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Do, Jimmy Hoang

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Comparative Genomics of Transport Proteins in Probiotic and Pathogenic *Escherichia coli* strains

A Thesis submitted in partial satisfaction of the requirements for the degree
Master of Science

in

Biology

by

Jimmy Hoang Do

Committee in charge:

Professor Milton Saier, Chair
Professor Suckjoon Jun
Professor Eduardo Macagno

2016

The Thesis of Jimmy Hoang Do is approved, and it is acceptable in quality and form for publication on microfilm and electronically:

Chair

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ABSTRACT OF THE THESIS

Comparative Genomics of Transport Proteins in Probiotic and Pathogenic *Escherichia coli* strains

by

Jimmy Hoang Do

Master of Science in Biology

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Professor Milton Saier, Chair

Escherichia coli is a genetically diverse species, representing pathogenic, probiotic, and commensal strains, while *E. coli* K-12 is a commonly laboratory strain. Pathogenic strains of *E. coli* are known to cause urinary tract infections, diarrhea, hemorrhagic colitis, and pyelonephritis worldwide. In addition, there are two probiotic strains, *E. coli* Nissle 1917 and O83, which have been shown to combat inflammatory bowel disease. In this study, we identify the transport systems and their substrates within five *E. coli* strains, two pathogens, two probiotics, and K-12, to identify transport systems characteristic of either probiotic or pathogenic species. We found that the probiotic and pathogenic strains generally contain more iron-siderophore and sugar transporters than *E. coli* K-12. Pathogens have an increased number of pore-forming toxins and protein secretion systems than the probiotic strains do. Both pathogens and probiotic strains encode sugar transporters that reflect their intracellular or extracellular environments. In general, both groups seem to show high similarity, suggesting that only a few virulence factors can convert a beneficial microorganism into a pathogenic one. Taken together, these results provide a starting point for future engineering or other applied studies on probiotic bacteria.

INTRODUCTION

Probiotic bacteria are live microorganisms that, when administered orally in adequate quantities, can colonize the intestines and confer upon the host health benefits. By contrast, prebiotic substances are defined as nutrients that stimulate the growth of probiotic species. Adaptive co-evolution of humans and bacteria over millennia has resulted in symbiotic relationships in which both partners benefit (1-3). The mechanisms of action of probiotics have been generalized to (1) strengthening the intestinal barrier, (2) modulating the immune response, (3) secreting antimicrobial compounds, and (4) competing with pathogens for mucosal binding sites (4). However, some mechanisms are strain-specific or are poorly defined (5).

Escherichia coli is the leading cause of preventable infant mortality worldwide, and it causes several pathogenic conditions. However, it also includes commensal and probiotic strains (6). As such, *E. coli* genomes are composed of two gene pools: the core and the variable portion of the genomes, in which the core pool is conserved between strains, and the flexible pool is variable and strain-specific (4). *E. coli* Nissle 1917 is a well-studied probiotic strain that has been shown to exhibit anti-invasive effects on bacterial pathogens without requiring physical contact with the invasive bacteria or the epithelial cells (7, 8). However, the mechanism of action of probiotic *E. coli* O83 is less well understood, and it is thought to directly compete with bacterial pathogens through adhesion, iron acquisition, and bacteriocin secretion (8). Regardless, both strains have been shown to be clinically useful in ameliorating diseases, such as inflammatory bowel disease (9).

In a previous study, Tang and Saier reported that pathogenic strains of *E. coli* each possess a complement of transport proteins that provided clues as to the systems that imparted virulence to these strains (10). Many transporters were unique to certain pathogens, and their presence or absence explained, in part, their virulence properties. For example, sets of protein secretion systems for export to the cell surface or for injecting effector proteins into host cells were generally strain-specific. Pathogens also have increased numbers of iron siderophore receptors and ABC iron uptake transporters compared to *E. coli* K-12, but the numbers and types of low-affinity secondary iron carriers were uniform in all strains. Each pathovar encodes a different set of pore-forming toxins and virulence-related outer membrane proteins lacking in the non-virulent K-12 strain (10).

The goal of this study was to extend these results to probiotic *E. coli* strains for comparative purposes. Five *E. coli* strains, two representative pathogens (*E. coli* strains CFT073 and O157), two probiotic lines (*E. coli* strains O83 and Nissle 1917), and *E. coli* K-12, were examined to analyze the distribution of transport systems and their substrates in order to elucidate differences between substrates transported, and transporter types that might confer probiotic versus pathogenic character. Table 1 presents the basic traits of these five strains.

METHODS

Genome-BLAST (G-BLAST) search for transport proteins

The proteomes of five *E. coli* strains (O83, Nissle 1917, CFT073, O157, and K-12) were obtained from GenBank and were screened against the Transporter Classification Database (TCDB; www.tcdb.org) for transport protein homologues in January, 2015 using G-BLAST (11). G-BLAST is especially designed for this purpose, as it uses FASTA-formatted protein sequences from the genome as a query to search for homologous transport proteins within TCDB and then retrieves information from the TC top hit (TCID number, number of amino acyl residues (aas), predicted numbers of transmembrane segments (TMSs), TMS overlap between query and hit, and e-value for the query and hit proteins) (12). To predict the number of TMSs, G-BLAST uses another program, HMMTOP 2.0, to highlight regions of both hydrophobicity and amphipathicity along hydropathy profiles (13). The Web-based Amphipathicity and Topology (WHAT) program was used to display hydropathy and amphipathicity profiles of individual proteins with a window size of 19 aas and a viewing angle of 100° for α-helices or 180° for β-strands in order to compare the topologies of the query proteins and their top TC hits (14). Proteins with no TMSs were not automatically excluded since many multicomponent systems contain soluble components, and were therefore considered to be potential transport protein homologues.

Examination of transport protein homologues

An arbitrary e-value cutoff of 0.0001 was initially used. The remaining proteins that had e-values of 0.0001 or less were manually examined using topological data to determine if they were indeed true homologues of recognized transport proteins or if they were false positive. Since two proteins showing homology in hydrophilic regions can give small e-values, manual examination was required in order to avoid including well-scoring proteins that were not actual homologues of known transport proteins. By using the hydropathy profile generated by WHAT, it could be seen whether HMMTOP 2.0 has missed a TMS or predicted a TMS in an incorrect region. This also allowed for the inclusion or exclusion of TC hits based on the numbers of TMSs, as well as the locations of the TMSs. However, it is ultimately up to the user to judge the actual numbers and locations of TMSs.

Proteins with poor e-values, between 0.0001 and e^{-8}, represent a range in which there could be distant transport protein homologues, and thus, they were examined in closer detail using the aforementioned steps. Low-scoring hits that proved to be recognizable transport proteins were incorporated into TCDB.

Identification of substrates transported

Authentic transport protein homologues were assigned substrates according to TCDB entries. For entries of unknown function, the genome context of genes encoded within an operon or the scientific literature was used to deduce their functions.

RESULTS

Overview of transporter types

Following the conventions of TCDB, transporters are organized into five well-defined categories, classes one to five, and two less well-defined categories, classes eight and nine. The five well-defined classes are (1) channels (2) secondary carriers (3) primary active transporters, (4) group translocators, and (5) transmembrane electron flow carriers. Meanwhile, the latter two classes include (8) auxiliary transport proteins and (9) transporters or putative transporters of unknown function or mechanism of transport (15, 16).

To analyze the distribution of transport proteins within each of the five *E. coli* strains, their proteomes were blasted against TCDB using G-BLAST. The results are shown in detail in Table S1, while Table 2 summarizes the distribution of the subclasses of transporters found in each of the five *E. coli* strains according to TC number. Surprisingly, the probiotic strains and *E. coli* K-12 all contain fewer transport proteins than their pathogenic counterparts (891, 908, and 897 versus 942 and 958). In general, all five strains show a similar distribution of the different transporter classes. The most obvious differences are among pore-forming toxins, auxiliary transport proteins, and putative transport proteins, TC subclass 9.B. The probiotic *E. coli* strains have fewer of each class than the other three strains.

TC subclass 1.A represents α-type channels except for holins (17). The probiotic and pathogenic strains show a similar distribution of these proteins, each falling in the range of 30-40 proteins. Similar to our previous study, K-12 contains fewer such systems; it only has 30 channel systems (10).

TC subclass 1.B includes β-barrel porins that are located in the outer membrane (18). Similar to the distribution of TC subclass 1.A, the probiotic and pathogenic strains each contain more of these types of proteins than K-12. K-12 contains 73 of these proteins, whereas the remaining four strains number 92-106. Altogether, approximately 3-8% of a bacterial transportosome is dedicated to channel-type transporters (19). However, all five strains of *E. coli* do not adhere to this pattern, as the percentage of subclass 1.B alone already surpasses 8% in each strain; thus, all five show an unusually high number of channel-type transporters.

TC subclass 1.C includes pore-forming toxins (17). The two pathogenic strains, CFT073 and O157, contain 14 and 13 such proteins, respectively. Not surprisingly, the remaining three strains show substantially fewer such proteins. The probiotic strains, O83 and Nissle 1917, contain two and four toxins, respectively, while K-12 contains six.

TC subclass 1.E consists of holins. The five strains show large variation within this subclass and show no consistent pattern. *E. coli* Nissle 1917 and CFT073 contain nine and eight holins, respectively. The largest number of holins, 30, is present within O157, while O83 and K-12 fall somewhere in between with 14 and 11, respectively.

Secondary carriers comprise the second largest number of transport proteins in all five strains, with 30% of the transporters in each strain falling within this class. However, these proteins and primary active transport proteins are found in similar number. Within TC subclass 2.A (porters), each strain contains 271-293 proteins. The remaining class 2 proteins fall into TC subclass 2.C, ion-gradient-driven energizers of motility and outer membrane transport, with three to five such proteins in all five strains.

The largest number of transport proteins across all five strains is relegated to primary active transporters, which comprise 31-33% of all transport proteins in these strains, but because many of these systems are multicomponent, there are far fewer systems than in class 2. TC subclass 3.A includes phosphate bond-hydrolysis-driven transporters. The probiotic strains contain approximately 264 of these proteins, while the three remaining strains contain 218-240. While the numbers are smaller, the percentage differences can be considered to be minimal due to the sheer numbers. TC subclass 3.B includes decarboxylation-driven transporters, which are absent in the probiotic strains, though the remaining three strains all contain two such proteins. TC subclass 3.D includes oxidoreduction-driven transporters. The probiotic strains contain about 36 such proteins, while the remaining three strains contain 40-49.

TC subclass 4.A consists of phosphotransfer-driven sugar transporting group translocators. These include 48-55 proteins, 5-6% of all transport proteins within each of the five strains. TC subclass 4.B includes nicotinamide ribonucleoside uptake transporters and their homologues, which number two or three across all five strains. TC subclass 4.C includes acyl-CoA ligase-coupled transporters, which also number two across all strains. TC subclass 4.D includes polysaccharide synthase/exporters. All strains contain three or four of these proteins.

TC subclass 5.A includes transmembrane two-electron carriers. There are 28-30 of these proteins in each of the five strains. TC subclass 5.B includes transmembrane one-electron carriers. While these are absent in the probiotic strains as well as *E. coli* CFT073, O157 and K-12 each contains two to four of these carriers.

TC subclass 8.A includes auxiliary transport proteins that do not participate directly in the transport process, but facilitate this process. The probiotic strains contain 19 such proteins; the pathogens contain 37 and 35, while K-12 contains 33.

The remainder of the proteins in each strain falls into TC subclasses 9.A, known transporters that function by unknown mechanism of action, or 9.B, putative transporters. Each *E. coli* strain shows 7-12 proteins from TC subclass 9.A, but in TC subclass 9.B, the probiotic strains show 51 and 54 proteins, while the remaining strains show 69-72.

Differences in transported substrates between probiotic and pathogenic strains

To better understand the contribution of transport systems to probiotic or pathogenic character, the probable substrate specificity of each transport protein was predicted. While the results are extensively tabulated in Table S1, Table 3 provides an overview of predicted substrate types transported, and it can be seen that the probiotic strains and *E. coli* K-12 each contain fewer complete transport systems than the pathogenic strains of *E. coli* (581-591 versus 640-649). In general, the distribution of transported substrates is similar across all five strains, though there are notable differences.

The results in Table 3 show that the probiotic *E. coli* strains contain fewer DNA transporters (10-11 versus 2-3) and transporters of unknown function (41-62 versus 70-83) than the other three strains. Similarly, the pathogenic strains contain far more protein and peptide transporters than the probiotic strains or *E. coli* K-12 (90-116 versus 75-81), many probably for secretion of virulence factors. With regards to siderophore transport, both the probiotic and pathogenic strains contain more such systems than *E. coli* K-12

(20-30 versus 16). Interestingly, *E. coli* CFT073 contains more drug exporters than the other four strains (43 versus 33-38), while *E. coli* O157 contains fewer polysaccharide transporters than the other four strains (12 versus 17-24).

Carbon utilization by probiotic and pathogenic strains

From the lists of transporters and their substrates (Tables 2 and 3), transporters that are unique to the probiotic strains are summarized in Table S2, while those unique to the pathogenic strains are summarized in Table S3.

To better understand the carbon source usage of the five strains, the occurrence of carboxylate and sugar transporters were examined more closely. These two categories of transport proteins are summarized in Tables S4 and 4, respectively. With regards to carboxylate transporters, most are shared between the five strains. There are two probiotic-exclusive transporters, which catalyze uptake of gluconate and ascorbate (TC#s 2.A.8.1.1 and 4.A.7.1.2, respectively) (Table S4). In contrast, there are eight pathogen-exclusive carboxylate transporters, six of which catalyze uptake (TC#s 2.A.1.15.1 and 2, 2.A.8.1.3, 2.A.16.2.2, 2.A.23.1.6, 2.A.68.1.1) and two that catalyze bidirectional transport of formate and C_4-dicarboxylates (TC#s 1.A.1.16.2 and 2.A.61.1.2, respectively).

Of the sugar transporters, the numbers of probiotic-exclusive systems are small, numbering only eight (Table 4). One of these proteins (TC# 2.A.1.2.18) probably catalyzes efflux of galactosides, including lactose and melibiose. The remaining seven (TC#s 3.A.1.1.25, 28, 34, 41, and 44; 3.A.1.2.14, and 20) catalyze uptake of various sugars that are found either intracellularly or extracellularly. In the pathogens, there are

12 exclusive sugar transporters. One catalyzes efflux of xylose (TC# 2.A.1.1.3), and the other eleven catalyze uptake of oligogalacturonates (TC# 1.B.35.2.2), sucrose (TC# 2.A.1.5.3), melibiose (TC# 2.A.2.1.1), β-xylosides (TC# 2.A.2.3.5), cellobiose (TC# 2.A.2.3.6), rhamnose (TC# 3.A.1.2.9), glucose (TC#s 4.A.1.1.9, 4.A.6.1.6), α-glucosides (TC# 4.A.1.1.10), mannose (TC# 4.A.2.1.6), and fructose (TC# 4.A.2.1.14).

Both the probiotic and pathogenic strains share a high number of sugar uptake transporters. Upon closer inspection, it can be seen that *E. coli* CFT073, the only strain that resides intracellularly within the host, contains more sugar transporters that are specific to sugars that reside within the cytoplasm (i.e., glucose, fructose, trehalose, etc.), while strains that reside extracellularly, the two probiotic strains and *E. coli* O157, contain more sugar transporters that are specific to sugars that are found outside of the cell (i.e., raffinose, lactose, melibiose, etc.). This consistent trend has been noticed previously when larger numbers of these pathogens were analyzed (10). In addition, it can be seen that the probiotic-exclusive sugar transporters all catalyze uptake of mono- and oligosaccharides, such as trehalose, maltose, sucrose, ribose, and arabinose, whereas the single probiotic-exclusive transporter catalyzes efflux of lactose and melibiose (Table 4).

Transporters that contribute to pathogenesis are also found in probiotic strains

Protein and DNA secretion systems, total iron transporters, and toxins were examined because of their involvement in pathogenicity. The results are summarized in Tables 5, 6, and 7, respectively. As presented in Table 5, the occurrence of protein secretion systems is very disparate and shows no obvious patterns. The Drug Exporter-1 system in the type I secretion system (T1SS), 3.A.1.105.4, is unique to the probiotic strains; both strains contain five components, and therefore one complete system. Like our previous studies, the presence of type VI secretion system (T6SS) constituents is common to pathogenic strains, but there are proteins also present in the probiotic strains (10). Nevertheless, it can be seen that the pathogenic strains contain more of these secretion proteins than the probiotic or commensal strains, numbering 21-24 versus 6-14 (Table 5). This suggests that while the former are complete, the latter are not. As expected, common to all five strains is the presence of the general secretory pathway in the type 2 secretion system (T2SS), 3.A.5.1.1.

With regards to iron transporters, it can be seen that the pathogenic strains share with the probiotic strains most of their secondary iron transport systems and some primary active transporters (Table 6). It appears that five of the iron transport systems are unique to the probiotic strains and may catalyze the uptake of Fe^{3+}-pseudobactin (1.B.14.1.15), Fe^{3+}-ferrioxamine (1.B.14.1.20), heme (1.B.14.10.1), Fe^{3+}-dicitrate (3.A.1.14.1), and Fe^{3+}-vibriobactin (3.A.1.14.8). However, both probiotic and pathogenic strains contain more high-affinity than low-affinity iron transporters, consistent with previous results (Table 6) (10). Unlike the other two categories of transport systems, toxins are virtually absent from the probiotic strains except for colicin V (1.C.31.1.3) and cytotoxic fimbrial subunit transporters (1.C.80.1.2 and 3), as shown in Table 7.

DISCUSSION

Probiogenomics, the sequencing and analysis of probiotic and commensal gut bacteria, is a powerful tool that can facilitate the comparative analyses of large numbers of proteins to glean similarities and differences between different species or strains of organisms (4). The genomes of five *E. coli* strains, two probiotic strains, two pathogenic strains, and one commensal strain were blasted against TCDB to identify homologues of established or putative transport proteins. This allowed us to obtain nearly complete sets of transport systems, based on current knowledge of transporters. The sum total of the proteins comprises the organisms' "transportosomes" (20). These transportomes were then used to compare and contrast the presence or absence of transport systems, as well as the substrates transported, in each of the five strains.

Analysis of potential carbon sources, particularly carboxylates and sugars, revealed that most uptake transporters are shared between the probiotic and pathogenic strains, but the large number of probiotic-exclusive sugar uptake transporters is likely to confer upon the probiotic strains an advantage over the pathogens. The probiotic strains as well as the extracellular pathogen, *E. coli* O157, contain many sugar uptake transporters specific for sugars found in the extracellular environment, leading to the conclusion that their primary site of action is extracellular. Intracellular *E. coli* pathogens preferentially transport a very different set of sugars, those found in the cytoplasm of animal cells (10). It is interesting to note that most sugar transport in the probiotic strains occurs through permeases, secondary carriers and ABC systems, rather than through PTS sugar uptake systems, and that they each contain more ABC systems (3.A.1) than in *E. coli* O157 or the other two strains. It has been shown that ABC-type systems in general possess higher affinities for their substrates than secondary carriers (TC family 2.A). Therefore, in addition to have increased numbers of sugar uptake systems, these high-affinity sugar transporters may confer an advantage to the probiotic strains when scavenging for sugars present at low concentrations.

It has been shown that many ingested bacteria can ferment non-digestible carbohydrates into short-chain fatty acids, such as acetate, lactate, proprionate, and butyrate (21, 22). While acetate and proprionate are used by the liver for lipogenesis and gluconeogenesis, butyrate is metabolized in the colonic epithelium and may function as a histone deacetylase inhibitor, and thereby regulate mammalian transcription (22). These short-chain fatty acids have also been shown to signal, by binding to G-protein-coupled receptors, for different functions, depending on the cell type. This effect can range from suppression of inflammation by neutrophils to improvement of insulin secretion by enteroendocrine L-cells (22). Therefore, *E. coli* Nissle 1917 and O83 may antagonize gut pathogens by affecting the host immune system by virtue of sugar metabolism.

In *E. coli*, iron is required to sustain cellular respiration and is crucial to the activities of ferric oxidase, NADH oxidase, succinate dehydrogenase, and many cytochromes. As such, iron sequestration is a major defense mechanism employed to ward off pathogens. Not surprisingly, iron and iron-siderophore transporters were found to be present in high numbers within the probiotic strains, as well as in the pathogens.

TC family 1.B.14 represents outer membrane receptors that are involved in the uptake of iron-siderophore complexes and are found in lower numbers in *E. coli* K-12 than in the other four strains. However, this is not especially surprising, as the probiotic *E. coli* strains, like the pathogens, must also compete with the host for iron. The probiotic strains and the pathogens also contain more high-affinity inner membrane iron-siderophore uptake porters (TC class 3.A.1) than *E. coli* K-12. Interestingly, the numbers of outer membrane and inner membrane receptors coincide, suggesting that these two types of receptors co-evolved, as discussed previously (10). While these numbers are similar to those seen in the pathogens, this probably confers to the probiotic strains an advantage over some other microbes in the gut (23).

Not surprisingly, *E. coli* O83 Nissle 1917 lacks almost all of the toxins that are found in the two pathogens. Both probiotic strains contain cytotoxic fimbrial subunit transporters, though the relevance of these transporters is not clear since *E. coli* strains produce dozens of fimbriae with a variety of functions in adhesion, biofilm formation, motility, conjugation, and virulence (24, 25). Consistent with previous studies, *E. coli* Nissle 1917 contains an additional toxin, colicin V, which is toxic to other bacteria, but not to humans (6). This may allow *E. coli* Nissle 1917 to antagonize pathogens, conferring upon it a competitive advantage over pathogens.

