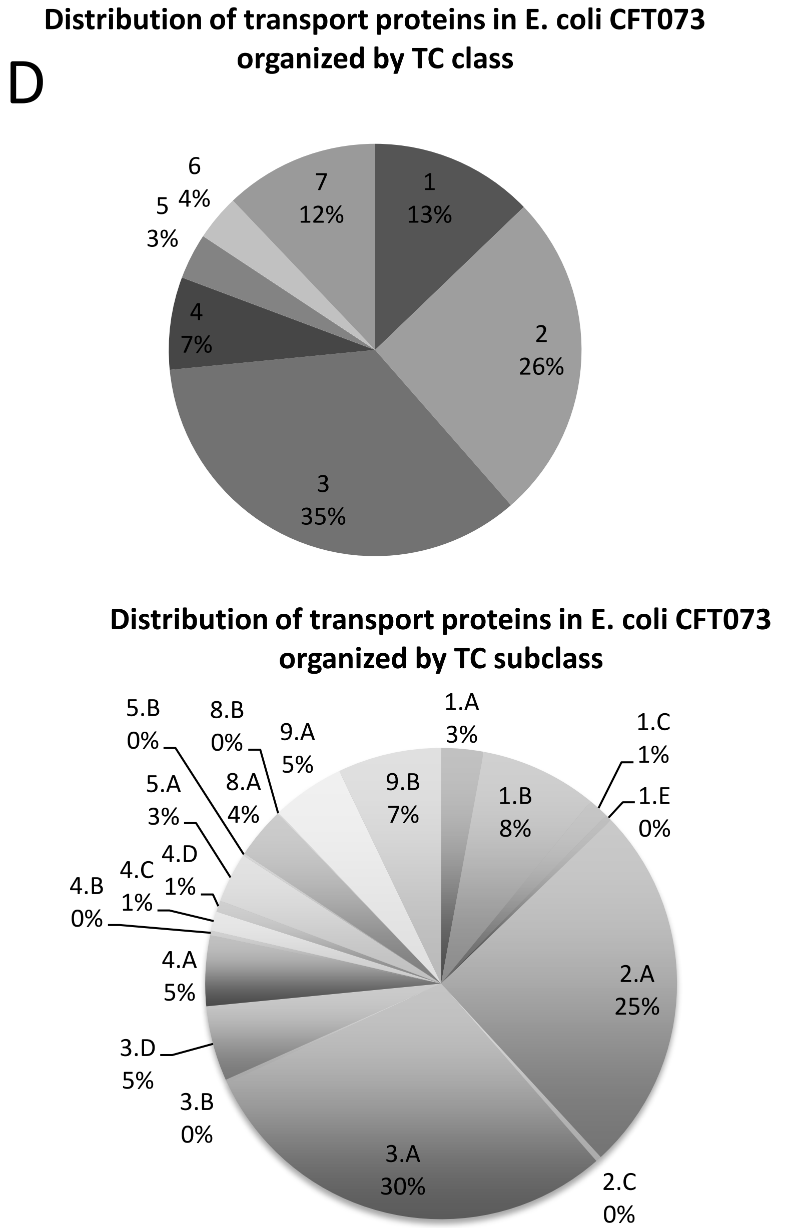
Figure S1



Distribution of transport proteins in E. coli APEC O1 organized by TC class

Distribution of transport proteins in E. coli APEC O1 organized by TC subclass

Figure S1



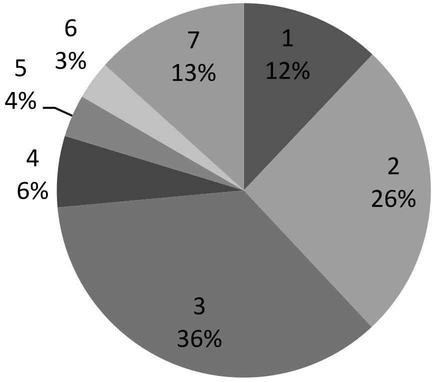
Distribution of transport proteins in E. coli CFT073 organized by TC class