The presence of protein secretion systems in all five strains shows very disparate patterns, as most strains contain many constituents of various systems, though some are incomplete and therefore nonfunctional. This suggests that the common ancestor had these systems but they were partially lost by some of their progeny. The T6SS has been shown to be important in antagonizing other bacteria and in use as a defense mechanism through “T6SS dueling” (26). Studies have shown that intercellular T6SS dynamics involve targeting prey cells by translocation, or “injection” of effector proteins that puncture the prey’s membrane (26). The absence of a T6SS in both probiotic strains is noteworthy, as it was possible that *E. coli* O83 could have inhibited growth of pathogens via T6SS dueling. However, this observation is consistent with the previous finding that *E. coli* Nissle 1917 does not inhibit pathogens through physical contact (7).

Our studies have shown that some virulence factors that are present in pathogenic *E. coli* strains are also present in the probiotic strains, such as increased numbers of high-affinity sugar and iron uptake systems. Other virulence factors, such as toxins and T6SSs, are not found in the probiotic strains. Previous studies had shown that most factors that contribute to pathogenesis have been acquired through horizontal gene transfer (HGT), which are found in genomic islands on the chromosome (6). The results provided by G-BLAST allows detailed comparative analyses, though there are shortcomings, such as its inability to infer HGT. Future efforts will seek to detect HGT and to integrate transporter proteomic with these genomic analyses. Based on the presented data, it is possible that some transporters will prove to be useful for diagnostic purposes, or for genetically engineering probiotic strains.

SUPPLEMENTAL FILES

Table S1. Accepted list of transport proteins and their substrates in all five *E. coli* strains. True homologues of transport proteins are marked in blue.

NCBI Acc. #	O83	Nissle 1917	CFT073	O157	K-12	TCID	E-Value	Acc #	General Substrate	Specific Substrate
YP_002402432.1	+	+	+	+	+	1.A.1.13.1	0	P31069	Cations	K+
YP_006120312.1	+	+	-	-	-	1.A.4.10.1	e-168	P0AA70	Cations	Ca2+ uptake
YP_006120378.1	+	-	-	-	-	1.A.8.1.1	e-105	P0AER0	Sugar alcohols	Glycerol
YP_002405308.1	+	+	+	+	+	1.A.8.1.1	e-150	P0AER0	Sugar alcohols	Glycerol
YP_002402016.1	+	+	+	+	+	1.A.8.3.1	e-100	P60844	Water	Water
YP_002401581.1	+	+	+	+	+	1.A.11.1.1	0	P69681	Cations	Ammonia
NP_312496.1	+	-	+	+	-	1.A.12.2.2	e-10	Q8F2Y8	None	Unknown
YP_002404595.1	+	+	+	+	-	1.A.12.3.1	e-121	P0ACA3	Anions	Cl-
NP_311212.1	+	+	+	+	-	1.A.12.3.2	e-123	B7LBF5	Peptides	Glutathione
YP_006106641.1	-	+	+	-	-	1.A.13.2.3	0	P76481	None	Unknown
AAN80949.1	-	+	+	-	-	1.A.13.5.1	e-150	A1ACJ3	None	Unknown
YP_002402112.1	+	+	+	+	+	1.A.14.2.1	e-118	P0AAC6	Proteins	Proteins
YP_006104938.1	+	+	+	-	-	1.A.14.2.2	e-09	P0AAC4	Carboxylates	Acetate
YP_002401926.1	-	-	+	+	+	1.A.14.2.2	e-118	P0AAC4	Carboxylates	Acetate
NP_308892.1	-	-	+	+	-	1.A.14.2.4	e-119	B7LC70	None	Unknown
YP_002402044.1	+	+	+	+	+	1.A.16.1.1	e-157	P0AC23	Carboxylates	Formate
YP_002403786.1	-	-	+	+	+	1.A.16.1.2	e-160	P77733	Carboxylates	Formate
AAN82581.1	+	+	+	-	-	1.A.16.3.1	e-152	P0AC26	Anions	Nitrite
YP_002403614.1	+	+	+	+	+	1.A.16.4.1	e-180	P37327	Anions	Formate, nitrite
YP_002404650.1	+	+	+	+	+	1.A.22.1.1	e-60	P0A742	Ions	Ions

Table S1, continued.

YP_002401594.1	+	+	+	+	+	1.A.23.1.1	0	P77338	Cations	K+ efflux
YP_002405578.1	+	+	+	+	+	1.A.23.1.3	0	P39285	Cations	K+ efflux
YP_002404184.1	+	+	+	+	+	1.A.23.2.1	e-129	P0C0S1	Ions	Ions
YP_002401949.1	+	+	+	+	+	1.A.23.3.2	0	P75783	Cations	K+ efflux
YP_002402572.1	+	+	+	+	+	1.A.23.4.3	e-179	P0AEB5	Ions	Ions
YP_002401684.1	+	+	+	+	+	1.A.23.4.5	0	P0AAT4	Ions	Ions
YP_002403123.1	+	+	+	+	+	1.A.30.1.1	e-163	P09348	Cation	H+
YP_002403122.1	+	+	+	+	+	1.A.30.1.1	e-175	P0AF06	Cation	H+
YP_002404382.1	+	+	+	+	+	1.A.30.2.1	e-133	P0ABU7	Cation	H+
YP_002404381.1	+	+	+	+	+	1.A.30.2.1	e-77	P0ABV2	Cation	H+
YP_002401828.1	+	+	+	+	+	1.A.30.2.2	e-126	P0ABU9	Cation	H+
YP_002401829.1	+	+	+	+	+	1.A.30.2.2	e-67	P0ABV8	Cation	H+
NP_414555.1	+	-	+	+	+	1.A.33.1.2	0	P0A6Y8	Ions	Ions
NP_311623.1	+	+	-	+	-	1.A.34.1.2	0	B7LEG0	Proteins	Lipoprotein
AID79903.1	-	+	-	-	-	1.A.34.1.2	e-50	B7LEG0	Proteins	Lipoprotein
YP_002405200.1	+	+	+	+	+	1.A.35.1.1	e-175	P0ABI4	Cations	Mg2+, Co2+, Ni2+
YP_002402584.1	+	+	+	+	+	1.A.35.4.1	e-165	Q9EYX5	Cations	Zn2+, Cd2+ efflux
YP_006118849.1	+	+	-	-	-	1.A.40.5.2	0	P77328	Nucleosides	Purines
NP_415157.1	+	+	+	+	+	1.A.43.1.1	e-67	P37002	Anions	F-, Cl-
YP_002271840.1	+	-	-	+	-	1.A.45.1.1	e-39	Q01074	Nucleic acids	DNA
YP_002271841.1	+	-	-	+	-	1.A.45.1.1	e-49	Q01076	Nucleic acids	DNA
YP_002402725.1	+	+	+	+	+	1.A.46.3.4	e-173	B2N0W4	Nucleic acids	DNA
YP_002401290.1	+	+	+	+	+	1.A.62.2.1	e-24	A0M015	Cations	Cations
NP_414699.1	+	+	+	+	+	1.A.62.2.2	e-91	I7MT28	None	Unknown

Table S1, continued.

NP_418195.2	+	+	-	+	+	1.A.77.3.11	e-52	S0WRQ6	Cations	Ca2+, Mg2+
YP_002402071.1	+	+	+	+	+	1.B.1.1.1	0	P02931	Peptides	Peptides
YP_002328485.1	+	+	+	+	+	1.B.1.1.2	0	P02932	Anions	Phosphate
YP_853015.1	+	+	-	+	+	1.B.1.1.3	0	P06996	Cations	Cations
YP_002329865.1	-	-	+	-	+	1.B.1.1.3	e-130	P06996	Cations	Cations
YP_002412976.1	-	-	-	+	-	1.B.1.1.3	e-29	P06996	Cations	Cations
YP_002402589.1	+	+	+	+	-	1.B.1.1.4	e-101	P21420	MDR	Methyl benzyl viologen, ceftriaxone, hydrogen peroxide
YP_006106282.1	+	+	+	-	-	1.B.1.1.5	0	P07238	None	Unknown
YP_006105475.1	-	-	+	-	-	1.B.1.1.5	0	P07238	None	Unknown
AAN80842.1	+	+	+	-	-	1.B.1.1.12	e-116	Q6RW54	MDR	MDR
NP_310729.1	+	+	+	+	-	1.B.1.1.19	e-143	D6QLX8	MDR	MDR
NP_310730.1	-	-	-	+	-	1.B.1.1.20	e-54	J9VK71	None	Unknown
YP_002405410.1	+	+	+	+	+	1.B.3.1.1	0	P02943	Monosaccharides	Maltose, maltoheptose
YP_002405110.1	+	+	+	-	+	1.B.3.1.3	0	P26218	Oligosaccharides	β-glucosides
YP_002402738.1	+	+	+	-	-	1.B.3.1.3	e-161	P26218	Oligosaccharides	β-glucosides
YP_002402099.1	+	+	+	+	+	1.B.6.1.1	0	P0A910	Ions	Ions
YP_006120938.1	+	-	-	-	-	1.B.6.1.4	e-15	Q8KWW6	MDR	Cephalothin, cephaloridine
YP_002403896.1	+	+	+	+	+	1.B.6.1.4	e-15	Q8KWW6	MDR	Cephalothin, cephaloridine
AID79680.1	-	+	-	-	-	1.B.6.1.4	e-15	Q8KWW6	MDR	Cephalothin, cephaloridine
AAN81834.1	+	+	+	-	-	1.B.6.1.14	e-14	K1LZ89	None	Unknown
YP_002402760.1	+	+	-	+	-	1.B.6.2.1	e-19	P0A917	None	Unknown

Table S1, continued.

YP_002270304.1	+	-	-	+	-	1.B.6.2.1	e-19	P0A917	None	Unknown
YP_002271473.1	-	-	-	+	-	1.B.6.2.1	e-19	P0A917	None	Unknown
YP_002270238.1	-	-	-	+	-	1.B.6.2.1	e-20	P0A917	None	Unknown
YP_002401907.1	-	-	-	+	-	1.B.6.2.1	e-20	P0A917	None	Unknown
YP_002271095.1	-	-	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002271189.1	-	-	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002271413.1	-	-	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002273579.1	-	-	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002269436.1	-	-	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002328284.1	-	-	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002328598.1	-	-	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002402169.1	-	-	+	-	-	1.B.6.2.1	e-22	P0A917	None	Unknown
NP_753376.1	-	-	+	-	-	1.B.6.2.1	e-23	P0A917	None	Unknown
YP_002401955.1	-	-	+	+	+	1.B.6.2.1	e-88	P0A917	None	Unknown
YP_002271766.1	-	-	-	+	-	1.B.6.2.2	e-19	Q0WCZ9	None	Unknown
YP_002330699.1	-	-	-	+	-	1.B.6.2.2	e-24	Q0WCZ9	None	Unknown
YP_002403610.1	+	+	-	+	+	1.B.9.1.1	0	P10384	Lipids	Fatty acids
YP_006106711.1	-	-	+	-	-	1.B.9.1.1	0	P10384	Lipids	Fatty acids
YP_006108391.1	+	+	+	-	-	1.B.10.1.1	e-105	P0A927	Nucleosides	Nucleosides
YP_002401539.1	+	+	+	+	+	1.B.10.1.1	e-176	P0A927	Nucleosides	Nucleosides
NP_416903.1	+	+	+	-	-	1.B.10.3.1	e-138	P45564	None	Unknown
NP_416903.1	+	+	+	-	+	1.B.10.3.1	e-138	P45564	None	Unknown
YP_002271749.1	+	+	-	+	-	1.B.11.2.1	0	P07110	Proteins	Fimbrial subunit
YP_006108762.1	-	-	+	-	-	1.B.11.2.1	0	P07110	Proteins	Fimbrial subunit

Table S1, continued.

NP_755465.1	-	-	+	-	-	1.B.11.2.1	0	P07110	Proteins	Fimbrial subunit
YP_006106705.1	-	-	+	-	-	1.B.11.2.1	e-171	P07110	Proteins	Fimbrial subunit
YP_002401808.1	+	+	-	-	+	1.B.11.2.2	0	P75750	None	Unknown
YP_002269340.1	-	-	-	+	-	1.B.11.2.2	0	P75750	None	Unknown
YP_006107455.1	-	-	+	-	-	1.B.11.2.2	0	P75750	None	Unknown
YP_002403394.1	+	+	+	-	+	1.B.11.3.2	e-119	P21647	Proteins	Fimbrial subunit
YP_002271391.1	-	-	-	+	-	1.B.11.3.2	e-122	P21647	Proteins	Fimbrial subunit
YP_002401272.1	+	+	-	-	+	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_002268748.1	-	-	-	+	-	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_006104298.1	-	-	+	-	-	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_006107825.1	+	+	+	-	-	1.B.11.3.5	0	Q8CVM4	Proteins	Fimbrial subunit
YP_002404518.1	-	-	-	+	+	1.B.11.3.6	0	P42915	Proteins	Fimbrial subunit
NP_309305.1	-	-	-	+	-	1.B.11.3.7	e-130	Q9HWU4	Proteins	Proteins
YP_006108861.1	+	+	-	+	+	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
YP_002402082.1	+	+	-	-	+	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
YP_006108861.1	+	+	+	+	+	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
YP_002402709.1	-	-	+	+	-	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
YP_006105297.1	-	-	+	-	-	1.B.11.3.9	e-146	P30130	Proteins	Fimbrial subunit
YP_002273255.1	-	-	-	+	-	1.B.11.3.9	e-164	P30130	Proteins	Fimbrial subunit
YP_002401420.1	-	-	-	+	+	1.B.11.4.1	e-12	P25733	Proteins	Fimbrial subunit
NP_417683.1	-	-	-	-	+	1.B.11.5.1	0	P45420	Proteins	Proteins
YP_002401441.1	-	-	-	+	-	1.B.12.1.2	e-115	Q7BCK4	Proteins	Fimbrial subunit
YP_002402715.1	-	+	-	+	-	1.B.12.1.3	e-105	Q9Z625	Proteins	Fimbrial subunit
NP_754776.1	-	-	+	-	-	1.B.12.1.3	e-85	Q9Z625	Proteins	Fimbrial subunit

Table S1, continued.

YP_002402383.1	+	+	+	-	+	1.B.12.2.1	e-38	P14283	Proteins	Proteins
AID77359.1	-	+	-	-	-	1.B.12.4.5	0	Q7BS42	Proteins	Proteins
AID80026.1	-	+	-	-	-	1.B.12.4.6	0	Q8FDW4	Proteins	Proteins
AID77388.1	-	+	-	-	-	1.B.12.4.7	0	A1A7W8	Proteins	Proteins
YP_006118631.1	+	-	-	-	-	1.B.12.4.7	0	A1A7W8	Proteins	Proteins
AAN81229.1	-	-	+	-	-	1.B.12.5.4	e-27	Q9XCJ4	Proteins	Proteins
NP_416736.1	+	+	+	-	+	1.B.12.5.4	e-45	Q9XCJ4	Proteins	Proteins
NP_310034.1	+	-	-	+	-	1.B.12.5.5	0	P25927	Proteins	Proteins
YP_002269864.1	+	+	-	+	-	1.B.12.8.2	0	P39180	Proteins	Proteins
YP_006105327.1	-	+	+	-	-	1.B.12.8.2	0	P39180	Proteins	Proteins
YP_006107322.1	-	+	+	-	-	1.B.12.8.2	0	P39180	Proteins	Proteins
YP_002402894.1	-	+	+	+	+	1.B.12.8.2	e-28	P39180	Proteins	Proteins
YP_001463964.1	+	+	-	+	+	1.B.12.8.3	e-12	Q9XD84	Proteins	Proteins
YP_002402354.1	-	-	+	+	-	1.B.12.8.3	e-13	Q9XD84	Proteins	Proteins
YP_006104536.1	-	-	+	-	-	1.B.12.8.3	e-31	Q9XD84	Proteins	Proteins
YP_002413240.1	-	-	-	+	-	1.B.12.8.3	e-93	Q9XD84	Proteins	Proteins
NP_309694.1	+	+	-	+	-	1.B.12.8.4	e-37	Q1C5U1	Proteins	Proteins
YP_002402302.1	+	+	+	+	+	1.B.14.1.1	0	P16869	Siderophores	Fe3+-coprogen
AID78195.1	-	+	-	-	-	1.B.14.1.1	0	P16869	Siderophores	Fe3+-coprogen
AID81695.1	-	+	-	-	-	1.B.14.1.1	0	P16869	Siderophores	Fe3+-coprogen
YP_002401283.1	+	+	-	+	+	1.B.14.1.2	0	P06971	Siderophores	Ferrichrome
YP_006104308.1	-	-	+	-	-	1.B.14.1.2	0	P06971	Siderophores	Ferrichrome
YP_006105304.1	-	+	+	-	-	1.B.14.1.3	0	O54507	Siderophores	Fe3+-enterobactin
YP_002403435.1	+	+	+	+	+	1.B.14.1.4	0	P17315	Siderophores	Fe3+-catecholate

Table S1, continued.

YP_854314.1	-	+	+	-	-	1.B.14.1.4	e-102	P17315	Siderophores	Fe3+-catecholate
YP_006106341.1	-	-	+	+	-	1.B.14.1.4	e-33	P17315	Siderophores	Fe3+-catecholate
YP_002401946.1	+	+	+	+	+	1.B.14.1.9	0	P75780	Siderophores	Fe3+-catecholate
AAN78782.1	-	-	+	-	-	1.B.14.1.11	e-55	P11461	Siderophores	Fe3+-coprogen
YP_002405537.1	-	+	+	+	-	1.B.14.1.13	e-109	A3ZKG8	Cations	Fe3+
AID81624.1	-	+	-	-	-	1.B.14.1.15	e-46	Q05202	Siderophores	Ferrichrome
NP_418711.1	-	+	-	-	+	1.B.14.1.20	0	P13036	Siderophores	Fe3+-citrate
NP_415116.1	+	+	+	+	+	1.B.14.1.22	0	P05825	Siderophores	Ferrichrome
NP_311944.1	+	+	+	+	-	1.B.14.1.24	e-55	Q21EL3	Siderophores	Fe3+-enterobactin
YP_006107909.1	-	+	+	-	-	1.B.14.2.2	0	P31499	Siderophore	Heme
YP_006105316.1	-	-	+	-	-	1.B.14.2.2	e-144	P31499	Siderophore	Heme
NP_312407.1	+	+	+	+	-	1.B.14.2.14	0	P72412	Siderophores	Heme
YP_002405349.1	+	+	+	+	+	1.B.14.3.1	0	P06129	Vitamins	Vitamin B12
AID78345.1	-	+	-	-	-	1.B.14.3.1	e-10	P06129	Vitamins	Vitamin B12
YP_002403258.1	+	+	+	-	-	1.B.14.7.2	0	P0C2M9	Siderophores	Fe3+-yersiniabactin
YP_002405516.1	-	+	+	-	-	1.B.14.9.3	0	Q7CGN6	Siderophore	Ferrichrome
NP_310082.1	+	-	-	+	+	1.B.14.9.4	e-23	H8BDK1	Siderophores	Fe3+-yersiniabactin, bacteriocin
YP_006119583.1	+	-	-	-	-	1.B.14.10.1	e-9	P95494	Siderophores	Heme
NP_418453.1	+	+	+	+	+	1.B.14.16.4	0	D8EPC3	None	Unknown
YP_006108348.1	+	+	+	+	-	1.B.15.1.1	e-97	P77076	Oligosaccharides	Raffinose
YP_002404408.1	+	+	+	+	+	1.B.17.1.1	0	P02930	Multiple substrates	Hemolysin, drugs, siderophores
YP_002411289.1	-	-	-	+	-	1.B.17.1.4	e-19	Q92Q38	Multiple substrates	Proteins, polysaccharides, drugs
YP_002401679.1	+	+	+	+	+	1.B.17.3.5	0	P77211	Cations	Cu+, Ag+

Table S1, continued.

YP_002405456.1	+	+	+	+	+	1.B.17.3.9	0	P32714	Drugs	Puromycin, acriflavin, tetraphenyl arsonium chloride
YP_002403417.1	+	+	+	+	-	1.B.17.3.9	e-62	P32714	Drugs	Puromycin, acriflavin, tetraphenyl arsonium chloride
YP_006107341.1	+	+	+	-	-	1.B.18.1.2	0	Q03961	Polysaccharides	Capsular polysaccharide
YP_002403352.1	+	+	+	+	+	1.B.18.3.1	0	P0A930	Polysaccharides	Capsular polysaccharide, colanic acid
YP_002402183.1	-	-	-	+	+	1.B.18.3.1	e-145	P0A930	Polysaccharides	Capsular polysaccharide, colanic acid
NP_754476.1	-	-	+	-	+	1.B.18.3.1	e-92	P0A930	Polysaccharides	Capsular polysaccharide, colanic acid
YP_002269765.1	-	-	-	+	-	1.B.20.1.4	0	Q8XAN8	Proteins	Proteins
NP_309409.1	-	-	+	+	+	1.B.20.1.7	e-141	B5YV25	None	Unknown
YP_002402561.1	+	+	+	+	+	1.B.21.1.1	0	P76045	None	Unknown
AAN78813.1	-	+	+	-	-	1.B.21.2.1	0	F4VWJ2	None	Unknown
YP_006107718.1	+	+	+	-	+	1.B.22.1.1	0	P15644	Proteins	Proteins
YP_006121284.1	+	-	-	-	-	1.B.22.1.1	e-152	P15644	Proteins	Proteins
AID80097.1	-	+	-	-	-	1.B.22.1.1	e-152	P15644	Proteins	Proteins
YP_002413888.1	-	-	-	+	-	1.B.22.3.2	e-151	P35672	Proteins	Proteins
YP_002331417.1	-	-	-	+	-	1.B.22.3.3	e-72	Q01244	Proteins	Proteins
YP_002404738.1	+	+	+	+	+	1.B.22.4.2	0	Q1R5P6	Nucleic acids	DNA
YP_002402844.1	+	+	+	-	+	1.B.25.1.5	0	Q47706	Monosaccharides	Glucuronide
YP_002401776.1	+	+	+	-	+	1.B.25.1.13	0	P75733	Monosaccharides	Chitosugars

Table S1, continued.

YP_002401309.1	+	+	+	+	+	1.B.33.1.3	0	P0A943	None	Unknown
YP_002403806.1	+	+	+	+	+	1.B.33.1.3	0	P77774	None	Unknown
YP_002403887.1	+	+	+	+	+	1.B.33.1.3	e-140	P0AC02	None	Unknown
YP_002403773.1	+	+	+	+	+	1.B.33.1.3	e-160	P0A903	None	Unknown
YP_002403907.1	+	+	+	+	+	1.B.33.1.3	e-53	P0A937	None	Unknown
NP_418641.1	+	+	+	-	+	1.B.33.2.4	0	P0ADE4	None	Unknown
YP_006108860.1	+	+	+	+	+	1.B.35.2.1	e-144	P69856	Anions	Anions
YP_006107305.1	-	+	+	+	+	1.B.35.2.1	e-84	P69856	Anions	Anions
NP_312824.2	-	-	-	+	+	1.B.35.2.2	e-126	P76773	Oligosaccharides	Oligogalacturonate
YP_002402438.1	+	+	+	+	+	1.B.39.1.1	e-93	Q8ZP50	Drugs	Viologen
YP_002404993.1	+	+	-	+	-	1.B.40.2.3	0	A8A667	Proteins	Proteins
YP_006108010.1	-	-	+	-	-	1.B.40.2.3	0	A8A667	Proteins	Proteins
YP_002401193.1	+	+	+	+	+	1.B.42.1.2	0	P31554	Polysaccharides	LPS
YP_002405677.1	+	+	+	+	+	1.B.42.1.2	0	P0ADC6	Polysaccharides	LPS
YP_002404571.1	+	+	+	+	+	1.B.42.1.2	e-106	P0ADW0	Polysaccharides	LPS
YP_002404573.1	+	+	+	+	+	1.B.42.1.2	e-128	P0A9V1	Polysaccharides	LPS
AID80116.1	-	+	-	-	-	1.B.42.1.2	e-16	P0AF98	Polysaccharides	Murein
YP_006121302.1	+	-	-	-	-	1.B.42.1.2	e-17	P0AF98	Polysaccharides	LPS
AID80115.1	-	+	-	-	-	1.B.42.1.2	e-30	P0ADC6	Polysaccharides	Murein
YP_006121301.1	+	-	-	-	-	1.B.42.1.2	e-31	P0ADC6	Polysaccharides	LPS
YP_002404355.1	+	+	+	-	-	1.B.42.1.2	e-36	P0ADC6	Polysaccharides	LPS
YP_002401748.1	+	+	+	+	+	1.B.42.1.2	e-84	P0ADC1	Polysaccharides	LPS
YP_002404572.1	+	+	+	+	+	1.B.42.1.2	e-94	P0ADV1	Polysaccharides	LPS
YP_002402031.1	+	+	+	+	+	1.B.46.1.1	e-104	P61316	Proteins	Lipoprotein

Table S1, continued.

YP_002402390.1	+	+	+	+	+	1.B.46.1.1	e-113	P61320	Proteins	Lipoprotein
AID77913.1	-	+	-	-	-	1.B.46.1.1	e-118	P61316	Proteins	Lipoprotein
AID78362.1	-	+	-	-	-	1.B.46.1.1	e-119	P61320	Proteins	Lipoprotein
YP_002402239.1	+	+	+	+	+	1.B.48.1.1	e-151	P0A204	Proteins	Proteins
YP_006119363.1	+	-	-	-	-	1.B.48.1.1	e-73	P0AE95	Proteins	Proteins
AID78138.1	-	+	-	-	-	1.B.48.1.1	e-73	P0AE95	Proteins	Proteins
YP_006119362.1	+	-	-	-	-	1.B.48.1.1	e-77	P0AE98	Proteins	Proteins
AID78137.1	-	+	-	-	-	1.B.48.1.1	e-77	P0AE98	Proteins	Proteins
NP_309510.1	+	+	+	+	-	1.B.48.5.1	e-11	Q87R31	None	Unknown
YP_002273158.1	-	-	-	+	-	1.B.54.1.1	0	P43261	Proteins	Proteins
YP_002401426.1	+	+	-	+	-	1.B.54.1.2	e-107	P11922	Proteins	Proteins
YP_006104524.1	+	+	+	-	-	1.B.54.1.2	e-109	P11922	Proteins	Proteins
YP_002402403.1	+	+	+	+	+	1.B.54.1.2	e-53	P11922	Proteins	Proteins
YP_006106838.1	-	-	+	-	-	1.B.54.1.2	e-71	P11922	Proteins	Proteins
YP_002413033.1	-	-	-	+	-	1.B.54.1.2	e-88	P11922	Proteins	Proteins
YP_001463325.1	-	-	-	-	+	1.B.54.1.2	e-89	P11922	Proteins	Proteins
NP_308569.1	-	-	-	+	-	1.B.54.1.5	e-10	Q7W286	Proteins	Proteins
YP_002402227.1	+	+	+	+	+	1.B.55.1.1	0	P69434	Polysaccharides	6-N-acetyl-glucosamine
NP_308627.1	+	+	-	+	+	1.B.55.3.1	0	K3TS70	Proteins	Proteins
YP_026226.4	+	+	-	-	+	1.B.55.3.4	0	P37650	None	Unknown
NP_311165.2	+	+	-	+	+	1.B.68.1.1	e-99	Q8XE01	None	Unknown
NP_310455.1	+	+	-	+	+	1.B.75.1.3	e-147	P76206	None	Unknown
NP_308154.1	-	-	-	+	+	1.B.76.1.4	e-13	G9EQG6	Cations	Cu2+
YP_006105201.1	-	-	+	-	-	1.C.1.2.2	e-23	P02978	Proteins	Proteins

Table S1, continued.

YP_002412216.1	-	-	-	+	+	1.C.10.1.1	e-159	P77335	Proteins	Proteins
YP_006105538.1	-	-	+	-	-	1.C.10.1.1	e-45	P77335	Proteins	Proteins
YP_006108796.1	-	-	+	-	-	1.C.11.1.3	e-72	P09983	Proteins	Proteins
AID81862.1	-	+	-	-	-	1.C.31.1.3	e-39	Q83TS1	Peptides	Microcin
YP_002273154.1	-	-	-	+	-	1.C.36.1.1	e-168	O69413	Proteins	Proteins
YP_002273153.1	-	-	-	+	-	1.C.36.1.1	e-80	Q8XC86	Proteins	Proteins
NP_312582.1	-	-	-	+	-	1.C.36.6.1	0	Q7DB81	Proteins	Proteins
YP_002271220.1	-	-	-	+	-	1.C.54.1.1	e-23	P69178	Proteins	Proteins
YP_002271796.1	-	-	-	+	-	1.C.54.1.1	e-24	P69178	Proteins	Proteins
YP_002270020.1	-	-	-	+	-	1.C.57.3.3	e-17	Q47107	Proteins	Proteins
YP_002269764.1	-	-	-	+	-	1.C.75.1.1	e-34	P15320	Proteins	Proteins
YP_006104441.1	-	-	+	-	-	1.C.75.1.1	e-41	P15320	Proteins	Proteins
NP_757241.1	-	-	+	-	-	1.C.80.1.1	e-10	Q8KRT4	Proteins	Fimbrial subunit
NP_755467.1	-	+	+	-	-	1.C.80.1.1	e-13	Q8KRT4	Proteins	Fimbrial subunit
YP_006107454.1	-	-	+	-	-	1.C.80.1.1	e-14	Q8KRT4	Proteins	Fimbrial subunit
NP_757036.1	-	-	+	-	-	1.C.80.1.1	e-15	Q8KRT4	Proteins	Fimbrial subunit
YP_006105224.1	-	-	+	-	-	1.C.80.1.1	e-20	Q8KRT4	Proteins	Fimbrial subunit
NP_416021.1	+	+	+	+	+	1.C.80.1.2	e-102	E1PGF6	Proteins	Proteins
NP_416841.1	+	+	+	+	+	1.C.80.1.3	e-67	B7LBJ3	Proteins	Proteins
NP_415067.1	-	-	+	+	+	1.C.80.1.4	e-26	B7LAC5	Proteins	Proteins
YP_002402825.1	-	-	+	+	+	1.C.82.1.1	e-52	Q9ZK21	Proteins	Proteins
NP_417375.1	-	-	+	+	+	1.C.113.1.1	e-46	P54176	Proteins	Hemolysin
YP_002402784.1	+	+	+	-	+	1.E.1.1.2	e-33	P77237	Proteins	Endolysin
YP_002401881.1	+	+	-	-	+	1.E.1.1.2	e-34	P77237	Proteins	Endolysin

Table S1, continued.

NP_755064.1	-	-	+	-	+	1.E.1.1.2	e-35	P77237	Proteins	Endolysin
YP_002269671.1	-	-	-	+	-	1.E.1.1.3	e-12	O48430	Proteins	Endolysin
YP_002270281.1	-	-	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002271496.1	-	-	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002271791.1	-	-	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002402144.1	-	-	+	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002270568.1	-	-	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002270628.1	-	-	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002328258.1	-	-	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002328796.1	-	-	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002269991.1	-	-	-	+	-	1.E.1.1.3	e-22	O48430	Proteins	Endolysin
YP_002271119.1	-	-	-	+	-	1.E.1.1.3	e-22	O48430	Proteins	Endolysin
YP_002328577.1	-	-	-	+	-	1.E.1.1.3	e-33	O48430	Proteins	Endolysin
NP_308869.1	+	+	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_309148.1	+	-	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_309675.1	-	-	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_309833.1	-	-	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_310017.1	-	-	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_310188.1	-	-	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
YP_006119299.1	+	-	-	-	-	1.E.2.1.1	e-56	P03705	None	Unknown
YP_002403419.1	+	+	+	+	+	1.E.14.1.4	e-56	F4V3T5	Proteins	Proteins
YP_006108535.1	+	+	+	-	-	1.E.14.1.9	e-58	E7UC95	Proteins	Proteins
AAN79429.1	-	-	+	-	-	1.E.25.2.2	e-30	B2VHA2	None	Unknown
NP_417570.1	-	-	+	+	+	1.E.34.2.1	e-71	P64585	None	Unknown

Table S1, continued.

NP_416309.1	+	+	+	+	+	1.E.43.1.1	e-35	A6TAG3	None	Unknown
NP_308043.1	+	+	-	+	+	1.E.53.1.1	e-22	P0ACG4	Multiple substrates	Proteins, peptides, sugar derivatives
YP_026229.1	+	+	-	-	+	1.E.53.1.2	e-23	P37305	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309800.1	-	-	-	+	-	1.E.53.1.4	e-23	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_310781.1	-	-	-	+	-	1.E.53.1.4	e-27	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309107.1	-	-	-	+	-	1.E.53.1.4	e-28	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309547.1	+	-	-	+	+	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_944589.1	-	-	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309272.1	-	-	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_310225.1	-	-	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
YP_006121047.1	+	+	-	-	-	1.E.53.1.9	e-19	K4WL31	Multiple substrates	Peptides, proteins, sugar derivatives
YP_006118891.1	+	-	-	-	-	1.E.53.1.9	e-23	K4WL31	Multiple substrates	Peptides, proteins, sugar derivatives
NP_308648.1	+	-	-	+	+	1.E.53.1.9	e-42	K4WL31	Multiple substrates	Proteins, peptides, sugar derivatives
NP_418261.1	-	-	-	-	+	1.E.55.2.4	e-64	S1GB50	Multiple substrates	Proteins, peptides, sugar derivatives
YP_002404208.1	+	+	+	+	+	2.A.1.1.1	0	P0AEP1	Monosaccharides	Galactose:H+ symporter
YP_002404104.1	+	+	+	+	+	2.A.1.1.2	0	P0AE24	Monosaccharides	Arabinose:H+ symporter
YP_002405405.1	-	-	-	+	+	2.A.1.1.3	0	P0AGF4	Monosaccharides	Xylose:H+ symporter

Table S1, continued.

YP_002402995.1	+	+	+	+	+	2.A.1.1.92	0	P38055	Monosaccharides	Sugars
YP_002404037.1	+	+	+	-	+	2.A.1.1.95	0	Q46909	Monosaccharides	Xylose
YP_002405261.1	-	-	+	-	-	2.A.1.1.95	e-16	Q46909	Monosaccharides	Xylose
YP_002401184.1	+	+	+	+	+	2.A.1.1.114	0	P31679	Monosaccharides	Xylose
YP_002403001.1	+	+	+	+	+	2.A.1.1.115	0	P76230	Monosaccharides	Xylose
YP_002403464.1	+	+	+	+	+	2.A.1.2.7	0	P28246	MDR	Biocyclomycin, sulfathiazole, tetracycline, fosfomycin, acriflavin:H+ antiporter
YP_002270349.1	-	-	-	+	-	2.A.1.2.7	e-34	P28246	MDR	Biocyclomycin, sulfathiazole, tetracycline, fosfomycin, acriflavin:H+ antiporter
YP_006105663.1	-	-	+	-	-	2.A.1.2.7	e-35	P28246	MDR	Biocyclomycin, sulfathiazole, tetracycline, fosfomycin, acriflavin:H+ antiporter
YP_002405064.1	+	+	+	+	+	2.A.1.2.9	e-163	P31442	MDR	CCCP, benzalkonium, SDS:H+ antiporter
YP_002401523.1	+	+	+	+	+	2.A.1.2.14	0	P23910	Monosaccharides	Arabinose efflux
YP_002402732.1	+	+	+	+	+	2.A.1.2.15	0	P31122	Monosaccharides	Arabinose, isopropyl β-D-thio-galactopyranoside:H+ antiporter

Table S1, continued.

AID77864.1	-	+	-	-	-	2.A.1.2.18	0	P0AEY7	Oligosaccharides	Lactose, melibiose efflux
YP_002401983.1	+	-	+	+	+	2.A.1.2.19	0	P0AEY8	MDR	Chloramphenicol, tetracycline, norfloxacin, doxorubicin, trimethoprim, acriflavin, ethidium bromide, tetraphenylphosphonium, TPP, benzalkonium, ciprofloxacin, thiamphenicol, IPTG
YP_002402255.1	+	+	+	-	+	2.A.1.2.20	0	P25744	MDR	Multidrug
YP_002402266.1	+	+	+	+	+	2.A.1.2.21	0	P69367	MDR	Norfloxacin, enoxacin
YP_002405100.1	+	+	+	+	+	2.A.1.2.22	0	P31462	Drugs	Chloramphenicol
YP_002405051.1	+	+	+	-	+	2.A.1.2.26	0	P0ADL1	Nucleosides	Purine:H+ antiporter
YP_002411081.1	-	-	-	+	-	2.A.1.2.26	e-66	P0ADL1	Nucleosides	Purine:H+ antiporter
YP_002405849.1	-	+	-	+	+	2.A.1.2.52	0	P39386	MDR	Puromycin
YP_002402744.1	+	+	+	+	+	2.A.1.2.55	0	P31126	Peptides	Alanine-glutamine
YP_002401554.1	+	+	+	+	+	2.A.1.2.60	0	P77726	None	Unknown
YP_002402890.1	+	+	+	+	+	2.A.1.2.62	0	P37597	MDR	Unknown
YP_002402887.1	+	+	+	+	+	2.A.1.2.65	0	P77389	Monosaccharides	Arabinose efflux

Table S1, continued.

YP_002403949.1	+	+	+	+	+	2.A.1.3.2	0	P0AEJ0	MDR	CCCP, nalidixic acid, rhodamine-6G, methylviologen, deoxycholate, estradiol, progesterone, SDS, organomercurials:H+ antiporter
YP_002403061.1	+	+	+	+	+	2.A.1.3.17	0	P76269	Drugs	Trimethoprim
YP_002403545.1	-	-	+	+	+	2.A.1.3.17	e-31	P76269	Drugs	Trimethoprim
YP_852504.1	-	-	+	-	-	2.A.1.3.18	e-70	Q9KIH3	MDR	Phytoalexins, salicylate, drugs
YP_002403366.1	+	+	+	+	+	2.A.1.3.26	0	P36554	MDR	Novobiocin, deoxycholate exporter
YP_002403676.1	+	+	+	+	+	2.A.1.3.36	0	C5W789	Proteins	Proteins
YP_002403677.1	+	+	+	+	+	2.A.1.3.36	0	C5W790	Proteins	Proteins
YP_002405147.1	+	+	+	+	+	2.A.1.3.51	0	P31474	Drugs	Drug:H+ antiporter
YP_002405055.1	+	+	+	+	+	2.A.1.4.1	0	P0AGC0	Monosaccharides	Sugar-P:Pi antiporter
YP_854265.1	-	-	+	-	-	2.A.1.4.2	0	P12681	Anions	Phosphoglycerate:phosphate antiporter
YP_002403513.1	+	+	+	+	+	2.A.1.4.3	0	P08194	Sugar alcohols	Glycerol-P:Pi antiporter
YP_002405056.1	+	+	+	+	+	2.A.1.4.4	0	P09836	Monosaccharides	Hexose-P:Pi antiporter
YP_002269002.1	-	-	-	+	-	2.A.1.4.4	e-96	P09836	Monosaccharides	Hexose-P:Pi antiporter
YP_002401474.1	+	+	+	+	+	2.A.1.5.1	0	P02920	Oligosaccharides	Lactose:H+ symporter
NP_311268.1	-	-	-	+	-	2.A.1.5.3	0	P30000	Oligosaccharides	Sucrose:H+ symporter
YP_006108420.1	+	+	+	+	-	2.A.1.6.1	e-60	P16482	Carboxylates	Citrate:H+ symporter
YP_002403883.1	+	+	+	+	+	2.A.1.6.2	0	P0AEX3	Carboxylates	α-Ketoglutarate:H+ symporter

Table S1, continued.

YP_002405480.1	+	+	+	+	+	2.A.1.6.4	0	P0C0L7	Amino acids	Proline, glycine betaine:H+, Na+ symporter
YP_002403260.1	+	+	+	+	+	2.A.1.6.6	0	P76350	Carboxylates	Shikimate:H+ symporter
YP_002405262.1	-	-	+	-	-	2.A.1.6.6	e-85	P76350	Carboxylates	Shikimate:H+ symporter
YP_002402753.1	+	+	+	+	-	2.A.1.6.9	0	P77228	Metabolites	Non-specific
YP_006108502.1	-	-	+	-	-	2.A.1.6.9	e-60	P77228	Metabolites	Non-specific
YP_002404899.1	+	+	+	+	+	2.A.1.6.10	0	P37643	Metabolites	Non-specific
YP_002404067.1	+	+	+	+	+	2.A.1.7.1	0	P11551	Monosaccharides	Fucose:H+ symporter
YP_002405788.1	-	+	+	-	-	2.A.1.7.5	0	Q8XEV7	Monosaccharides	2-deoxyribose
NP_417823.1	+	+	+	+	+	2.A.1.7.14	0	P60778	Monosaccharides	Fucose:H+ symporter
YP_002402406.1	+	+	+	+	+	2.A.1.8.1	0	P10903	Anions	Nitrate:H+ symporter
YP_002402675.1	+	+	+	+	+	2.A.1.8.10	0	P37758	Anions	Nitrate uptake, nitrite efflux
YP_002404229.1	+	+	+	+	+	2.A.1.10.1	0	P0AFF4	Nucleosides	Guanosine, inosine, cytidine, thymidine
YP_002403708.1	+	+	+	-	+	2.A.1.10.2	0	P45562	Nucleosides	Xanthosine, inosine, adenosine, cytidine, thymidine
YP_002403383.1	+	+	+	+	+	2.A.1.10.4	0	P76417	Nucleosides	Unknown
YP_002404931.1	+	+	+	+	+	2.A.1.11.3	e-177	P37662	Carboxylates	Oxalate:formate antiporter
YP_002404590.1	+	+	+	+	+	2.A.1.12.1	0	P41036	Carboxylates	Sialic acid:H+ symporter
YP_006107307.1	-	-	+	-	-	2.A.1.12.1	0	P41036	Carboxylates	Sialic acid:H+ symporter
YP_002415427.1	-	-	-	-	+	2.A.1.12.1	e-76	P41036	Carboxylates	Sialic acid:H+ symporter

Table S1, continued.

YP_002404464.1	+	+	+	+	+	2.A.1.14.2	0	P0AA78	Carboxylates	Glucuronate, galacturonate
NP_756357.1	-	-	+	-	-	2.A.1.14.2	e-103	P0AA78	Carboxylates	Glucuronate, galacturonate
YP_006108681.1	-	-	+	-	-	2.A.1.14.2	e-120	P0AA78	Carboxylates	Glucuronate, galacturonate
YP_002405080.1	+	+	+	-	+	2.A.1.14.7	0	P0AA76	Carboxylates	Galactonate
YP_002404499.1	+	+	+	+	+	2.A.1.14.14	0	Q8FDB7	Carboxylates	Galactarate
YP_002405861.1	+	+	-	+	+	2.A.1.14.33	0	P39398	Carboxylates	Galactonate
YP_002405343.1	-	-	+	-	-	2.A.1.14.33	e-132	P39398	Carboxylates	Galactonate
YP_006106617.1	+	+	+	+	+	2.A.1.14.35	0	P76470	Carboxylates	Rhamnonate
YP_002271658.1	-	-	-	+	+	2.A.1.14.35	e-95	P76470	Carboxylates	Rhamnonate
NP_417269.1	+	+	+	+	+	2.A.1.14.40	0	C4ZZU4	Carboxylates	Glucarate
YP_001463490.1	-	-	-	+	-	2.A.1.15.1	e-82	Q51955	Carboxylates	4-hydroxybenzoate, protocatachuate
YP_002401484.1	-	-	-	+	+	2.A.1.15.2	e-180	P77589	Carboxylates	3-(3-hydroxyphenyl)propionate
YP_002402918.1	+	+	+	+	+	2.A.1.15.12	0	P76197	Carboxylates	Quinate, shikimate
YP_002402919.1	+	+	+	+	+	2.A.1.15.13	0	P76198	Carboxylates	Quinate, shikimate
YP_002401472.1	-	-	-	+	+	2.A.1.17.1	e-165	P17583	Anions	Cyanate
YP_002403017.1	+	+	+	+	+	2.A.1.17.3	0	P76242	Anions	Cyanate
YP_002401207.1	-	-	-	-	+	2.A.1.20.1	0	P31675	Monosaccharides	Lactose, glucose, aromatic glucosides, galactosides, cellobiose, maltose, α-methylglucoside, IPTG, amino-glycosides

Table S1, continued.