Distribution of transport proteins in E. coli CFT073 organized by TC subclass

Figure S1

E

Distribution of transport proteins in E. coli E24377A organized by TC class



Distribution of transport proteins in E. coli E24377A organized by TC subclass

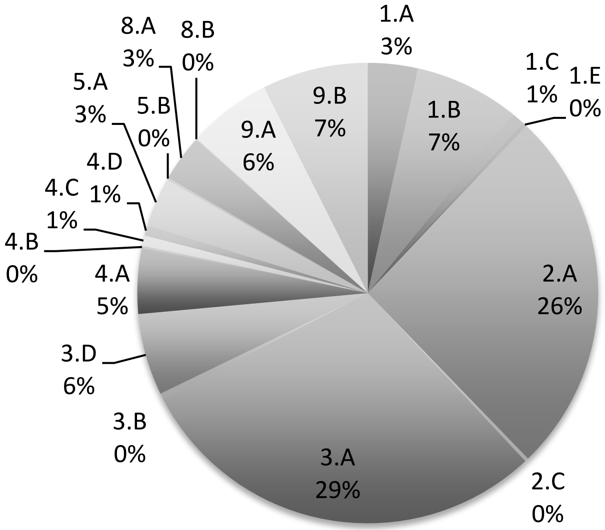
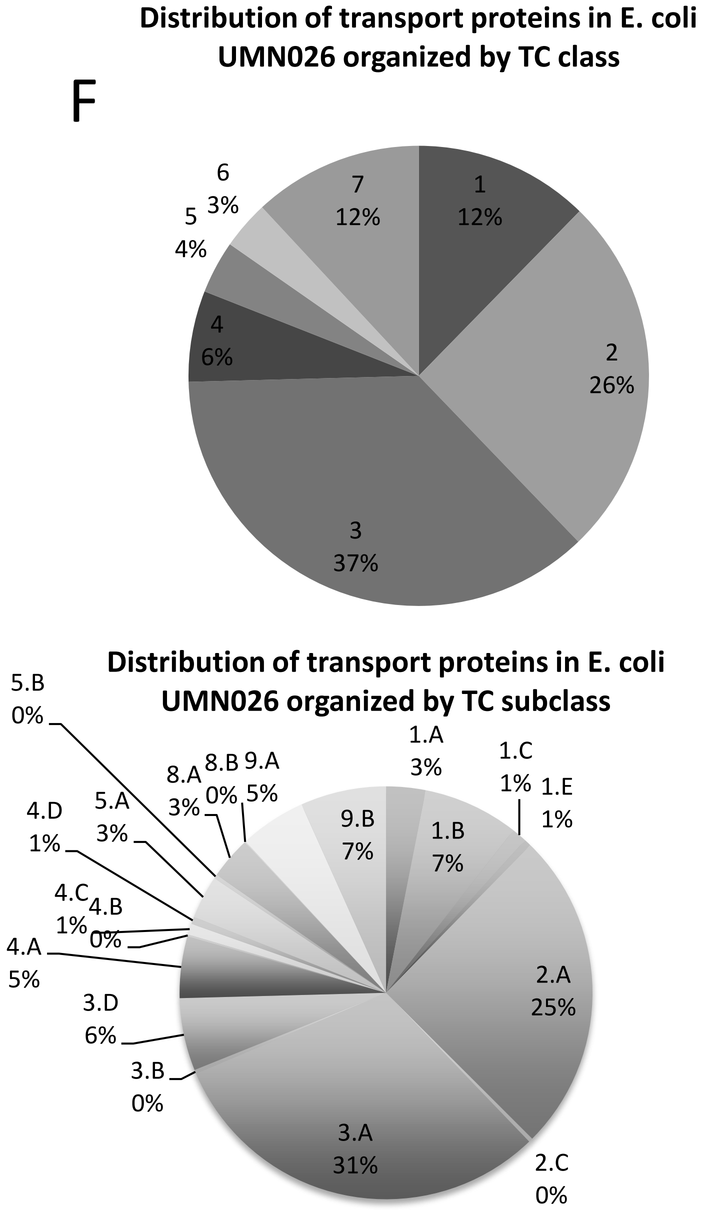