YP_002403451.1	+	+	+	+	+	2.A.1.20.2	0	P33026	Oligosaccharides	Lactose, glucose efflux
YP_002405047.1	-	-	-	-	+	2.A.1.20.3	0	P31436	Monosaccharides	Arabinose
YP_002401563.1	+	+	+	+	+	2.A.1.25.2	0	P0AE16	Peptides	Muropeptide
YP_002402038.1	+	+	+	+	+	2.A.1.26.1	0	P21503	None	Unknown
YP_002403830.1	+	+	+	+	+	2.A.1.27.1	0	Q47142	Carboxylates	Phenylproprionate
YP_002401608.1	+	+	+	+	+	2.A.1.35.1	0	P52067	Drugs	Fosmidmycin
YP_002405358.1	-	+	+	+	+	2.A.1.36.1	0	P43531	Drugs	Acriflavin
YP_002403944.1	+	+	+	+	-	2.A.1.36.3	0	P76628	Monosaccharides	Arabinose
YP_002401699.1	+	+	+	+	+	2.A.1.38.1	e-163	P24077	Siderophores	Enterobactin
YP_002404098.1	+	+	+	+	+	2.A.1.42.1	0	P39196	Lipids	Lysophospholipid
YP_002404099.1	-	-	+	+	+	2.A.1.42.2	e-176	Q89SS6	Lipids	Lysophospholipid
YP_002413287.1	-	-	-	+	-	2.A.1.46.5	e-52	C2UR80	MDR	Quinolone
YP_002403588.1	+	+	-	+	+	2.A.1.46.6	0	P77549	Monosaccharides	Arabinose efflux
YP_002404823.1	+	+	+	+	+	2.A.1.46.7	0	P37621	Monosaccharides	Arabinose export
YP_002405843.1	+	+	+	-	+	2.A.1.51.2	e-162	D6IHN4	Monosaccharides	Sugars
YP_002273858.1	-	-	-	+	-	2.A.1.51.2	e-174	D6IHN4	Monosaccharides	Sugars
YP_002405255.1	+	+	+	+	+	2.A.1.52.1	0	P32135	Monosaccharides	Sugars
YP_002404040.1	+	+	+	+	+	2.A.1.52.2	0	F4TJX1	Monosaccharides	Sugars
AAN80879.1	+	+	+	-	-	2.A.1.57.3	0	B7L8Z4	Siderophores	Fe3+
YP_002401986.1	+	+	+	+	+	2.A.1.60.2	0	P75810	Monosaccharides	Sugars
YP_002405489.1	-	-	-	+	+	2.A.2.1.1	0	A7ZUZ0	Oligosaccharides	Melibiose
YP_002402845.1	+	+	+	+	+	2.A.2.3.1	0	P0CE45	Monosaccharides	Glucuronide
YP_002405045.1	+	+	+	+	+	2.A.2.3.4	0	P31435	Monosaccharides	α-xyloside uptake
YP_002414739.1	-	-	-	+	-	2.A.2.3.4	e-72	P31435	Monosaccharides	α-xyloside uptake

Table S1, continued.

NP_414804.1	-	-	-	-	+	2.A.2.3.5	0	P75683	Monosaccharides	β-xyloside
NP_312485.1	-	-	-	+	-	2.A.2.3.6	e-79	A1S5F2	Oligosaccharides	Cellobiose:Na+
YP_001465361.1	-	-	-	+	+	2.A.2.3.9	0	P32137	None	Unknown
YP_001465360.1	-	-	-	+	+	2.A.2.3.9	e-179	P32137	None	Unknown
YP_006104421.1	-	-	+	-	-	2.A.2.5.1	e-153	Q93KC2	Oligosaccharides	Oligogalacturonide
YP_002401683.1	+	+	+	+	+	2.A.3.1.1	0	P24207	Amino acids	Phenylalanine
YP_002403437.1	+	+	+	+	+	2.A.3.1.2	0	P25737	Amino acids	Lysine
YP_002401245.1	+	+	+	+	+	2.A.3.1.3	0	P15993	Amino acids	Asparagine
YP_002403927.1	+	+	+	+	+	2.A.3.1.4	0	P25527	Carboxylates	GABA
YP_002401530.1	+	+	+	+	+	2.A.3.1.6	0	P37460	Amino acids	Proline
YP_002405628.1	+	+	+	+	+	2.A.3.1.7	0	P0AAE0	Amino acids	Serine
YP_002402662.1	+	+	+	+	+	2.A.3.1.8	0	P40812	Amino acids	Asparagine
NP_414794.4	-	-	-	-	+	2.A.3.1.10	0	Q47689	Amino acids	Methylmethionine
YP_002402539.1	-	-	-	+	+	2.A.3.1.13	0	P76037	Amines	Putrescine
YP_002403306.1	+	+	+	+	+	2.A.3.1.14	0	P0AA47	Amines	Putrescine:spermidine transporter
YP_002405181.1	+	+	+	+	+	2.A.3.1.15	0	P27837	Amino acids	Alanine, serine, glycine
YP_002401785.1	+	+	+	+	+	2.A.3.2.1	0	P0AAF1	Amines	Putrescine:ornithine antiporter
YP_002405502.1	+	+	+	+	+	2.A.3.2.2	0	P0AAE8	Amines	Cadaverine:lysine antiporter
YP_002405484.1	+	+	+	+	+	2.A.3.2.5	0	P60061	Amino acids	Arginine:agmatine antiporter
YP_859796.1	-	-	+	-	-	2.A.3.2.7	e-128	Q9Z6M8	Amino acids	Arginine:agmatine antiporter
YP_002402834.1	+	+	+	+	+	2.A.3.2.8	0	P0AAE5	Amino acids	Arginine:ornithine antiporter

Table S1, continued.

YP_002401615.1	+	+	+	+	+	2.A.3.6.4	0	P77400	Amino acids	Glutamine
YP_002402039.1	-	-	-	+	+	2.A.3.7.2	0	P75835	None	Unknown
YP_002402696.1	+	+	+	+	+	2.A.3.7.3	0	C8U8G2	Carboxylates	Glutamate:GABA antiporter
YP_002404449.1	+	+	+	+	+	2.A.3.7.4	0	P42590	Proteins	Proteins
YP_002405575.1	+	+	+	+	+	2.A.3.7.5	0	P39282	Carboxylates	Glutamate:GABA antiporter
YP_002404718.1	-	-	-	+	+	2.A.3.8.17	0	P45539	Sugar derivatives	Fructoselysine
YP_002405558.1	+	+	+	+	+	2.A.3.13.1	0	P39277	Amino acids	Methionine
YP_002401836.1	+	-	+	+	+	2.A.4.1.4	e-153	P75757	Cations	Zn2+, Cd2+ efflux
YP_002405296.1	+	+	+	+	+	2.A.4.7.1	e-160	P69380	Cations	Zn2+, Cd2+, Hg2+, Fe2+:H+ antiporter
YP_002404412.1	+	+	+	+	+	2.A.5.5.1	e-123	P0A8H3	Cations	Fe2+, Co2+, Mn2+, Cd2+, Zn2+ uptake
YP_002401681.1	+	+	+	+	+	2.A.6.1.4	0	P77239	Cations	Cu+, Ag+
YP_002401682.1	+	+	+	+	+	2.A.6.1.4	0	P38054	Cations	Cu+, Ag+
YP_002401680.1	+	+	+	+	+	2.A.6.1.4	e-58	P77214	Cations	Cu+, Ag+
NP_417732.1	+	+	+	-	+	2.A.6.2.1	0	P24181	MDR	MDR

Table S1, continued.

YP_002401591.1	+	+	+	+	+	2.A.6.2.2	0	P31224	MDR	Chloramphenicol, tetracycline, erythromycin, nalidixic acid, fusidic acid, fluoroquinolones, lipophilic β-lactams, norfloxacin, doxorubicin, novobiocin, rifampin, trimethoprim, acriflavin, crystal violet, ethidium, rhodamine-6G, TPP, benzalkonium, SDS, Triton X-100, deoxycholate, estradiola, progesterone, phospholipids
YP_859756.1	-	-	+	-	-	2.A.6.2.6	e-138	P52002	MDR	N-(3-oxododecanoyl)-L-homoserine lactone autoinducer
YP_002403763.1	+	+	+	+	+	2.A.6.2.7	0	P24177	MDR	Amikacin, gentamicin, neomycin, kanamycin, tobramycin, SDS, dexoycholate, estradiol, progesterone
YP_006106806.1	-	-	-	-	+	2.A.6.2.7	e-27	P24177	MDR	Amikacin, gentamicin, neomycin, kanamycin, tobramycin, SDS, dexoycholate, estradiol, progesterone

Table S1, continued.

YP_006120458.1	+	+	-	-	-	2.A.6.2.12	0	P76398	MDR	Nalidixic acid, norfloxacin, cloxicillin, enoxacin, kanamycin, benzalkonium, bilte salts, SDS, deoxycholate
YP_002403364.1	+	+	+	+	+	2.A.6.2.12	0	P76398	MDR	Nalidixic acid, norfloxacin, cloxicillin, enoxacin, kanamycin, benzalkonium, bilte salts, SDS, deoxycholate
NP_417971.1	+	+	+	+	+	2.A.6.2.13	0	P37637	MDR	Erythromycin, doxorubicin, crystal violet, ethidium, rhodamine 6G, TPP, benzalkonium, SDS, deoxycholate, estradiol, progesterone
YP_006119690.1	+	+	-	-	-	2.A.6.2.19	0	Q8GC83	MDR	Chloramphenicol, ciprofloxacin, erythromycin, tetracycline, doxycycline
YP_006105662.1	+	+	+	+	-	2.A.6.2.19	0	Q8GC82	MDR	Chloramphenicol, ciprofloxacin, erythromycin, tetracycline, doxycycline

Table S1, continued.

YP_006105660.1	+	+	+	+	-	2.A.6.2.19	e-157	Q8GC84	MDR	Chloramphenicol, ciprofloxacin, erythromycin, tetracycline, doxycycline
YP_002401536.1	+	+	+	+	+	2.A.6.4.1	0	P0AG90	Proteins	Proteins
AID81729.1	-	+	-	-	-	2.A.6.4.1	e-180	P0AG90	Proteins	Proteins
YP_002401537.1	-	-	+	+	+	2.A.6.4.3	e-47	Q5SKE6	Proteins	Proteins
NP_312363.1	-	+	+	+	-	2.A.6.8.2	0	Q7AA53	MDR	Unknown
YP_002403208.1	+	+	-	+	+	2.A.7.1.3	e-60	P23895	MDR	Cationic lipophilic drugs
YP_002401872.1	-	-	+	+	+	2.A.7.1.3	e-61	P23895	MDR	Cationic lipophilic drugs
YP_002405567.1	+	+	+	+	+	2.A.7.1.4	e-42	P69937	Cations	Quaternary ammonium compound efflux
YP_002402828.1	+	+	+	+	+	2.A.7.1.9	e-48	P69210	Amines	Spermidine
YP_002402829.1	+	+	+	+	+	2.A.7.1.9	e-63	P69213	Amines	Spermidine
YP_002405215.1	+	+	+	+	+	2.A.7.3.1	e-71	O06933	Carboxylates	Acetate
YP_002402743.1	+	+	+	+	+	2.A.7.3.2	e-154	P31125	Amino acids	O-acetylserine, cysteine, asparagine, glutamine
YP_002401954.1	+	+	+	+	+	2.A.7.3.6	e-148	P0AA67	Amino acids	Threonine, homoserine
YP_002405048.1	+	+	+	+	+	2.A.7.3.12	e-138	P31437	Amino acids	Amino acid efflux
YP_002404556.1	+	+	+	+	+	2.A.7.3.18	e-170	E1ILD8	Amino acids	Amino acid efflux
YP_002405630.1	+	+	+	+	+	2.A.7.3.19	e-176	P39314	Amino acids	Amino acid efflux
YP_002403230.1	-	-	+	+	+	2.A.7.3.22	e-131	p0aa70	None	Unknown
YP_002405325.1	+	+	+	+	+	2.A.7.3.26	e-153	P0ABT9	Amino acids	Amino acid efflux

Table S1, continued.

YP_002405289.1	+	+	+	-	+	2.A.7.6.1	e-172	P27125	Monosaccharides	Rhamnose:H+ symporter
YP_002405207.1	+	+	+	+	+	2.A.7.7.2	e-168	P27844	Drugs	Chloramphenicol
YP_002402678.1	+	+	+	+	+	2.A.7.17.2	e-145	P46136	Amino acids	Phenylalanine, tyrosine, tryptophan, histidine
AID81840.1	-	+	-	-	-	2.A.7.19.2	e-13	Q9ZPR7	Amines	Allantoin
YP_002402656.1	+	+	+	+	+	2.A.7.21.2	e-79	P76111	None	Unknown
AAN80950.1	-	+	+	-	-	2.A.7.21.7	e-26	F6FW65	MDR	MDR
YP_002403527.1	+	+	+	+	+	2.A.7.22.1	e-46	Q47377	Sugar derivatives	4-amino-4-deoxy-L-arabinose phosphoundecaprenol
YP_002403528.1	+	+	+	+	+	2.A.7.22.1	e-51	P76474	Sugar derivatives	4-amino-4-deoxy-L-arabinose phosphoundecaprenol
YP_002402811.1	+	+	+	+	+	2.A.7.26.1	e-61	P76169	None	Unknown
YP_002415475.1	-	+	-	-	+	2.A.8.1.1	e-107	P12012	Carboxylates	Gluconate:H+ symporter
YP_002405680.1	+	-	+	-	+	2.A.8.1.2	0	P39344	Carboxylates	L-idonate, D-gluconate: H+ symporter
YP_002405830.1	-	-	+	+	+	2.A.8.1.3	0	P0AC94	Carboxylates	Fructuronate/gluconate :H+ symporter
YP_002404765.1	+	+	+	+	+	2.A.8.1.4	0	P39835	Carboxylates	D-gluconate:H+ symporter
YP_006106719.1	+	+	+	-	+	2.A.8.1.5	0	P08555	Amino acids	Serine
YP_002404001.1	+	+	+	-	+	2.A.8.1.7	0	Q46892	Carboxylates	Gluconate:H+ symporter
YP_002404787.1	+	+	+	+	+	2.A.8.1.8	0	P0AC96	Carboxylates	Gluconate
YP_002405095.1	+	+	+	+	+	2.A.9.3.1	0	P25714	Proteins	Proteins

Table S1, continued.

YP_002405291.1	+	+	+	+	+	2.A.10.1.2	e-124	P0A712	Carboxylates	2-keto-3-deoxygluconate
YP_002405555.1	+	+	+	+	+	2.A.13.1.1	0	P0ABN5	Carboxylates	Aspartate:fumarate antiporter
YP_002405492.1	+	+	+	+	+	2.A.13.1.2	0	P0ABN9	Carboxylates	Fumarate:malate antiporter
YP_002404994.1	+	+	+	+	+	2.A.14.1.1	0	P33231	Carboxylates	L-lactate, D-lactate, glycolate
YP_002404346.1	+	+	+	-	+	2.A.14.1.2	0	Q46839	Carboxylates	L-lactate, D-lactate, glycolate
YP_002401440.1	+	+	+	+	+	2.A.15.1.4	0	P0ABC9	Cations	Choline:Na+ symporter
YP_002401179.1	+	+	+	+	+	2.A.15.2.1	0	P31553	Amines	Carnitine:γ-butyrobetaine antiporter
YP_006122712.1	+	-	-	-	-	2.A.15.2.2	e-62	B4EY22	Amines	Carnitine:γ-butyrobetaine antiporter
YP_002403030.1	-	-	-	+	+	2.A.15.2.3	0	P0ABD2	Amines	Glycine betaine
YP_002402636.1	+	+	+	+	+	2.A.16.1.1	e-178	P25396	Anions	Tellurite efflux
YP_002405210.1	-	-	+	+	+	2.A.16.2.2	e-25	Q5EAK4	Carboxylates	Malate
YP_002402864.1	+	+	+	+	+	2.A.17.1.2	0	P77304	Peptides	Di/tripeptide:H+ symporter
YP_002404869.1	+	+	+	+	+	2.A.17.1.3	0	P36837	Peptides	Di/tripeptide:H+ symporter
YP_002401799.1	+	+	+	+	+	2.A.17.1.4	0	P75742	Peptides	Peptides
YP_002405500.1	+	+	+	+	+	2.A.17.1.5	0	P39276	Peptides	Peptides
YP_002402399.1	+	+	+	+	+	2.A.19.1.1	e-166	P31801	Cations	Ca2+, Na2+, K+:H+ antiporter
YP_002404568.1	+	+	+	+	+	2.A.19.5.1	e-149	P45394	Cations	Ca2+:H+ antiporter
YP_002404866.1	+	+	+	+	+	2.A.20.1.1	0	P0AFJ7	Anions	Pi:H+ symporter

Table S1, continued.

YP_002404363.1	+	+	+	+	+	2.A.20.1.2	0	P43676	Anions	Pi:H+ symporter
YP_002404624.1	+	+	+	+	+	2.A.21.1.1	0	P16256	Carboxylates	Pantothenate:Na+ symporter
YP_002402218.1	+	+	+	+	+	2.A.21.2.1	0	P07117	Amino acids	Proline:Na+ symporter
YP_002405070.1	+	+	+	+	+	2.A.21.3.9	e-74	A8H019	Monosaccharides	Galactose
YP_002405443.1	+	+	+	+	+	2.A.21.7.2	0	P32705	Carboxylates	Acetate, glyoxylate
YP_002405453.1	+	+	+	+	+	2.A.23.1.1	0	P21345	Amino acids	Glutamate, aspartate:H+ symporter
YP_006120091.1	+	+	-	-	-	2.A.23.1.4	e-116	P54596	Amino acids	Cystine, selenocystine: H+ symporter
NP_308785.1	-	-	-	+	-	2.A.23.1.6	e-70	P96603	Carboxylates	Dicarboxylate:H+ symporter
YP_002404905.1	+	+	+	+	+	2.A.23.1.7	0	P0A830	Carboxylates	Dicarboxylates
NP_416243.1	-	-	+	+	+	2.A.23.1.8	0	P77529	Amino acids	Cysteine
YP_002404460.1	+	+	+	+	+	2.A.23.4.1	e-177	P0AGE4	Amino acids	Serine, threonine:Na+ symporter
YP_002401150.1	+	+	+	+	+	2.A.25.1.5	e-96	Q45068	Amino acids	Na+:alanine symporter
P0A8K2.1	-	-	+	-	-	2.A.25.1.6	e-45	B0SM05	Amino acids	Glycine
YP_002401529.1	+	+	-	+	+	2.A.26.1.2	e-158	P25185	Amino acids	Isoleucine, valine:H+ symporter
YP_002405041.1	+	+	+	+	+	2.A.27.1.1	e-178	P0AER8	Amino acids	Glutamate:H+ symporter
YP_002401158.1	+	+	+	+	+	2.A.33.1.1	e-174	P13738	Cations	Na+:H+ antiporter
YP_002402367.1	+	+	+	+	+	2.A.34.1.1	0	P0AFA7	Cations	Na+:H+ antiporter
YP_006122719.1	+	-	-	-	-	2.A.35.1.1	e-61	P27611	Cations	Na+:H+ antiporter
YP_002405441.1	+	+	+	+	+	2.A.36.3.1	0	P32703	Cations	Na+:H+ antiporter
YP_006108896.1	-	-	+	-	-	2.A.36.3.1	e-160	P32703	Cations	Na+:H+ antiporter

Table S1, continued.

YP_002402372.1	+	+	+	+	-	2.A.36.6.3	e-155	Q87KV8	Cations	K+:H+ antiporter
NP_415709.2	-	-	-	-	+	2.A.36.6.5	0	Q9KNM9	Cations	K+:H+ antiporter
YP_002401186.1	+	+	+	+	+	2.A.37.1.1	0	P03819	Cations	K+ efflux
YP_002401185.1	+	+	+	+	+	2.A.37.1.1	e-108	P0A754	Cations	K+ efflux
YP_002404697.1	+	+	+	-	+	2.A.37.1.2	0	P45522	Cations	K+ efflux
YP_002404698.1	+	+	+	+	+	2.A.37.1.2	e-108	P0A756	Cations	K+ efflux
YP_002401607.1	+	+	+	+	+	2.A.37.1.5	0	P39830	Cations	K+:H+ antiporter
YP_002404649.1	+	+	+	+	+	2.A.38.1.1	0	P0AGI8	Cations	K+:H+ antiporter
YP_002405235.1	+	+	+	+	+	2.A.38.1.1	0	P0AFZ7	Cations	K+:H+ antiporter
YP_852529.1	-	-	-	-	+	2.A.38.1.6	0	P23849	Cations	K+ uptake
NP_755569.1	-	-	+	-	-	2.A.38.4.5	e-10	P73948	Cations	K+
YP_002401467.1	+	+	+	+	+	2.A.39.1.1	0	P0AA82	Nucleosides	Cytosine
YP_006108271.1	-	-	+	-	-	2.A.39.1.1	e-26	P0AA82	Nucleosides	Cytosine
YP_002401641.1	+	+	+	+	+	2.A.39.3.8	0	P75712	Amines	Allantoin
YP_002403791.1	+	+	+	+	+	2.A.40.1.1	0	P0AGM7	Nucleosides	Uracil
YP_002402209.1	+	+	+	+	+	2.A.40.1.3	0	P75892	Nucleosides	Pyrimidines
YP_852115.1	-	-	-	-	+	2.A.40.1.3	e-96	P75892	Nucleosides	Pyrimidines
YP_002404150.1	+	+	+	+	+	2.A.40.3.3	0	Q46821	Carboxylates	Urate
YP_002405042.1	+	+	+	+	+	2.A.40.4.2	0	P0AGM9	Nucleosides	Xanthine
YP_002404145.1	+	+	+	+	+	2.A.40.4.3	0	P67444	Nucleosides	Xanthine
NP_415046.4	-	-	+	+	+	2.A.40.5.1	0	P77328	Nucleosides	Purines
YP_002405053.1	+	+	+	+	+	2.A.40.7.4	0	P31440	Nucleosides	Adenine
YP_002405440.1	+	+	+	+	+	2.A.40.7.5	0	P0AF52	Nucleosides	Guanine, hypoxanthine, xanthine

Table S1, continued.

YP_002404147.1	-	-	+	+	+	2.A.40.7.5	e-171	P0AF52	Nucleosides	Guanine, hypoxanthine, xanthine
YP_002405104.1	+	+	+	+	+	2.A.40.7.6	0	P31466	Nucleosides	Adenine
YP_026186.1	+	+	+	+	+	2.A.40.7.7	0	Q46817	Nucleosides	Guanine, hypoxanthine
YP_002403702.1	+	+	+	+	+	2.A.41.1.1	0	P0AFF2	Nucleosides	Nucleoside (except guanosine):H+ symporter
YP_002403445.1	+	+	+	+	+	2.A.41.2.9	0	P33024	Cations	Na+:H+ symporter
YP_002403442.1	-	-	-	+	+	2.A.41.2.10	0	P33021	Nucleosides	Nucleosides
YP_002403138.1	+	+	+	+	+	2.A.42.1.1	0	P0AAD4	Amino acids	Tyrosine
YP_002404535.1	+	+	+	+	+	2.A.42.1.2	0	P0AAD2	Amino acids	Tryptophan
YP_002405099.1	+	+	+	+	+	2.A.42.1.3	0	P23173	Amino acids	Tryptophan
YP_002404062.1	+	+	+	+	+	2.A.42.2.1	0	P0AAD6	Amino acids	Serine
YP_002404489.1	+	+	+	+	+	2.A.42.2.2	0	P0AAD8	Amino acids	Threonine, serine
YP_002404918.1	+	+	+	+	+	2.A.42.2.3	0	P37660	Amino acids	Serine
YP_002404484.1	+	-	-	+	+	2.A.42.2.4	0	P42628	Amino acids	Serine
YP_002404108.1	+	+	+	+	+	2.A.42.2.5	0	P63340	Amino acids	Serine
YP_002401958.1	+	+	+	+	+	2.A.45.3.2	0	P75788	Anions	Arsenite, antimonite efflux
YP_002402642.1	+	+	+	+	+	2.A.46.1.1	e-69	P07775	Carboxylates	Benzoate
YP_002401855.1	+	+	+	+	+	2.A.47.3.1	e-83	Q41364	Carboxylates	2-oxoglutarate:malate antiporter
YP_002401720.1	+	+	+	+	+	2.A.47.3.2	0	P0AE74	Carboxylates	Citrate:succinate antiporter
YP_006108517.1	+	-	+	-	-	2.A.47.3.2	e-21	P0AE74	Carboxylates	Citrate:succinate antiporter

Table S1, continued.

YP_002404435.1	+	+	+	+	+	2.A.47.3.3	0	P39414	Carboxylates	L-tartate:succinate antiporter
YP_002403558.1	-	-	+	+	+	2.A.47.4.1	e-52	P72958	Cations	Na+:K+ symporter
AAN79230.1	-	-	+	-	-	2.A.47.4.7	0	E4P9F4	Ions	Na+:Sulfate symporter
YP_002401288.1	+	+	+	+	+	2.A.49.5.1	0	P37019	Anions	Cl-:H+ antiporter
YP_002402821.1	+	+	+	+	+	2.A.49.5.3	0	Q8FHC1	Anions	Cl-
YP_002403699.1	+	+	+	+	+	2.A.49.7.1	e-175	H5KWQ5	Anions	Cl-
NP_415724.2	+	+	+	+	+	2.A.53.3.11	0	P0AFR2	Anions	Bicarbonate
YP_002403701.1	+	+	+	+	-	2.A.55.3.1	0	P0A769	Cations	Mn2+, Fe2+, Cd2+, Co2+, Zn2+, Ni2+:H+ symporter
YP_002404963.1	+	+	+	-	-	2.A.56.1.2	0	P37676	Carboxylates	2,3-diketo-L-gulonate
YP_006107990.1	+	+	+	-	-	2.A.56.1.2	e-178	P37675	Carboxylates	2,3-diketo-L-gulonate
YP_006107989.1	+	+	+	-	-	2.A.56.1.2	e-42	P37674	Carboxylates	2,3-diketo-L-gulonate
YP_006107419.1	+	+	+	-	-	2.A.56.1.5	e-20	Q8ZKR9	Oligosaccharides	Rhamnogalacturonide
YP_006107418.1	+	+	+	-	-	2.A.56.1.5	e-58	P43020	Oligosaccharides	Rhamnogalacturonide
YP_006107420.1	+	+	+	-	-	2.A.56.1.5	e-97	Q8ZKS0	Oligosaccharides	Rhamnogalacturonide
AAN83851.1	+	-	+	-	-	2.A.56.1.8	0	Q8FA80	Carboxylates	Sialic acid
YP_006122745.1	+	-	-	-	-	2.A.56.1.8	e-157	Q8FA78	Carboxylates	Sialic acid
YP_006122744.1	+	-	-	-	-	2.A.56.1.8	e-86	Q8FA79	Carboxylates	Sialic acid
YP_002405389.1	+	+	+	+	+	2.A.58.2.1	0	P0AF43	Cations	Pi:Na+ symporter
YP_002401729.1	+	+	+	+	+	2.A.61.1.1	0	P0ABP3	Carboxylates	C4-dicarboxylates
YP_002404593.1	-	-	-	+	+	2.A.61.1.2	0	P45428	Carboxylates	C4-dicarboxylates
YP_002401734.1	+	+	+	+	+	2.A.64.1.1	e-12	P0A843	Peptides	Diarginine
YP_002405226.1	+	+	+	+	+	2.A.64.1.1	e-129	P69423	Peptides	Diarginine
YP_002405224.1	+	+	+	+	+	2.A.64.1.1	e-39	P69428	Peptides	Diarginine

Table S1, continued.

YP_002405225.1	+	+	+	+	+	2.A.64.1.1	e-84	P69425	Peptides	Diarginine
YP_002402893.1	+	+	+	+	+	2.A.66.1.3	0	P37340	MDR	Chloramphenicol, norflaxin, enoxacin, phosphomycin, doxorubicin, trimethoprim, ethidium, deoxycholate
YP_002405419.1	-	-	+	+	+	2.A.66.1.4	0	P28303	Proteins	Proteins
YP_002403263.1	+	+	+	-	+	2.A.66.1.23	0	P76352	MDR	Drug:Na+ antiporter
YP_006106319.1	-	+	+	-	-	2.A.66.1.26	e-44	Q58119	None	Unknown
NP_416541.1	-	-	-	-	+	2.A.66.2.1	0	P37746	Polysaccharides	LPS
YP_002405177.1	+	+	+	+	+	2.A.66.2.3	0	P0AAA7	Sugar derivatives	Undecaprenol-pyrophosphate O-antigen
YP_006120425.1	+	-	-	-	-	2.A.66.2.6	e-49	O32273	Carboxylates	Teichuronic acid exporter
YP_002403336.1	+	+	+	+	+	2.A.66.2.7	0	P77377	Polysaccharides	LPS
NP_754454.1	-	+	+	-	-	2.A.66.2.10	e-26	O26447	Polysaccharides	O-antigen
YP_002402270.1	+	+	+	+	+	2.A.66.4.3	0	P0AF16	Polysaccharides	Murein
NP_310869.1	-	-	-	+	-	2.A.66.10.1	0	F1XYT9	Polysaccharides	O-antigen
YP_026192.1	-	-	+	-	+	2.A.66.12.6	0	L8CW92	Polysaccharides	Polysaccharides
YP_002402577.1	-	-	-	+	+	2.A.68.1.1	0	P46133	Carboxylates	p-aminobenzoyl-glutamate uptake
YP_002403681.1	+	+	+	+	+	2.A.69.3.5	e-159	P0AA50	Carboxylates	Auxin efflux
YP_002405140.1	+	+	+	+	+	2.A.72.1.1	0	P63183	Cations	K+ uptake
YP_006106596.1	+	+	+	-	+	2.A.73.1.1	0	P76460	Lipids	Short-chain fatty acid uptake
YP_002404183.1	+	+	+	+	+	2.A.75.1.2	e-119	P11667	Amino acids	Arginine

Table S1, continued.

YP_002405212.1	+	+	+	+	+	2.A.76.1.1	e-102	P0AG34	Peptides	Homoserine, homoserine lactone:H+ antiporter
YP_002405211.1	+	+	+	+	+	2.A.76.1.2	e-100	P0AG38	Amino acids	Threonine:H+ antiporter
YP_002401459.1	+	+	+	+	+	2.A.76.1.3	e-116	P75693	Amino acids	Neutral amino acids
YP_002403873.1	+	+	+	+	+	2.A.76.1.4	e-109	P38101	Amino acids	O-acetylserine, cysteine, azaserine export
YP_002403027.1	+	+	+	+	+	2.A.76.1.5	e-116	P76249	Amino acids	Leucine export
YP_002403945.1	+	+	+	+	+	2.A.78.1.3	e-129	P76630	Amino acids	Methionine efflux
YP_002403946.1	+	+	+	+	+	2.A.78.1.3	e-52	P43667	Amino acids	Methionine efflux
YP_002405869.1	+	+	+	+	+	2.A.79.2.1	e-144	Q8FA71	None	Unknown
YP_006108282.1	+	+	+	-	-	2.A.80.1.1	e-21	Q9FA46	Carboxylates	Tricarboxylates
YP_006108280.1	-	-	+	-	-	2.A.80.1.1	e-72	Q9FA44	Carboxylates	Tricarboxylates
AAN83209.1	+	+	+	-	-	2.A.80.1.3	e-38	D0J060	Carboxylates	Tricarboxylates
YP_002401988.1	+	+	+	+	+	2.A.81.1.4	0	A7ZJR5	Amino acids	Aspartate:alanine antiporter
YP_002405074.1	+	+	+	+	+	2.A.81.1.5	0	B7L824	Amino acids	Aspartate:alanine antiporter
YP_002402102.1	+	+	+	+	+	2.A.85.1.1	0	P75870	Carboxylates	Fusaric acid
YP_002404606.1	+	+	+	+	+	2.A.85.1.2	0	P46481	Carboxylates	p-hydroxybenzoate efflux
YP_002404706.1	+	+	+	+	+	2.A.85.1.3	0	P45537	Carboxylates	Fusaric acid
YP_002402875.1	+	+	+	+	+	2.A.85.1.6	0	Q8X638	Carboxylates	Fusaric acid
YP_002405457.1	+	+	+	+	+	2.A.85.6.1	0	P32715	MDR	Puromycin, acriflavin, tetraphenyl arsonium chloride
YP_002403300.1	+	+	+	+	+	2.A.85.7.1	0	P33011	Carboxylates	Fusaric acid

Table S1, continued.

YP_002403787.1	+	+	+	+	+	2.A.86.1.1	e-145	P0AFI9	Amines	Pheromone autoinducer 2 exporter
YP_002404824.1	+	+	+	+	+	2.A.86.1.2	0	P0AGM0	Amines	Pheromone autoinducer 2 exporter
YP_002402830.1	+	+	+	+	+	2.A.86.1.4	e-159	P0AFS5	Amines	Pheromone autoinducer 2 exporter
YP_002403790.1	-	-	-	-	+	2.A.86.1.5	e-06	C9VRY8	Proteins	Proteins
YP_002402916.1	+	+	+	+	+	2.A.86.2.1	e-169	B1LE48	Amines	Pheromone autoinducer 2 exporter
YP_002404821.1	+	+	+	+	+	2.A.88.8.6	e-125	B3WJF3	Vitamins	Vitamins
YP_002403712.1	+	+	+	+	+	2.A.93.1.4	0	P39836	Cations	Na+
YP_002402733.1	+	+	+	+	+	2.A.95.1.1	e-120	P0AEY1	Amino acids	Neutral amino acids
YP_006119636.1	+	+	-	-	-	2.A.95.1.3	e-28	O32244	MDR	Unknown
YP_002404786.1	+	+	+	+	+	2.A.95.1.5	e-89	P67143	MDR	Unknown
NP_415758.1	-	-	+	+	+	2.A.95.1.7	e-121	P25743	Amino acids	Amino acids
YP_002401153.1	+	+	+	+	+	2.A.96.1.1	e-96	P0AC98	Carboxylates	Acetate, succinate
YP_002403439.1	+	+	+	+	+	2.A.98.1.3	e-160	P62723	Anions	Sulfate efflux
YP_002403593.1	+	+	+	+	+	2.A.102.3.1	e-142	P0AD30	Anions	4-toluenesulfonate uptake
YP_002401225.1	+	+	+	+	+	2.A.103.1.1	0	P0ABG4	Lipids	Lipid II
YP_002401741.1	+	+	+	+	+	2.A.103.1.2	e-164	P0ABG7	None	Unknown
YP_002403934.1	+	+	+	+	+	2.A.104.1.1	e-72	A8ANM6	Amino acids	Alanine export
NP_416335.4	+	+	-	+	+	2.A.107.1.1	e-103	P76264	Polysaccharides	Murein
YP_006119349.1	+	+	-	-	-	2.A.108.2.3	0	P31545	Cations	Fe2+ uptake
NP_309291.1	+	+	+	+	-	2.A.108.2.3	0	P0AB24	Cations	Fe2+ uptake
YP_006119347.1	+	+	-	-	-	2.A.108.2.3	e-151	P75901	Cations	Fe2+ uptake
NP_309381.1	-	-	-	+	-	2.A.109.1.1	0	Q7B1W8	Cations	Tellurium

Table S1, continued.

YP_026201.1	+	+	+	+	+	2.A.109.1.2	e-88	F0N2E7	Cations	Tellurium
NP_417309.1	+	+	+	+	+	2.A.109.2.3	e-62	L5DDD7	Cations	Tellurium
NP_416609.1	+	+	+	+	+	2.A.113.1.1	e-159	P76425	Cations	Ni2+, Co2+
YP_006120488.1	+	+	-	-	-	2.A.113.1.1	e-63	P64534	Cations	Ni2+, Co2+ export
NP_415130.1	+	+	+	+	+	2.A.114.1.1	0	P15078	Peptides	Peptides
AAN83769.1	+	+	+	-	-	2.A.118.1.2	e-163	Q11G42	Carboxylates	Dicarboxylates
NP_416801.2	+	+	+	-	+	2.A.118.1.3	e-72	F9Z4G3	Carboxylates	C4 carboxylates
NP_417620.1	-	-	+	-	+	2.A.119.1.2	e-12	A8VTI4	None	Unknown
NP_416908.1	+	+	+	+	+	2.A.121.1.1	e-146	P0A6J3	Anions	Sulfate
NP_416647.1	+	-	+	+	+	2.A.122.1.1	e-130	C6EAH0	Polysaccharides	Murein
YP_006105480.1	+	+	+	-	-	2.C.1.1.1	e-13	P02929	Proteins	Bacteriocin
YP_002402434.1	-	-	+	+	+	2.C.1.1.1	e-79	P02929	Proteins	Bacteriocin
AID77771.1	-	+	-	-	-	2.C.1.2.1	0	P0A855	Proteins	Colicin
YP_002401833.1	+	-	+	+	+	2.C.1.2.1	e-108	P45955	Proteins	Colicin
NP_752753.1	+	-	+	-	+	2.C.1.2.1	e-31	P45955	Proteins	Colicin
YP_002401830.1	+	+	+	+	+	2.C.1.2.1	e-55	P19934	Proteins	Colicin
YP_006119026.1	+	+	-	-	-	2.C.1.2.1	e-99	C6EJJ6	Proteins	Colicin
YP_002405407.1	+	+	+	+	+	3.A.1.1.1	0	P02916	Oligosaccharides	Maltose
YP_002405408.1	+	+	+	+	+	3.A.1.1.1	0	P0AEX9	Oligosaccharides	Maltose
YP_002405409.1	+	+	+	+	+	3.A.1.1.1	0	P68187	Oligosaccharides	Maltose
YP_002405406.1	+	+	+	+	+	3.A.1.1.1	e-153	P68183	Oligosaccharides	Maltose
YP_002404800.1	+	+	+	+	+	3.A.1.1.3	0	P10907	Sugar alcohols	Glycerol-phosphate
YP_002404803.1	+	+	+	+	+	3.A.1.1.3	0	P0AG80	Sugar alcohols	Glycerol-phosphate
YP_002404801.1	+	+	+	+	+	3.A.1.1.3	e-151	P10906	Sugar alcohols	Glycerol-phosphate

Table S1, continued.

YP_002404802.1	+	+	+	+	+	3.A.1.1.3	e-158	P10905	Sugar alcohols	Glycerol-phosphate
AID78461.1	-	+	-	-	-	3.A.1.1.25	e-36	Q72H67	Oligosaccharides	Trehalose, maltose, sucrose, palatinose
YP_006119707.1	+	+	-	-	-	3.A.1.1.28	e-12	Q00749	Oligosaccharides	Glucose uptake
YP_006119715.1	+	+	-	-	-	3.A.1.1.34	e-135	P94360	Monosaccharides	Arabinose
YP_006119709.1	+	+	-	-	-	3.A.1.1.41	e-45	G4FGN6	Oligosaccharides	Trehalose
YP_006119708.1	+	-	-	-	-	3.A.1.1.44	e-36	Q9KZ07	Oligosaccharides	Maltose
YP_002405142.1	+	+	+	+	+	3.A.1.2.1	0	P04983	Monosaccharides	Ribose
YP_002405143.1	+	+	+	+	+	3.A.1.2.1	e-122	P0AGI1	Monosaccharides	Ribose
YP_002405144.1	+	+	+	+	+	3.A.1.2.1	e-152	P02925	Monosaccharides	Ribose
YP_002403130.1	+	+	+	+	+	3.A.1.2.2	0	P0AAF3	Monosaccharides	Arabinose
YP_002403131.1	+	+	+	+	+	3.A.1.2.2	0	P02924	Monosaccharides	Arabinose
YP_002403129.1	+	+	+	+	+	3.A.1.2.2	e-168	P0AE26	Monosaccharides	Arabinose
YP_002403427.1	+	+	+	+	+	3.A.1.2.3	0	P0AAG8	Monosaccharides	Galactose, glucose
YP_002403426.1	+	+	+	+	+	3.A.1.2.3	e-153	P23200	Monosaccharides	Galactose, glucose
YP_002403428.1	+	+	+	+	+	3.A.1.2.3	e-178	P0AEE5	Monosaccharides	Galactose, glucose
YP_002404950.1	+	+	+	+	+	3.A.1.2.4	0	P37388	Monosaccharides	Xylose
YP_002404951.1	+	+	+	+	+	3.A.1.2.4	e-172	P0AGI4	Monosaccharides	Xylose
YP_002404949.1	+	+	+	+	+	3.A.1.2.4	e-178	P37387	Monosaccharides	Xylose
YP_006108564.1	+	+	+	-	+	3.A.1.2.6	0	P32721	Monosaccharides	Allose
YP_006108563.1	+	+	+	-	+	3.A.1.2.6	e-157	P32720	Monosaccharides	Allose
YP_006108565.1	+	+	+	-	+	3.A.1.2.6	e-162	P39265	Monosaccharides	Allose
YP_002402718.1	-	-	-	+	+	3.A.1.2.8	0	P77257	Amines	Autoinducer-2 uptake
YP_002402720.1	-	-	-	+	+	3.A.1.2.8	e-133	P0AFS1	Amines	Autoinducer-2 uptake
YP_002402719.1	-	-	-	+	+	3.A.1.2.8	e-156	P77672	Amines	Autoinducer-2 uptake

Table S1, continued.

YP_002402721.1	-	-	-	+	+	3.A.1.2.8	e-174	P76142	Amines	Autoinducer-2 uptake
YP_002401453.1	-	-	-	+	-	3.A.1.2.9	e--87	Q7BSH4	Oligosaccharides	Rhamnose
YP_002401452.1	-	-	-	+	-	3.A.1.2.9	e-25	Q7BSH5	Oligosaccharides	Rhamnose
YP_006107651.1	+	+	+	+	+	3.A.1.2.13	e-53	A6VKS9	Amines	Autoinducer-2 uptake
YP_002405646.1	+	+	-	-	+	3.A.1.2.14	e-137	Q0HIQ7	Monosaccharides	Arabinose
YP_002405647.1	+	+	-	-	+	3.A.1.2.14	e-59	Q0HIQ6	Monosaccharides	Arabinose
YP_002405648.1	+	+	-	-	+	3.A.1.2.14	e-75	Q0HIQ5	Monosaccharides	Arabinose
YP_002403972.1	+	+	-	-	+	3.A.1.2.14	e-98	Q0HIQ8	Monosaccharides	Arabinose
AAN81518.1	+	+	+	-	-	3.A.1.2.16	e-48	Q1M4Q8	Sugar alcohols	Erythritol
YP_006121570.1	+	+	-	-	-	3.A.1.2.20	e-116	G4FGN3	Monosaccharides	Ribose
YP_002403574.1	+	+	+	+	+	3.A.1.3.1	e-105	P0A2I9	Amino acids	Histidine, lysine, arginine, ornithine
YP_002403573.1	+	+	+	+	+	3.A.1.3.1	e-106	P0A2I7	Amino acids	Histidine, lysine, arginine, ornithine
YP_002403572.1	+	+	+	+	+	3.A.1.3.1	e-131	P02915	Amino acids	Histidine, lysine, arginine, ornithine
YP_002403575.1	+	+	+	+	+	3.A.1.3.1	e-132	P02910	Amino acids	Histidine, lysine, arginine, ornithine
YP_002403576.1	+	-	-	+	+	3.A.1.3.1	e-133	P09551	Amino acids	Histidine, lysine, arginine, ornithine
YP_002401951.1	+	+	+	+	+	3.A.1.3.2	e-103	P0AEQ6	Amino acids	Glutamine
YP_002401950.1	+	+	+	+	+	3.A.1.3.2	e-124	P10346	Amino acids	Glutamine
YP_002401952.1	+	+	+	+	+	3.A.1.3.2	e-140	P0AEQ3	Amino acids	Glutamine
YP_002402002.1	+	+	+	+	+	3.A.1.3.3	e-110	P0AE30	Amino acids	Arginine
YP_002402003.1	+	+	+	+	+	3.A.1.3.3	e-125	P0AE34	Amino acids	Arginine
YP_002402005.1	+	+	+	+	+	3.A.1.3.3	e-127	P0AAF6	Amino acids	Arginine
YP_002402001.1	+	+	+	+	+	3.A.1.3.3	e-128	P30860	Amino acids	Arginine

Table S1, continued.