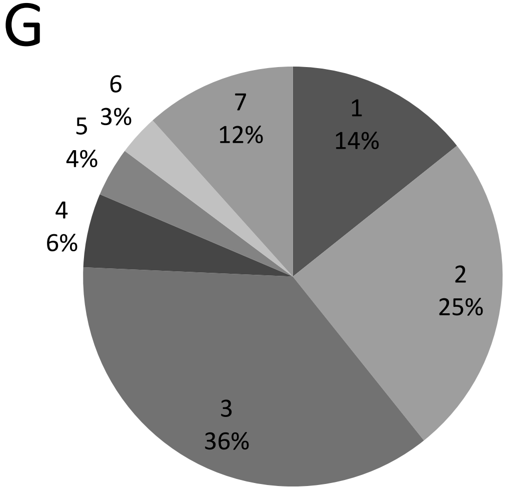
Figure S1



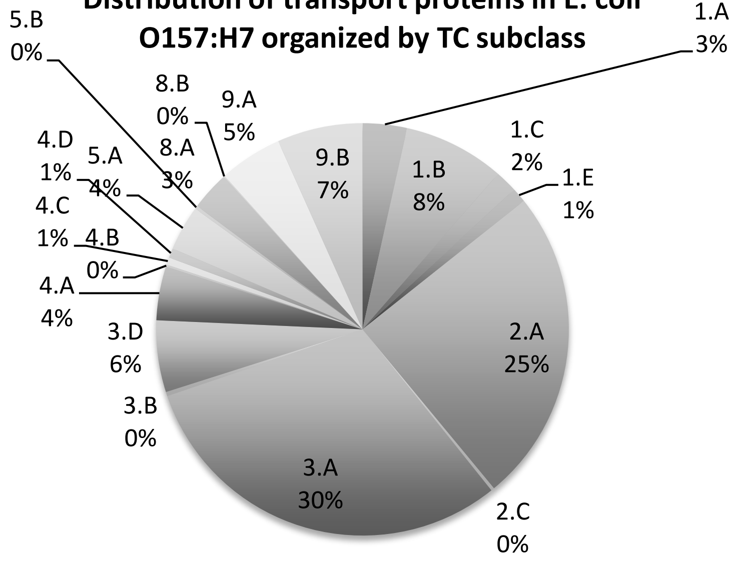
Distribution of transport proteins in E. coli UMN026 organized by TC class