YP_002402004.1	+	+	+	+	+	3.A.1.3.3	e-139	P30859	Amino acids	Arginine
YP_002401760.1	+	+	+	+	+	3.A.1.3.4	e-122	P0AER5	Amino acids	Glutamate
YP_002401759.1	+	+	+	+	+	3.A.1.3.4	e-126	P0AAG3	Amino acids	Glutamate
YP_002401761.1	+	+	+	+	+	3.A.1.3.4	e-140	P0AER3	Amino acids	Glutamate
YP_002401762.1	+	+	+	+	+	3.A.1.3.4	e-156	P37902	Amino acids	Glutamate
AID80410.1	-	+	-	-	-	3.A.1.3.8	e-111	Q52815	Amino acids	Amines
AID80407.1	-	+	-	-	-	3.A.1.3.8	e-118	Q52812	Amino acids	Amines
AID80408.1	-	+	-	-	-	3.A.1.3.8	e-94	Q52813	Amino acids	Amines
AID80409.1	-	+	-	-	-	3.A.1.3.8	e-98	Q52814	Amino acids	Amines
YP_002403192.1	+	+	+	+	+	3.A.1.3.10	e-101	P0AFT2	Amino acids	Cysteine, DAP
YP_002403191.1	+	+	+	+	+	3.A.1.3.10	e-121	P37774	Amino acids	Cysteine, DAP
YP_002403194.1	+	+	+	+	+	3.A.1.3.10	e-130	P0AEM9	Amino acids	Cysteine, DAP
YP_002404806.1	+	+	+	+	+	3.A.1.4.1	0	P22729	Amino acids	Leucine, isoleucine, valine
YP_002404808.1	+	+	+	+	+	3.A.1.4.1	0	P04816	Amino acids	Leucine, isoleucine, valine
YP_002404810.1	+	+	+	+	+	3.A.1.4.1	0	P0AD96	Amino acids	Leucine, isoleucine, valine
YP_002404804.1	+	+	+	+	+	3.A.1.4.1	e-132	P22731	Amino acids	Leucine, isoleucine, valine
YP_002404807.1	+	+	+	+	+	3.A.1.4.1	e-143	P0AEX7	Amino acids	Leucine, isoleucine, valine
YP_002404805.1	+	+	+	+	+	3.A.1.4.1	e-144	P0A9S7	Amino acids	Leucine, isoleucine, valine
YP_002402424.1	+	+	+	+	+	3.A.1.5.1	0	P06202	Peptides	Oligopeptides
YP_002402428.1	+	+	+	+	+	3.A.1.5.1	0	P08007	Peptides	Oligopeptides
YP_002402571.1	+	+	+	+	+	3.A.1.5.1	0	P77348	Peptides	Oligopeptides

Table S1, continued.

YP_002402426.1	+	+	+	+	+	3.A.1.5.1	e-128	P08006	Peptides	Oligopeptides
YP_006107424.1	+	+	+	+	+	3.A.1.5.1	e-133	P06202	Peptides	Oligopeptides
YP_002402425.1	+	+	+	+	+	3.A.1.5.1	e-166	P08005	Peptides	Oligopeptides
YP_002402427.1	+	+	+	+	+	3.A.1.5.1	e-177	P04285	Peptides	Oligopeptides
YP_002402534.1	+	+	+	+	+	3.A.1.5.5	0	P36636	Peptides	Peptides
YP_002402537.1	+	+	+	+	+	3.A.1.5.5	0	P36634	Peptides	Peptides
YP_002402533.1	+	+	+	+	+	3.A.1.5.5	e-148	P36638	Peptides	Peptides
YP_002402535.1	+	+	+	+	+	3.A.1.5.5	e-152	P0A2J5	Peptides	Peptides
YP_002402536.1	+	+	+	+	+	3.A.1.5.5	e-152	P0A2J3	Peptides	Peptides
YP_002401970.1	+	+	+	+	+	3.A.1.5.11	0	P75796	Peptides	Glutathione
YP_002401971.1	+	+	+	+	+	3.A.1.5.11	0	P75797	Peptides	Glutathione
YP_002401972.1	+	+	+	+	+	3.A.1.5.11	e-150	P75798	Peptides	Glutathione
YP_002401973.1	+	+	+	+	+	3.A.1.5.11	e-157	P75799	Peptides	Glutathione
YP_002403459.1	+	+	+	+	+	3.A.1.5.21	0	P33913	Peptides	Microcin C
YP_002403460.1	+	+	+	+	+	3.A.1.5.21	0	P0AFU1	Peptides	Microcin C
YP_002403461.1	+	+	+	+	+	3.A.1.5.21	0	P33915	Peptides	Microcin C
YP_002403462.1	+	+	+	+	+	3.A.1.5.21	0	Q8ZNJ8	Peptides	Microcin C
YP_002404922.1	+	+	+	+	+	3.A.1.5.27	e-114	P45096	Peptides	Glutathione
YP_002404920.1	+	+	+	+	+	3.A.1.5.27	e-117	P45095	Peptides	Glutathione
YP_002404919.1	+	+	+	+	+	3.A.1.5.27	e-143	P45094	Peptides	Glutathione
YP_002404924.1	+	+	+	+	+	3.A.1.5.27	e-168	P33950	Peptides	Glutathione
YP_002404921.1	+	+	+	+	+	3.A.1.5.27	e-92	P51000	Peptides	Glutathione
NP_416003.1	-	-	-	+	+	3.A.1.5.38	0	P77308	Peptides	Dialanine
NP_418000.1	-	-	-	+	+	3.A.1.5.39	e-127	W0WN20	Peptides	Di-, tri-peptides

Table S1, continued.

YP_002403724.1	+	+	+	+	+	3.A.1.6.1	0	P16676	Anions	Sulfate, thiosulfate
YP_002405298.1	+	+	+	+	+	3.A.1.6.1	0	P0AG78	Anions	Sulfate, thiosulfate
YP_002403726.1	+	+	+	+	+	3.A.1.6.1	e-125	P16701	Anions	Sulfate, thiosulfate
YP_002403725.1	+	+	+	+	+	3.A.1.6.1	e-155	P0AEB0	Anions	Sulfate, thiosulfate
YP_002403727.1	+	+	+	+	+	3.A.1.6.1	e-175	P16700	Anions	Sulfate, thiosulfate
YP_002405117.1	+	+	+	+	+	3.A.1.7.1	0	P0AG82	Anions	Phosphate
YP_002405114.1	+	+	+	+	+	3.A.1.7.1	e-139	P0AAH0	Anions	Phosphate
YP_002405115.1	+	+	+	+	+	3.A.1.7.1	e-153	P07654	Anions	Phosphate
YP_002405116.1	+	+	+	+	+	3.A.1.7.1	e-153	P0AGH8	Anions	Phosphate
YP_002401850.1	+	+	+	+	+	3.A.1.8.1	0	P09833	Anions	Molybdate
YP_002401848.1	+	+	+	+	+	3.A.1.8.1	e-141	P37329	Anions	Molybdate
YP_002401849.1	+	+	+	+	+	3.A.1.8.1	e-85	P0AF01	Anions	Molybdate
YP_002405474.1	+	+	+	+	+	3.A.1.9.1	0	P16682	Anions	Phosphonate, organophosphate ester
YP_002405473.1	+	+	+	+	-	3.A.1.9.1	e-119	P16683	Anions	Phosphonate, organophosphate ester
YP_002405475.1	+	+	+	+	+	3.A.1.9.1	e-146	P16677	Anions	Phosphonate, organophosphate ester
YP_002402323.1	+	+	+	+	+	3.A.1.11.1	0	P0AFK9	Amines	Putrescine, spermidine
YP_002402326.1	+	+	+	+	+	3.A.1.11.1	0	P69874	Amines	Putrescine, spermidine
YP_002402324.1	+	+	+	+	+	3.A.1.11.1	e-135	P0AFK6	Amines	Putrescine, spermidine
YP_002402325.1	+	+	+	+	+	3.A.1.11.1	e-155	P0AFK4	Amines	Putrescine, spermidine
YP_002401995.1	+	+	+	+	+	3.A.1.11.2	0	P31133	Amines	Putrescine
YP_002401996.1	+	+	+	+	+	3.A.1.11.2	0	P31134	Amines	Putrescine
YP_002401998.1	+	+	+	+	+	3.A.1.11.2	e-133	P0AFL1	Amines	Putrescine
YP_002401997.1	+	+	+	+	+	3.A.1.11.2	e-159	P31135	Amines	Putrescine

Table S1, continued.

YP_002403941.1	+	+	+	+	+	3.A.1.12.1	0	P14175	Amines	Glycine betaine, proline
YP_002403943.1	+	+	+	+	+	3.A.1.12.1	0	P0AFM2	Amines	Glycine betaine, proline
YP_002403942.1	+	+	+	+	+	3.A.1.12.1	e-169	P14176	Amines	Glycine betaine, proline
YP_006120509.1	+	+	-	-	-	3.A.1.12.4	e-73	O34992	Amino acids	Choline, carnitine, glycine betaine, proline betaine, crotonobetaine, γ-butyrobetaine, dimethylsulfonioacetate, dimethylsulfonionproprionate, ectoine, choline-O-sulfate
YP_006120510.1	+	+	-	-	-	3.A.1.12.10	e-26	Q87WH4	Amino acids	Glycine, betaine, choline uptake
YP_006120511.1	+	+	-	-	-	3.A.1.12.10	e-32	Q87WH3	Amino acids	Glycine betaine, choline, acetylcholine, carnitine, proline betaine
YP_006120508.1	+	+	-	-	-	3.A.1.12.14	e-34	Q8ZPK1	Amino acids	Glycine betaine, choline-O-sulfate uptake
YP_002401291.1	+	+	+	+	+	3.A.1.13.1	e-123	Q8ZRP7	Vitamins	Vitamin B12
YP_002402940.1	+	+	+	+	+	3.A.1.13.1	e-136	P06609	Vitamins	Vitamin B13
YP_002402938.1	+	+	+	+	+	3.A.1.13.1	e-140	P06611	Vitamins	Vitamin B14
YP_002405808.1	-	+	-	-	+	3.A.1.14.1	e-131	P15029	Siderophores	Fe3+-citrate
YP_002405806.1	-	+	-	-	+	3.A.1.14.1	e-137	P15031	Siderophores	Fe3+-citrate
YP_002405809.1	-	+	-	-	+	3.A.1.14.1	e-145	P15030	Siderophores	Fe3+-citrate

Table S1, continued.

YP_002405810.1	-	+	-	-	+	3.A.1.14.1	e-166	P15028	Siderophores	Fe3+-citrate
YP_002401698.1	+	+	+	+	+	3.A.1.14.2	e-128	P23876	Siderophores	Fe3+-enterobactin
YP_002401697.1	+	+	+	+	+	3.A.1.14.2	e-142	P23877	Siderophores	Fe3+-enterobactin
YP_002401696.1	+	+	+	+	+	3.A.1.14.2	e-149	P23878	Siderophores	Fe3+-enterobactin
YP_002401700.1	+	+	+	+	+	3.A.1.14.2	e-163	C8U2V6	Siderophores	Fe3+-enterobactin
YP_002401286.1	+	+	+	+	+	3.A.1.14.3	0	P06972	Siderophores	Fe3+-hydroxamate, albomycin
YP_002401284.1	+	+	+	+	+	3.A.1.14.3	e-151	P07821	Siderophores	Fe3+-hydroxamate, albomycin
YP_002401285.1	+	+	+	+	+	3.A.1.14.3	e-162	P07822	Siderophores	Fe3+-hydroxamate, albomycin
YP_006107438.1	+	+	+	+	-	3.A.1.14.6	e-72	Q9RCF3	Siderophores	Fe3+-vibriobactin/enterobactin
YP_006121358.1	+	+	-	-	-	3.A.1.14.8	e-44	Q8GRB2	Siderophores	Fe3+-vibrioferrin
YP_006119586.1	+	+	-	-	-	3.A.1.14.11	e-34	Q57399	Anions	Molybdate, tungstate
YP_006105556.1	+	+	+	-	-	3.A.1.14.11	e-47	Q57130	Anions	Molybdate, tungstate
NP_311941.1	+	+	-	+	-	3.A.1.14.15	e-43	P40411	Siderophores	Fe3+-vibriobactin
YP_006107916.1	+	+	+	+	-	3.A.1.14.18	e-129	Q32AY3	Siderophores	Heme
YP_006107915.1	+	+	+	+	-	3.A.1.14.18	e-141	Q32AY2	Siderophores	Heme
YP_006107911.1	+	+	+	+	-	3.A.1.14.18	e-164	Q32AX9	Siderophores	Heme
YP_002403092.1	+	+	+	+	+	3.A.1.15.5	e-106	P39832	Cations	Zn2+
YP_002403091.1	+	+	+	+	+	3.A.1.15.5	e-143	P0A9X1	Cations	Zn2+
YP_002403090.1	+	+	+	+	+	3.A.1.15.5	e-150	P39172	Cations	Zn2+
YP_006105507.1	+	+	+	-	-	3.A.1.15.7	e-113	Q9XCS1	Cations	Mn2+, Fe2+
YP_006105506.1	+	+	+	-	-	3.A.1.15.7	e-115	Q9XCS0	Cations	Mn2+, Fe2+
YP_006105508.1	+	+	+	-	-	3.A.1.15.7	e-134	Q9XCS2	Cations	Mn2+, Fe2+

Table S1, continued.

YP_006105505.1	+	+	+	-	-	3.A.1.15.7	e-91	Q9XCR9	Cations	Mn2+, Fe2+
YP_002401496.1	+	+	+	+	+	3.A.1.17.1	e-137	Q47539	Amino acids	Taurine
YP_002401495.1	+	+	+	+	+	3.A.1.17.1	e-142	Q47538	Amino acids	Taurine
YP_002401494.1	+	+	+	+	+	3.A.1.17.1	e-171	Q47537	Amino acids	Taurine
YP_006119215.1	+	+	-	-	-	3.A.1.17.2	e-108	O85765	Anions	Aromatic sulfonates
YP_006119217.1	+	+	-	-	-	3.A.1.17.2	e-71	O85763	Anions	Aromatic sulfonates
YP_006119214.1	+	+	-	-	-	3.A.1.17.2	e-91	Q8KZQ6	Anions	Aromatic sulfonates
YP_002401204.1	+	+	+	+	+	3.A.1.19.1	0	P31549	Vitamins	Thiamin, thiamin monophosphate, thiamin pyrophosphate
YP_002401203.1	+	+	+	+	+	3.A.1.19.1	e-117	P31548	Vitamins	Thiamin, thiamin monophosphate, thiamin pyrophosphate
YP_002401205.1	+	+	+	+	+	3.A.1.19.1	e-174	P31550	Vitamins	Thiamin, thiamin monophosphate, thiamin pyrophosphate
YP_006120115.1	+	+	-	-	-	3.A.1.19.4	0	B7L6M8	Anions	Sulfate, thiosulfate
NP_416269.4	+	+	+	+	+	3.A.1.19.4	0	B7L6M9	Anions	Sulfate, thiosulfate
YP_006120117.1	+	+	-	-	-	3.A.1.19.4	e-116	B7L6N0	Anions	Sulfate, thiosulfate
YP_002403250.1	+	+	+	-	-	3.A.1.21.1	0	Q9Z375	Siderophores	Fe3+-yersiniabactin
YP_002403251.1	+	+	+	-	-	3.A.1.21.1	0	Q9R7V3	Siderophores	Fe3+-yersiniabactin
YP_002401332.1	+	+	+	+	+	3.A.1.24.1	0	P30750	Amino acids	Methionine
YP_002401330.1	+	+	+	+	+	3.A.1.24.1	e-144	P28635	Amino acids	Methionine
YP_002401331.1	+	+	+	+	+	3.A.1.24.1	e-91	P31547	Amino acids	Methionine
YP_006119038.1	+	+	-	-	-	3.A.1.26.1	e-27	A9WGB0	Vitamins	Vitamin B12
YP_002404564.1	+	+	+	+	+	3.A.1.27.3	e-119	P0ADV7	Lipids	Outer membrane lipid
YP_002404566.1	+	+	+	+	+	3.A.1.27.3	e-143	P64606	Lipids	Outer membrane lipid

Table S1, continued.

YP_002404567.1	+	+	+	+	+	3.A.1.27.3	e-145	P63386	Lipids	Outer membrane lipid
YP_002403612.1	+	+	+	+	+	3.A.1.27.3	e-149	P76506	Lipids	Outer membrane lipid
YP_002404563.1	+	+	+	+	+	3.A.1.27.3	e-44	P64602	Lipids	Outer membrane lipid
YP_002404565.1	+	+	+	+	+	3.A.1.27.3	e-91	P64604	Lipids	Outer membrane lipid
YP_002404190.1	+	+	+	+	-	3.A.1.28.1	e-105	Q8Z3V9	Nucleoside	Queosine
NP_311827.1	+	+	+	+	-	3.A.1.28.1	e-74	Q8XGV9	Nucleoside	Queosine
NP_311830.1	+	+	+	+	-	3.A.1.28.1	e-80	Q8Z3V7	Nucleoside	Queosine
NP_311828.1	+	+	-	+	-	3.A.1.28.1	e-88	Q8Z3V8	Nucleoside	Queosine
NP_755572.1	+	+	+	-	-	3.A.1.101.1	e-102	P24586	Polysaccharides	Capsular polysaccharides
YP_006107351.1	+	+	+	-	-	3.A.1.101.1	e-137	P24584	Polysaccharides	Capsular polysaccharides
YP_006119073.1	+	+	-	-	-	3.A.1.105.4	e-135	Q4VWC9	Drugs	Pyoluteorin
YP_006119074.1	+	+	-	-	-	3.A.1.105.4	e-57	Q4VWD0	Drugs	Pyoluteorin
YP_006119072.1	+	+	-	-	-	3.A.1.105.4	e-78	Q4VWC8	Drugs	Pyoluteorin
YP_006119071.1	+	+	-	-	-	3.A.1.105.4	e-78	Q4VWC7	Drugs	Pyoluteorin
YP_006118499.1	+	+	-	-	-	3.A.1.105.12	e-40	F8D412	MDR	Unknown
YP_006118498.1	+	+	-	-	-	3.A.1.105.12	e-62	F8D413	MDR	Unknown
YP_002402054.1	+	+	+	-	+	3.A.1.106.1	0	P60752	Lipids	Phospholipids
YP_002401578.1	+	+	-	+	-	3.A.1.106.5	0	A7VN01	MDR	Norfloxacin, tetracycline, DAPI
YP_006118788.1	+	+	-	-	-	3.A.1.106.5	0	A7VN02	MDR	Norfloxacin, tetracycline, DAPI
YP_006105307.1	-	+	+	-	-	3.A.1.106.7	0	Q8RMB7	Siderophores	Salmonchellin, enterobactin
YP_002403477.1	+	+	+	+	+	3.A.1.107.3	e-12	P0ABM7	Siderophores	Heme
YP_002403479.1	+	+	+	+	+	3.A.1.107.3	e-70	P0ABM0	Siderophores	Heme

Table S1, continued.

YP_002403480.1	+	+	+	+	+	3.A.1.107.3	e-99	Q8XE58	Siderophores	Heme
YP_006104453.1	-	+	+	-	-	3.A.1.109.3	e-119	Q88RG3	Proteins	Proteins
YP_006104452.1	-	-	+	-	-	3.A.1.109.4	e-09	Q9I2M2	MDR	MDR
YP_002411291.1	-	-	-	+	-	3.A.1.109.4	e-115	Q9I2M1	MDR	MDR
YP_006104454.1	-	-	+	-	-	3.A.1.109.4	e-65	Q9I2M0	MDR	MDR
YP_002411292.1	-	-	-	+	-	3.A.1.109.4	e-73	Q9I2M0	MDR	MDR
YP_006105216.1	-	+	+	-	-	3.A.1.110.1	0	Q93GK4	Proteins	Microcin
YP_006105217.1	-	+	+	-	-	3.A.1.110.1	0	Q93GK5	Proteins	Microcin
NP_752270.1	-	+	+	-	-	3.A.1.110.1	e-49	Q93GK6	Proteins	Microcin
YP_002403491.1	+	+	+	+	+	3.A.1.113.3	0	P33941	Peptides	Microcin
YP_002402091.1	-	+	+	+	+	3.A.1.120.6	0	P43672	Siderophores	Heme
YP_002405894.1	+	-	+	+	+	3.A.1.120.6	e-74	P43672	Siderophores	Heme
YP_002402019.1	+	+	+	+	+	3.A.1.122.1	0	P75830	MDR	Macrolides
YP_002402020.1	+	-	+	+	+	3.A.1.122.1	0	P75831	MDR	Macrolides
YP_002402316.1	+	+	+	+	+	3.A.1.125.1	0	P0ADC3	Proteins	Lipoproteins
YP_002402318.1	+	+	+	+	+	3.A.1.125.1	0	P75958	Proteins	Lipoproteins
YP_002402317.1	+	+	+	+	+	3.A.1.125.1	e-129	P75957	Proteins	Lipoproteins
YP_002402026.1	+	+	+	+	+	3.A.1.129.1	0	P23886	Peptides	Cysteine, glutathione
YP_002402027.1	+	+	+	+	+	3.A.1.129.1	0	P29018	Peptides	Cysteine, glutathione
YP_006118833.1	+	+	-	-	-	3.A.1.139.2	e-130	P77279	Cations	Iron efflux
YP_002401620.1	+	-	-	+	+	3.A.1.139.2	e-131	P77307	Cations	Iron efflux
YP_006121777.1	+	+	-	-	-	3.A.1.140.1	e-128	P0A9R7	Proteins	Proteins
YP_002404812.1	+	+	+	+	+	3.A.1.140.1	e-180	P0AC31	Proteins	Proteins
YP_002402910.1	-	-	+	-	-	3.A.1.201.10	e-17	B0Y3B6	MDR	MDR

Table S1, continued.

YP_002402700.1	-	-	+	-	-	3.A.1.203.4	e-55	Q50614	MDR	MDR
NP_416013.1	-	+	+	+	+	3.A.1.203.11	0	P31826	Lipids	Fatty acids
YP_006122059.1	+	-	-	-	-	3.A.2.1.1	0	P0ABB4	Cations	H+
YP_002405125.1	+	+	+	+	+	3.A.2.1.1	0	P0ABB4	Cations	H+
YP_002405127.1	+	+	+	+	+	3.A.2.1.1	0	P0ABB0	Cations	H+
YP_002405131.1	+	+	+	+	+	3.A.2.1.1	e-143	P0AB98	Cations	H+
YP_002405126.1	+	+	+	+	+	3.A.2.1.1	e-152	P0ABA6	Cations	H+
YP_002405130.1	+	+	+	+	+	3.A.2.1.1	e-21	P68699	Cations	H+
YP_002405124.1	+	+	+	+	+	3.A.2.1.1	e-65	P0A6E6	Cations	H+
YP_002405129.1	+	+	+	+	+	3.A.2.1.1	e-66	P0ABA0	Cations	H+
YP_002405128.1	+	+	+	+	+	3.A.2.1.1	e-93	P0ABA4	Cations	H+
YP_002401613.1	+	+	+	+	+	3.A.3.5.5	0	Q59385	Cations	Cu+, Ag+ efflux
YP_002404819.1	+	+	+	+	+	3.A.3.6.2	0	P37617	Cations	Zn2+, Cd2+, Co2+, Hg2+, Ni2+, Cu2+, Pb2+ efflux
YP_002401790.1	+	+	+	+	+	3.A.3.7.1	0	P03960	Cations	K+ uptake
YP_002401791.1	+	+	+	+	+	3.A.3.7.1	0	P03959	Cations	K+ uptake
YP_002401789.1	+	+	+	+	+	3.A.3.7.1	e-98	P03961	Cations	K+ uptake
YP_002401234.1	+	+	+	+	+	3.A.5.1.1	0	P10408	Proteins	Preproteins
YP_002403901.1	+	+	+	+	+	3.A.5.1.1	0	P0AGD7	Proteins	Preproteins
YP_002404659.1	+	+	+	+	+	3.A.5.1.1	0	P0AGA2	Proteins	Preproteins
YP_002404814.1	+	+	+	+	+	3.A.5.1.1	0	P10121	Proteins	Preproteins
YP_002405355.1	+	+	+	+	+	3.A.5.1.1	e-48	P0AG96	Proteins	Preproteins
YP_002404547.1	+	+	+	+	+	3.A.5.1.1	e-57	P0AG99	Proteins	Preproteins
YP_002401585.1	+	+	+	+	+	3.A.5.1.1	e-65	P0AAQ6	Proteins	Preproteins

Table S1, continued.

YP_002331410.1	-	-	-	+	-	3.A.6.1.1	e-108	P40290	Proteins	Proteins
YP_002413886.1	-	-	-	+	-	3.A.6.1.1	e-126	P0C2V3	Proteins	Proteins
YP_002331411.1	-	-	-	+	-	3.A.6.1.1	e-133	P0C2V3	Proteins	Proteins
YP_001464196.1	-	-	-	+	-	3.A.6.1.1	e-14	Q7BFA7	Proteins	Proteins
YP_002405167.1	-	-	+	+	+	3.A.6.1.1	e-15	P40290	Proteins	Proteins
YP_002404120.1	-	-	-	+	-	3.A.6.1.1	e-22	Q7BFA4	Proteins	Proteins
YP_002331423.1	-	-	-	+	-	3.A.6.1.1	e-24	Q93KT5	Proteins	Proteins
YP_001464194.1	-	-	-	+	-	3.A.6.1.1	e-26	Q93KT4	Proteins	Proteins
YP_002331415.1	-	-	-	+	-	3.A.6.1.1	e-29	Q7BFA4	Proteins	Proteins
YP_002404126.1	-	-	-	+	-	3.A.6.1.1	e-32	Q9ZA77	Proteins	Proteins
YP_002331425.1	-	-	-	+	-	3.A.6.1.1	e-47	Q9ZA77	Proteins	Proteins
YP_002331422.1	-	-	-	+	-	3.A.6.1.1	e-57	Q93KT4	Proteins	Proteins
YP_002413885.1	-	-	-	+	-	3.A.6.1.1	e-99	P40290	Proteins	Proteins
YP_006119669.1	+	-	-	-	-	3.A.7.7.1	e-27	Q07711	Nucleic acids	DNA
YP_002402513.1	+	+	+	+	+	3.A.7.7.1	e-27	Q07711	Nucleic acids	DNA
YP_002402987.1	+	+	+	+	+	3.A.7.7.1	e-66	Q07711	Nucleic acids	DNA
YP_006121115.1	+	+	-	-	-	3.A.7.9.1	e-11	Q5ZYB4	Nucleic acids	DNA
YP_006122512.1	+	-	-	-	-	3.A.7.11.1	0	Q5EPC8	Nucleic acids	DNA
YP_852012.1	+	-	-	+	-	3.A.7.11.1	e-14	O30554	Nucleic acids	DNA
YP_002270067.1	-	-	-	+	-	3.A.7.11.1	e-19	O30554	Nucleic acids	DNA
YP_002404155.1	+	-	+	+	+	3.A.7.11.1	e-19	Q5K698	Nucleic acids	DNA
NP_754289.1	-	+	+	-	-	3.A.7.14.1	e-25	Q52001	Nucleic acids	DNA
YP_002402937.1	+	+	+	+	+	3.A.7.14.2	e-09	Q15HU6	Nucleic acids	DNA
AID78770.1	-	+	-	-	-	3.A.7.14.2	e-12	Q15HU4	Nucleic acids	DNA

Table S1, continued.

YP_002402282.1	+	+	+	+	+	3.A.7.14.2	e-20	Q15HU6	Nucleic acids	DNA
YP_002404645.1	-	-	+	+	+	3.A.11.1.3	e-33	Q8VRK4	Nucleic acids	DNA
YP_002402053.1	+	-	+	+	+	3.A.11.2.2	e-81	P44408	Nucleic acids	DNA
AID77931.1	-	+	-	-	-	3.A.11.2.2	e-98	P44408	Nucleic acids	DNA
AID77537.1	-	+	-	-	-	3.A.11.2.3	e-14	A1EMW4	Nucleic acids	DNA
YP_002405316.1	+	+	+	+	+	3.A.11.3.1	e-68	Q9ZKE4	Nucleic acids	DNA
YP_002402030.1	+	+	+	+	+	3.A.12.1.2	0	P46889	Nucleic acids	DNA
AID77912.1	-	+	-	-	-	3.A.12.1.2	0	P46889	Nucleic acids	DNA
YP_006107724.1	+	+	+	-	+	3.A.15.1.1	e-08	P15749	Proteins	Pullulanase
YP_006107726.1	+	+	+	-	+	3.A.15.1.1	e-09	P15751	Proteins	Pullulanase
NP_755965.1	+	+	+	-	+	3.A.15.1.1	e-09	P15748	Proteins	Pullulanase
YP_854398.1	+	+	-	-	+	3.A.15.1.1	e-12	P15752	Proteins	Pullulanase
YP_006107719.1	+	+	+	-	+	3.A.15.1.1	e-148	P15645	Proteins	Pullulanase
YP_006121638.1	+	+	-	-	-	3.A.15.1.1	e-154	P15645	Proteins	Pullulanase
YP_006121283.1	+	+	-	-	-	3.A.15.1.1	e-164	P15645	Proteins	Pullulanase
YP_002404333.1	+	+	+	-	-	3.A.15.1.1	e-38	P15750	Proteins	Pullulanase
YP_006107721.1	+	+	+	-	+	3.A.15.1.1	e-54	P15746	Proteins	Pullulanase
YP_006107720.1	+	+	+	-	+	3.A.15.1.1	e-71	P15745	Proteins	Pullulanase
YP_002272778.1	+	+	-	+	-	3.A.15.2.1	e-24	P22610	Proteins	Fimbrial subunit
YP_002401239.1	+	-	+	+	+	3.A.15.2.1	e-30	P22609	Proteins	Fimbrial subunit
YP_002404215.1	-	+	+	+	+	3.A.15.2.1	e-74	P24559	Proteins	Fimbrial subunit
YP_002401240.1	-	-	+	+	+	3.A.15.2.1	e-90	P22608	Proteins	Fimbrial subunit
YP_859985.1	-	-	-	-	+	3.A.17.1.1	0	P08956	Nucleic acids	DNA
YP_002403466.1	-	-	+	+	+	3.A.17.1.1	e-11	P08956	Nucleic acids	DNA

Table S1, continued.

YP_002405855.1	-	-	+	+	-	3.A.17.1.1	e-40	P08956	Nucleic acids	DNA
YP_002401352.1	+	-	-	+	-	3.A.23.1.1	0	Q9KN49	Proteins	Proteins
YP_006107110.1	-	-	+	-	-	3.A.23.1.1	e-08	Q9KN44	Proteins	Proteins
YP_002401348.1	-	-	-	+	-	3.A.23.1.1	e-09	Q9KN44	Proteins	Proteins
YP_006107095.1	+	-	+	-	-	3.A.23.1.1	e-10	Q9KN50	Proteins	Proteins
YP_002401365.1	-	-	-	+	-	3.A.23.1.1	e-104	B2D7K2	Proteins	Proteins
YP_002401354.1	+	+	-	+	-	3.A.23.1.1	e-106	Q9KN51	Proteins	Proteins
YP_002402664.1	-	+	-	+	-	3.A.23.1.1	e-107	B2D7K2	Proteins	Proteins
YP_002401676.1	+	+	-	+	-	3.A.23.1.1	e-110	B2D7K2	Proteins	Proteins
YP_006105771.1	+	+	+	-	-	3.A.23.1.1	e-123	B2D7K2	Proteins	Proteins
YP_006105776.1	+	-	+	-	-	3.A.23.1.1	e-125	B2D7K2	Proteins	Proteins
YP_006107104.1	+	-	+	-	-	3.A.23.1.1	e-13	Q9KN45	Proteins	Proteins
YP_002401358.1	+	+	-	+	-	3.A.23.1.1	e-135	Q9KN55	Proteins	Proteins
YP_001461389.1	-	-	-	+	-	3.A.23.1.1	e-14	Q9KN47	Proteins	Proteins
YP_002401355.1	-	-	-	+	-	3.A.23.1.1	e-19	Q9KN52	Proteins	Proteins
YP_002402382.1	-	-	+	-	+	3.A.23.1.1	e-23	Q9KN48	Proteins	Proteins
YP_006107094.1	-	-	+	-	-	3.A.23.1.1	e-32	Q9KN51	Proteins	Proteins
YP_002404771.1	-	-	+	+	+	3.A.23.1.1	e-33	Q9KN48	Proteins	Proteins
YP_002402565.1	-	-	+	+	+	3.A.23.1.1	e-41	Q9KN48	Proteins	Proteins
YP_002402546.1	-	-	+	+	+	3.A.23.1.1	e-44	Q9KN48	Proteins	Proteins
YP_002401353.1	-	-	-	+	-	3.A.23.1.1	e-45	Q9KN50	Proteins	Proteins
YP_002401356.1	-	-	-	+	-	3.A.23.1.1	e-45	Q9KN53	Proteins	Proteins
YP_006108519.1	+	-	+	-	-	3.A.23.1.1	e-47	Q9KN48	Proteins	Proteins
YP_002405248.1	-	-	+	+	+	3.A.23.1.1	e-48	Q9KN48	Proteins	Proteins

Table S1, continued.

YP_002403967.1	-	-	+	+	+	3.A.23.1.1	e-49	Q9KN48	Proteins	Proteins
YP_002401461.1	-	-	+	+	+	3.A.23.1.1	e-50	Q9KN48	Proteins	Proteins
YP_002403992.1	-	-	+	+	+	3.A.23.1.1	e-51	Q9KN48	Proteins	Proteins
YP_002403785.1	-	-	-	+	+	3.A.23.1.1	e-52	Q9KN48	Proteins	Proteins
YP_002405379.1	-	-	+	+	+	3.A.23.1.1	e-56	Q9KN48	Proteins	Proteins
YP_002268822.1	+	-	-	+	-	3.A.23.1.1	e-57	Q9KN46	Proteins	Proteins
YP_006106593.1	-	-	+	-	+	3.A.23.1.1	e-58	Q9KN48	Proteins	Proteins
YP_002403848.1	-	-	+	+	+	3.A.23.1.1	e-59	Q9KN48	Proteins	Proteins
YP_002404132.1	-	-	+	+	+	3.A.23.1.1	e-61	Q9KN48	Proteins	Proteins
YP_002401357.1	+	+	-	+	-	3.A.23.1.1	e-64	Q9KN54	Proteins	Proteins
YP_002402023.1	-	-	+	+	+	3.A.23.1.1	e-69	Q9KN49	Proteins	Proteins
YP_006107106.1	-	-	+	-	-	3.A.23.1.1	e-76	Q9KN55	Proteins	Proteins
YP_006107098.1	+	+	+	-	-	3.A.23.2.1	0	Q6EE14	Proteins	Proteins
YP_006121106.1	+	+	-	-	-	3.A.23.2.1	e-10	A8YQS0	Proteins	Proteins
YP_006107093.1	+	+	+	-	-	3.A.23.2.1	e-107	Q6EE20	Proteins	Proteins
YP_006118594.1	+	-	-	-	-	3.A.23.2.1	e-108	Q6EE20	Proteins	Proteins
YP_002403884.1	-	-	+	+	+	3.A.23.2.1	e-144	Q6EE14	Proteins	Proteins
YP_002401362.1	-	-	-	+	-	3.A.23.2.1	e-15	Q6EE21	Proteins	Proteins
YP_006107092.1	-	-	+	-	-	3.A.23.2.1	e-20	Q6EE21	Proteins	Proteins
YP_006107099.1	-	-	+	-	-	3.A.23.2.1	e-35	A8YQR5	Proteins	Proteins
YP_002404621.1	-	-	+	+	+	3.B.1.1.5	e-09	Q9V0A6	Cations	Na+
YP_002403582.1	-	-	+	+	+	3.B.1.1.5	e-11	Q9V0A4	Cations	Na+
YP_002403542.1	+	+	+	+	+	3.D.1.1.1	0	P0AFF0	Cations	H+
YP_002403543.1	+	+	+	+	+	3.D.1.1.1	0	P0AFE8	Cations	H+

Table S1, continued.

YP_002403544.1	+	+	+	+	+	3.D.1.1.1	0	P33607	Cations	H+
YP_002403549.1	+	+	+	+	+	3.D.1.1.1	0	P33602	Cations	H+
YP_002403550.1	+	+	+	+	+	3.D.1.1.1	0	P31979	Cations	H+
YP_002403552.1	+	+	+	+	+	3.D.1.1.1	0	P33599	Cations	H+
YP_002403547.1	+	+	+	+	+	3.D.1.1.1	e-107	P0AFD6	Cations	H+
YP_002403553.1	+	+	+	+	+	3.D.1.1.1	e-129	P0AFC7	Cations	H+
YP_002403548.1	+	+	+	+	+	3.D.1.1.1	e-179	P0AFD4	Cations	H+
YP_002401788.1	+	+	+	+	+	3.D.1.1.1	e-31	P0AFE4	Cations	H+
YP_002403554.1	+	+	+	+	+	3.D.1.1.1	e-81	P0AFC3	Cations	H+
YP_002403546.1	+	+	+	+	+	3.D.1.1.1	e-84	P0AFE0	Cations	H+
YP_002403551.1	+	+	+	+	+	3.D.1.1.1	e-97	P0AFD1	Cations	H+
YP_002403781.1	-	-	-	+	+	3.D.1.9.1	0	P77329	Cations	H+
YP_002413502.1	-	-	-	+	+	3.D.1.9.1	0	P77416	Cations	H+
YP_002403778.1	-	-	-	+	+	3.D.1.9.1	0	P23482	Cations	H+
YP_002403780.1	-	-	-	+	+	3.D.1.9.1	0	P77437	Cations	H+
YP_001463808.1	-	-	-	-	+	3.D.1.9.1	e-104	P0AEW1	Cations	H+
YP_002403777.1	-	-	-	+	+	3.D.1.9.1	e-118	P23481	Cations	H+
YP_001463807.1	-	-	-	+	+	3.D.1.9.1	e-124	P77858	Cations	H+
YP_002403783.1	-	-	-	+	+	3.D.1.9.1	e-140	P77668	Cations	H+
YP_002403782.1	-	-	-	+	+	3.D.1.9.1	e-91	P77423	Cations	H+
YP_002403982.1	+	+	+	+	+	3.D.1.9.2	0	P16431	Cations	H+
YP_002403984.1	+	+	+	+	+	3.D.1.9.2	0	P16429	Cations	H+
YP_002403981.1	+	+	+	+	+	3.D.1.9.2	e-105	P16432	Cations	H+
YP_002403985.1	+	+	+	+	+	3.D.1.9.2	e-107	P0AAK3	Cations	H+

Table S1, continued.

YP_002403980.1	+	+	+	+	+	3.D.1.9.2	e-148	P16433	Cations	H+
YP_002403983.1	+	+	+	+	+	3.D.1.9.2	e-148	P16430	Cations	H+
YP_002402831.1	+	+	+	+	+	3.D.2.1.1	0	P0AB67	Cations	H+
YP_002402832.1	+	+	+	+	+	3.D.2.1.1	0	P07001	Cations	H+
YP_002401824.1	+	+	+	+	+	3.D.4.3.2	0	P0ABJ9	Electrons	Electrons
YP_002401825.1	+	+	+	+	+	3.D.4.3.2	0	P0ABK2	Electrons	Electrons
YP_002402178.1	-	+	+	+	+	3.D.4.3.2	0	P0ABJ9	Electrons	Electrons
YP_002402179.1	-	+	+	+	+	3.D.4.3.2	e-118	P0ABK2	Electrons	Electrons
YP_002401561.1	+	+	+	+	+	3.D.4.5.1	0	P0ABI8	Electrons	Electrons
YP_002401562.1	+	+	+	+	+	3.D.4.5.1	0	P0ABJ1	Electrons	Electrons
YP_002401560.1	+	+	+	+	+	3.D.4.5.1	e-103	P0ABJ3	Electrons	Electrons
YP_002401559.1	+	+	+	+	+	3.D.4.5.1	e-60	P0ABJ6	Electrons	Electrons
YP_002402861.1	+	+	+	+	+	3.D.6.1.1	e-36	P97054	Electrons	Electrons
YP_002402862.1	+	+	+	+	+	3.D.6.1.1	e-37	P97055	Electrons	Electrons
YP_002402858.1	+	+	+	+	+	3.D.6.1.1	e-41	Q07394	Electrons	Electrons
YP_002402860.1	+	-	+	+	+	3.D.6.1.1	e-42	Q52715	Electrons	Electrons
YP_002402857.1	+	+	+	+	+	3.D.6.1.1	e-53	Q07396	Electrons	Electrons
YP_002402859.1	+	+	-	+	+	3.D.6.1.1	e-82	Q52716	Electrons	Electrons
AID78673.1	-	+	-	-	-	3.D.6.1.2	e-43	C4N8U1	Electrons	NADH:ferredoxin
YP_002404349.1	-	-	-	-	+	3.D.7.1.1	e-14	P96797	Cations	H+
YP_002403516.1	-	-	+	+	+	3.D.7.1.1	e-14	P96797	Cations	H+
YP_002402173.1	+	+	+	+	+	3.D.7.2.1	e-161	O67092	Electrons	Electrons
YP_002402172.1	+	+	+	+	+	3.D.7.2.1	e-92	O67095	Electrons	Electrons
NP_415493.1	-	-	+	+	+	3.D.7.2.3	e-66	T2K6Q3	Cations	H+

Table S1, continued.