Distribution of transport proteins in E. coli UMN026 organized by TC subclass

Figure S1

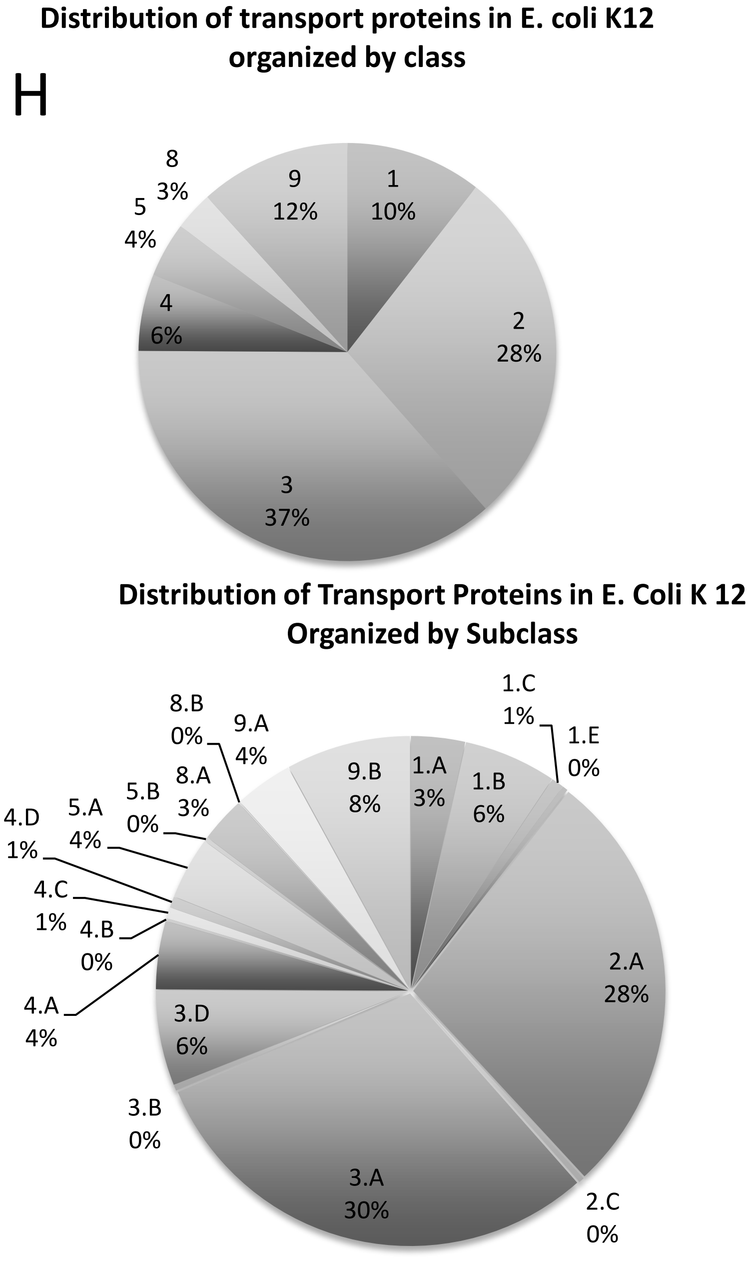


Distribution of transport proteins in E. coli O157:H7 organized by TC class



Distribution of transport proteins in E. coli O157:H7 organized by TC subclass

Figure S1



H

Distribution of transport proteins in E. coli K12 organized by class

Distribution of Transport Proteins in E. Coli K 12 Organized by Subclass

Figure S1

Figure

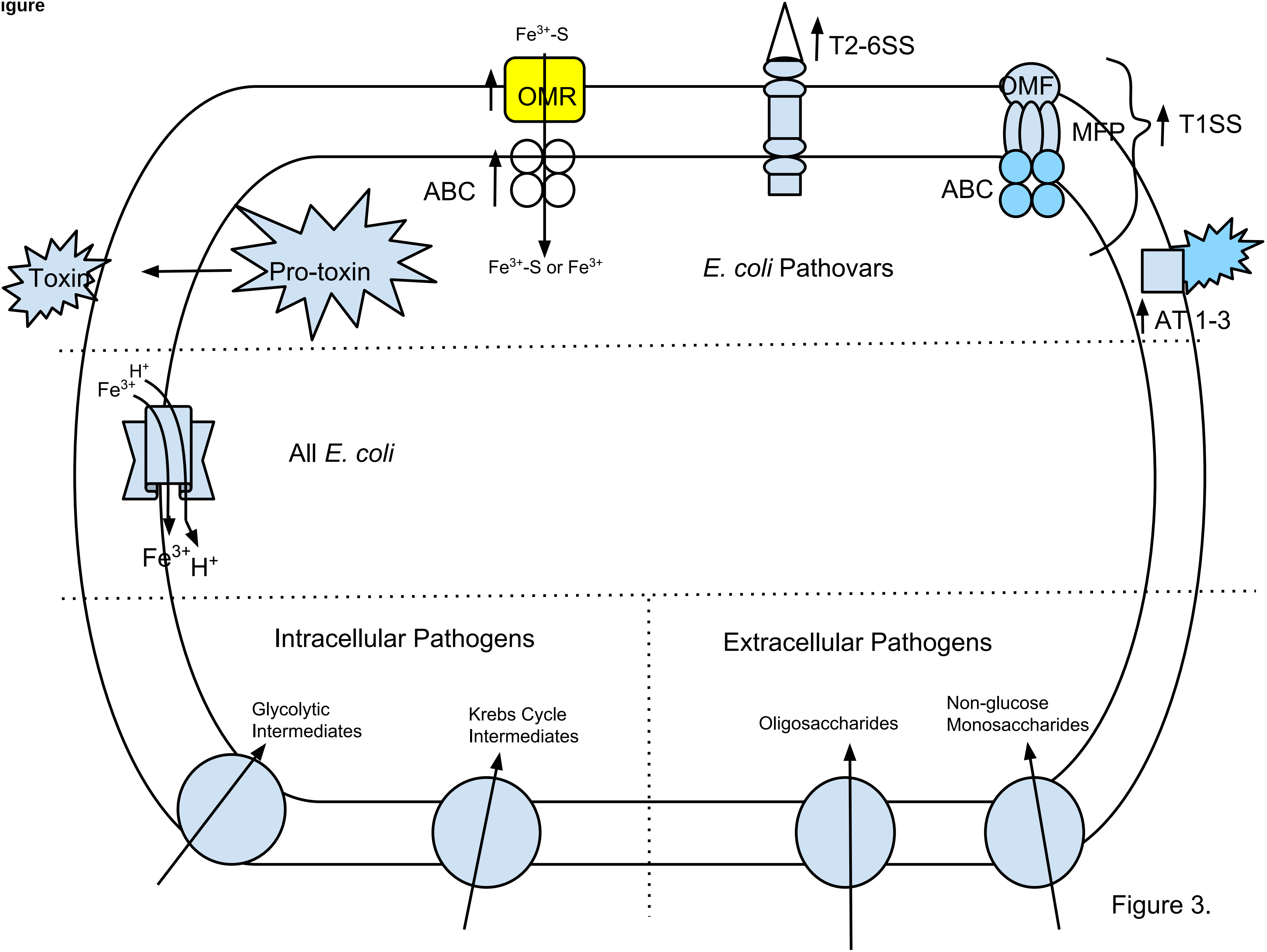


Figure 3.