YP_002401814.1	-	-	+	+	+	3.D.10.1.1	0	Q65GF4	Electrons	Electrons
YP_002405572.1	-	-	+	+	+	3.D.10.1.1	e-24	Q65GF5	Electrons	Electrons
YP_002402301.1	+	+	+	+	+	4.A.1.1.1	0	P69786	Monosaccharides	Glucose
YP_002403720.1	+	+	+	+	+	4.A.1.1.1	e-82	P69783	Monosaccharides	Glucose
YP_002401774.1	+	+	+	+	+	4.A.1.1.2	0	P09323	Sugar derivatives	NAG
YP_002402850.1	+	+	+	+	+	4.A.1.1.3	0	P19642	Oligosaccharides	Maltose
YP_006108267.1	-	-	+	-	-	4.A.1.1.9	e-116	P20166	Monosaccharides	Glucose
YP_002405072.1	-	-	-	+	-	4.A.1.1.10	0	Q9AGA7	Oligosaccharides	α-glucoside
YP_002405112.1	+	+	+	-	+	4.A.1.2.2	0	P08722	Oligosaccharides	β-glucoside
YP_002403973.1	+	-	-	+	+	4.A.1.2.3	0	P24241	Oligosaccharides	β-glucoside
YP_002405657.1	+	+	+	+	+	4.A.1.2.4	0	P36672	Oligosaccharides	Trehalose
YP_002403731.1	+	+	+	+	+	4.A.1.2.7	0	P77272	Sugar derivatives	NAM
YP_002403448.1	+	+	+	+	+	4.A.2.1.1	0	P20966	Monosaccharides	Fructose
YP_002403450.1	+	+	+	+	+	4.A.2.1.1	e-180	P69811	Monosaccharides	Fructose
YP_002404987.1	+	+	+	+	+	4.A.2.1.2	0	P00550	Sugar alcohols	Mannitol
YP_002401821.1	-	-	-	-	+	4.A.2.1.3	0	P54745	Carboxylates	2-O-α-mannosyl D-glycerate
YP_002404197.1	+	+	+	+	+	4.A.2.1.5	e-118	P42956	Sugar alcohols	Mannitol
YP_002405281.1	-	-	-	+	+	4.A.2.1.6	e-66	O31645	Monosaccharides	Mannose
YP_006108084.1	+	+	+	-	-	4.A.2.1.9	0	Q1R4T1	Monosaccharides	Fructose
YP_006108085.1	+	+	+	-	-	4.A.2.1.9	e-53	Q8FC73	Monosaccharides	Fructose
YP_006108086.1	+	+	+	-	-	4.A.2.1.9	e-84	Q1R4S9	Monosaccharides	Fructose
YP_002405329.1	+	+	+	+	+	4.A.2.1.10	0	P32670	Sugar derivatives	Phosphoenolpyruvate
YP_002405330.1	+	+	+	+	+	4.A.2.1.10	e-173	P32672	Sugar derivatives	Phosphoenolpyruvate
YP_002405331.1	+	+	+	+	+	4.A.2.1.10	e-46	P69816	Sugar derivatives	Phosphoenolpyruvate

Table S1, continued.

YP_002405334.1	+	+	+	+	+	4.A.2.1.10	e-59	P32676	Sugar derivatives	Phosphoenolpyruvate
YP_002403693.1	+	+	+	+	+	4.A.2.1.11	0	P77439	Monosaccharides	Fructose
YP_002403696.1	+	+	+	+	+	4.A.2.1.11	0	P77579	Monosaccharides	Fructose
YP_002403697.1	+	+	+	+	+	4.A.2.1.11	e-48	P69808	Monosaccharides	Fructose
YP_002404576.1	-	-	+	+	+	4.A.2.1.14	e-15	D2RXA7	Monosaccharides	Fructose
YP_002273416.1	-	-	-	+	+	4.A.2.1.14	e-16	D2RXA7	Monosaccharides	Fructose
NP_311713.1	-	-	-	+	-	4.A.2.1.17	e-85	Q9HY55	Monosaccharides	Fructose
YP_002402962.1	+	+	+	+	+	4.A.3.2.1	0	P17334	Sugar derivatives	N,N'-diacetylchitobiose
YP_002402739.1	+	+	+	-	-	4.A.3.2.1	e-21	P69791	Sugar derivatives	N,N'-diacetylchitobiose
YP_002402963.1	+	+	+	+	+	4.A.3.2.1	e-48	P69795	Sugar derivatives	N,N'-diacetylchitobiose
YP_002403961.1	+	+	+	-	+	4.A.4.1.1	e-169	P56580	Sugar alcohols	Glucitol
YP_002403962.1	+	+	+	+	+	4.A.4.1.1	e-67	P05706	Sugar alcohols	Glucitol
YP_002403960.1	+	+	+	-	+	4.A.4.1.1	e-92	P56579	Sugar alcohols	Glucitol
YP_002403378.1	+	+	+	+	+	4.A.5.1.1	0	P69831	Sugar alcohols	Galactitol
YP_002403379.1	+	+	+	+	+	4.A.5.1.1	e-50	P37188	Sugar alcohols	Galactitol
YP_002403380.1	+	+	+	+	+	4.A.5.1.1	e-82	P69828	Sugar alcohols	Galactitol
YP_002415483.1	-	+	-	-	+	4.A.5.1.3	0	P39365	Sugar alcohols	Galactitol
YP_002415484.1	-	+	-	-	+	4.A.5.1.3	e-48	P58035	Sugar alcohols	Galactitol
YP_002415481.1	-	+	-	-	+	4.A.5.1.3	e-81	P39363	Sugar alcohols	Galactitol
YP_006107885.1	+	+	+	+	-	4.A.5.1.4	0	Q8FCM4	Sugar alcohols	Galactitol
YP_006107884.1	+	+	+	+	-	4.A.5.1.4	e-47	Q8FCM5	Sugar alcohols	Galactitol
YP_002272943.1	+	+	-	+	-	4.A.5.1.4	e-85	Q8FCM6	Sugar alcohols	Galactitol
YP_006107883.1	-	-	+	-	-	4.A.5.1.4	e-88	Q8FCM6	Sugar alcohols	Galactitol

Table S1, continued.

YP_002403047.1	+	+	+	+	+	4.A.6.1.1	e-135	P69801	Monosaccharides	Mannose
YP_002403048.1	+	+	+	+	+	4.A.6.1.1	e-149	P69805	Monosaccharides	Mannose
YP_002403046.1	+	+	+	+	+	4.A.6.1.1	e-162	P69797	Monosaccharides	Mannose
YP_006108469.1	+	+	+	+	-	4.A.6.1.3	e-115	P37082	Monosaccharides	Sorbose
YP_006108468.1	+	+	+	+	-	4.A.6.1.3	e-127	P37083	Monosaccharides	Sorbose
YP_002273538.1	+	+	+	+	-	4.A.6.1.3	e-52	P37080	Monosaccharides	Sorbose
YP_006108470.1	+	+	+	-	-	4.A.6.1.3	e-77	P37081	Monosaccharides	Sorbose
YP_002404507.1	+	+	+	+	-	4.A.6.1.4	e-158	Q9KIQ2	Sugar derivatives	N-acetyl galactosamine
YP_002404505.1	+	+	+	+	+	4.A.6.1.4	e-86	Q9KIQ4	Sugar derivatives	N-acetyl galactosamine
YP_002404506.1	+	+	+	+	-	4.A.6.1.4	e-94	Q9KIQ3	Sugar derivatives	N-acetyl galactosamine
YP_002404514.1	+	+	+	+	+	4.A.6.1.5	e-140	P42911	Sugar derivatives	Galactosamine
YP_002404513.1	+	+	+	-	+	4.A.6.1.5	e-150	Q9KIP7	Sugar derivatives	Galactosamine
YP_002404512.1	+	+	+	+	+	4.A.6.1.5	e-76	P42909	Sugar derivatives	Galactosamine
YP_002404508.1	-	-	+	+	-	4.A.6.1.6	e-16	Q2QKM4	Monosaccharides	Glucose
YP_002405610.1	+	+	+	+	+	4.A.7.1.1	0	P39301	Carboxylates	Ascorbate
YP_002405611.1	+	+	+	+	+	4.A.7.1.1	e-54	P69822	Carboxylates	Ascorbate
YP_002405612.1	+	+	+	+	+	4.A.7.1.1	e-82	P69820	Carboxylates	Ascorbate
AID77350.1	-	+	-	-	-	4.A.7.1.2	0	B7LDR9	Carboxylates	Ascorbate
NP_311836.1	-	+	+	+	-	4.A.7.1.2	e-26	B7LDS1	Sugar alcohols	Mannitol
AID77351.1	-	+	-	-	-	4.A.7.1.2	e-47	B7LDS2	Carboxylates	Ascorbate
YP_002405893.1	+	+	+	+	+	4.B.1.1.1	0	P24518	Nucleosides	Nicotinamide riboside
YP_002401835.1	+	+	+	+	+	4.B.1.1.1	e-123	P24520	Nucleosides	Nicotinamide riboside
YP_006108509.1	-	-	+	-	-	4.B.1.1.4	e-18	Q8EDN0	Nucleosides	Nicotinamide riboside

Table S1, continued.

YP_002403034.1	+	+	+	+	+	4.C.1.1.4	0	P69451	Lipids	Long chain fatty acyl CoA
YP_002401176.1	+	+	+	+	+	4.C.1.1.6	0	P31552	Vitamins	Carnitine/crotonobetaine CoA
YP_002402225.1	+	+	+	+	+	4.D.1.1.3	0	P75905	Polysaccharides	Glucosyl residues
NP_415309.1	+	+	+	+	+	4.D.2.4.3	0	P75770	None	Unknown
NP_415567.1	+	+	+	+	+	4.D.3.1.1	0	P62517	Polysaccharides	Glycosyl residues
NP_417990.4	-	-	+	-	+	4.D.3.1.2	e-21	I7KBV6	Polysaccharides	Glycosyl residues
YP_002405553.1	+	+	+	+	+	5.A.1.1.1	0	P36655	Proteins	Proteins
YP_002402366.1	+	+	+	+	+	5.A.2.1.1	e-75	P0A6M2	Proteins	Proteins
YP_002402407.1	+	+	+	+	+	5.A.3.1.1	0	P09152	Electrons	Electrons
YP_002402408.1	+	+	+	+	+	5.A.3.1.1	0	P11349	Electrons	Electrons
YP_002402410.1	-	+	+	+	+	5.A.3.1.1	e-122	P11350	Electrons	Electrons
YP_002402673.1	+	+	+	+	+	5.A.3.1.2	0	P19318	Electrons	Electrons
YP_002402674.1	+	+	+	+	+	5.A.3.1.2	0	P19319	Electrons	Electrons
YP_002402671.1	+	+	+	+	+	5.A.3.1.2	e-120	P0AF32	Electrons	Electrons
YP_002402679.1	+	+	+	+	+	5.A.3.2.1	0	P24183	Electrons	Electrons
YP_002402681.1	+	+	+	+	+	5.A.3.2.1	e-107	P0AEK7	Electrons	Electrons
YP_002402680.1	+	+	+	+	+	5.A.3.2.1	e-172	P0AAJ3	Electrons	Electrons
YP_002402816.1	+	+	+	+	+	5.A.3.3.1	0	P77374	Electrons	Electrons
YP_002402817.1	+	+	+	+	+	5.A.3.3.1	0	P77783	Electrons	Electrons
YP_002402818.1	+	+	+	+	+	5.A.3.3.1	e-128	P0AAJ1	Electrons	Electrons
YP_002402819.1	+	+	+	+	+	5.A.3.3.1	e-145	P76173	Electrons	Electrons
YP_002402034.1	+	+	+	+	+	5.A.3.3.2	0	P18775	Electrons	Electrons
YP_002402035.1	+	+	+	+	+	5.A.3.3.2	e-128	P18776	Electrons	Electrons

Table S1, continued.

YP_002402036.1	+	+	+	+	+	5.A.3.3.2	e-146	P18777	Electrons	Electrons
YP_002402198.1	+	+	+	+	+	5.A.3.4.1	0	P33226	Electrons	Electrons
YP_002402199.1	+	+	+	+	+	5.A.3.4.1	0	P33225	Electrons	Electrons
YP_002402200.1	+	+	+	+	+	5.A.3.4.1	e-109	P36662	Electrons	Electrons
YP_002403105.1	+	+	+	+	+	5.A.3.4.2	0	P58362	Electrons	Electrons
YP_002403106.1	+	+	+	+	+	5.A.3.4.2	0	P52005	Electrons	Electrons
YP_002404935.1	+	+	+	+	+	5.A.3.4.3	0	P20099	Electrons	Electrons
YP_002402902.1	+	+	+	+	+	5.A.3.5.1	e-17	P0A1I1	Electrons	Electrons
YP_002402898.1	+	+	+	+	+	5.A.3.5.1	e-52	P37602	Electrons	Electrons
YP_002402899.1	-	-	+	+	+	5.A.3.5.1	e-56	P0A1I1	Electrons	Electrons
YP_859689.1	+	+	-	-	+	5.A.3.5.2	e-11	P31075	Electrons	Electrons
YP_002405449.1	+	+	+	+	+	5.A.3.5.2	e-39	P31077	Electrons	Electrons
YP_002405448.1	-	-	+	+	+	5.A.3.5.2	e-58	P31076	Electrons	Electrons
NP_418286.1	-	-	-	-	+	5.B.1.8.1	e-29	Q66DP5	Electrons	Electrons
NP_415910.1	-	-	-	-	+	5.B.1.8.2	e-10	Q7WTJ2	Electrons	Electrons
YP_002404894.1	-	-	+	+	+	5.B.3.1.1	e-59	Q74FY6	Electrons	Electrons
YP_002405447.1	-	-	+	+	+	5.B.5.1.1	e-14	Q8EG35	Electrons	Electrons
YP_002403948.1	+	+	+	+	+	8.A.1.1.1	0	P27303	None	Nontransport auxilliary
YP_002405458.1	+	+	+	+	+	8.A.1.1.3	e-149	B1LPP9	None	Nontransport auxilliary
YP_002404985.1	-	-	+	+	+	8.A.1.1.3	e-19	B1LPP9	None	Nontransport auxilliary
YP_002404970.1	-	-	-	+	+	8.A.1.1.3	e-22	B1LPP9	None	Nontransport auxilliary

Table S1, continued.

NP_418043.1	+	+	+	+	+	8.A.1.1.4	0	P37683	None	Nontransport auxilliary
YP_006108793.1	-	-	+	-	-	8.A.1.3.1	0	P06739	None	Nontransport auxilliary
YP_002401592.1	+	+	+	+	+	8.A.1.6.1	0	P0AE06	None	Nontransport auxilliary
YP_002404631.1	+	+	+	+	+	8.A.1.6.1	e-128	P0AE06	None	Nontransport auxilliary
YP_002403363.1	+	+	+	+	+	8.A.1.6.2	0	P76397	None	Nontransport auxilliary
YP_002404889.1	+	+	+	+	+	8.A.1.6.3	0	P37636	None	Nontransport auxilliary
YP_002404607.1	+	+	+	+	+	8.A.1.7.1	e-167	P46482	None	Nontransport auxilliary
YP_002402874.1	-	-	+	+	+	8.A.1.7.1	e-53	P46482	None	Nontransport auxilliary
YP_002401255.1	+	+	+	+	+	8.A.2.1.3	e-62	P0AA95	None	Nontransport auxilliary
YP_002402181.1	+	-	-	+	+	8.A.3.3.1	0	P38134	None	Nontransport auxilliary
YP_002403350.1	+	+	+	+	+	8.A.3.3.2	0	P76387	None	Nontransport auxilliary
YP_006107340.1	+	+	+	-	-	8.A.4.1.1	0	P42501	None	Nontransport auxilliary
YP_006121147.1	+	+	-	-	-	8.A.5.1.3	e-28	P63144	None	Nontransport auxilliary
YP_002401546.1	+	+	+	+	+	8.A.5.1.3	e-39	P63144	None	Nontransport auxilliary
YP_002404378.1	+	+	+	+	+	8.A.5.1.3	e-43	P63144	None	Nontransport auxilliary
YP_006104526.1	+	+	+	+	-	8.A.5.1.4	e-09	P80874	None	Nontransport auxilliary

Table S1, continued.

YP_002404388.1	+	+	+	+	+	8.A.5.1.4	e-15	P80874	None	Nontransport auxilliary
YP_002401335.1	-	-	+	+	+	8.A.5.1.4	e-16	P80874	None	Nontransport auxilliary
YP_006104523.1	-	-	+	+	-	8.A.5.1.4	e-17	P80874	None	Nontransport auxilliary
YP_002402877.1	-	-	+	-	+	8.A.5.1.4	e-18	P80874	None	Nontransport auxilliary
YP_002403007.1	-	-	+	+	+	8.A.5.1.4	e-23	P80874	None	Nontransport auxilliary
YP_002404097.1	-	-	+	+	+	8.A.5.1.4	e-27	P80874	None	Nontransport auxilliary
YP_006104522.1	-	-	+	-	-	8.A.5.1.4	e-37	P80874	None	Nontransport auxilliary
YP_002402997.1	-	-	+	+	+	8.A.5.1.4	e-47	P80874	None	Nontransport auxilliary
YP_002403719.1	+	-	+	+	+	8.A.7.1.1	0	P08839	None	Nontransport auxilliary
YP_006108870.1	-	+	+	-	-	8.A.7.1.4	e-26	D4GYE2	None	Nontransport auxilliary
YP_002402931.1	-	-	+	+	+	8.A.7.1.4	e-36	D4GYE2	None	Nontransport auxilliary
YP_002403718.1	+	+	+	+	+	8.A.8.1.1	e-42	P0AA04	None	Nontransport auxilliary
YP_002401531.1	+	+	+	+	+	8.A.9.1.1	e-15	Q05839	None	Nontransport auxilliary
YP_002405656.1	-	-	+	+	+	8.A.9.1.1	e-69	Q05839	None	Nontransport auxilliary
YP_002405591.1	-	-	+	+	+	8.A.21.2.1	e-08	O59180	None	Nontransport auxilliary
YP_002405590.1	-	-	+	+	+	8.A.21.2.1	e-09	O59180	None	Nontransport auxilliary

Table S1, continued.

YP_002401618.1	-	-	+	+	+	8.A.21.2.1	e-37	O59180	None	Nontransport auxilliary
YP_002268839.1	-	-	-	+	-	8.A.28.1.1	e-14	Q01484	None	Nontransport auxilliary
YP_002401445.1	-	-	+	+	+	8.A.28.1.1	e-14	Q01484	None	Nontransport auxilliary
NP_416160.1	-	-	+	+	+	8.A.48.1.1	e-39	G4PZW1	None	Nontransport auxilliary
NP_417709.2	-	-	+	+	+	8.A.48.1.2	e-32	D7XN98	None	Nontransport auxilliary
YP_002404217.1	+	+	+	+	+	9.A.4.1.2	e-86	P64564	Cations	K+ uptake
YP_002405841.1	+	+	+	+	+	9.A.5.4.1	e-48	D2YRH2	Amino acids	Arginine
YP_002404759.1	+	+	+	+	+	9.A.8.1.1	0	P33650	Cations	Fe2+
YP_006121717.1	+	+	-	-	-	9.A.8.1.1	e-39	P0AEL3	Cations	Fe2+
NP_417869.1	-	-	-	-	+	9.A.8.1.10	e-27	B5XTS6	Cations	Fe2+
YP_002403745.1	+	+	+	+	+	9.A.28.1.1	0	P41796	Amines	Ethanolamine
NP_752898.1	-	-	+	-	-	9.A.33.1.1	e-31	Q9KW03	None	Unknown
YP_002401764.1	+	+	+	+	+	9.A.40.1.2	e-153	P0A2L3	Cations	Co2+
YP_002405637.1	+	+	+	+	+	9.A.40.2.1	e-32	P54428	Cations	Mg2+, Co2+ uptake
YP_006122635.1	+	+	-	-	-	9.A.40.2.2	e-35	Q0PBV6	Proteins	Hemolysin
YP_002403820.1	+	+	+	+	+	9.A.41.1.1	0	P44669	Polysaccharides	Capsular polysaccharides
YP_006107343.1	+	+	+	-	-	9.A.41.1.2	0	P42217	Polysaccharides	Capsular polysaccharides
YP_006107344.1	+	+	+	-	-	9.A.41.1.3	0	P42218	Polysaccharides	Capsular polysaccharides
NP_416343.1	-	+	+	+	+	9.B.1.1.5	e-66	Q8EXN4	Proteins	Proteins
AAN79690.1	-	+	+	-	-	9.B.2.1.9	e-76	Q93GK6	None	Unknown

Table S1, continued.

YP_002404867.1	-	-	+	+	+	9.B.4.1.1	e-63	P0A8S5	None	Unknown
YP_002403455.1	-	-	+	+	+	9.B.10.1.1	e-10	P94400	Cations	Zn2+
YP_002405857.1	-	-	+	+	+	9.B.10.1.1	e-20	P94400	Cations	Zn2+
YP_006105318.1	-	-	+	-	-	9.B.10.1.1	e-26	P94400	Cations	Zn2+
YP_002403930.1	+	-	+	+	+	9.B.12.2.1	e-26	P0AE42	None	Unknown
YP_002403475.1	+	+	+	+	+	9.B.14.1.3	0	P33927	Siderophores	Heme
YP_002403478.1	+	+	+	+	+	9.B.14.2.3	e-145	P0ABM1	Siderophores	Heme
NP_417102.4	+	+	+	+	+	9.B.14.3.5	e-23	A6V120	None	Unknown
YP_002401932.1	+	+	+	+	+	9.B.15.1.1	e-61	P0AAW6	Siderophores	Heme
YP_002401535.1	+	+	+	+	+	9.B.18.1.1	e-57	P0ADZ7	Proteins	Proteins
YP_002404884.1	-	+	+	+	+	9.B.20.2.1	e-20	Q55026	None	Unknown
YP_002405188.1	+	+	+	+	+	9.B.21.2.1	e-61	P27838	Cations	Fe2+
YP_002405640.1	+	+	+	+	+	9.B.22.1.1	0	Q4JI69	Proteins	Leukotoxin
YP_002402975.1	+	+	+	+	+	9.B.27.1.1	e-101	P76219	None	Unknown
YP_002402977.1	+	+	+	+	+	9.B.27.1.2	e-120	P76221	None	Unknown
YP_002404385.1	+	+	+	+	+	9.B.27.2.1	e-102	P0AA60	None	Unknown
YP_002404470.1	+	+	+	+	+	9.B.27.2.2	e-118	P0AA63	None	Unknown
YP_002403583.1	-	+	+	+	+	9.B.27.2.3	e-113	P0ABP6	Anions	Selenite
NP_311050.1	-	-	-	+	-	9.B.27.2.7	e-107	E4PCL6	None	Unknown
NP_416640.2	-	-	+	+	+	9.B.27.2.7	e-107	E4PCL6	None	Unknown
NP_417174.1	-	+	+	-	+	9.B.27.3.1	e-76	E1P8P0	None	Unknown
NP_311049.1	+	+	+	+	-	9.B.29.3.1	e-35	J2MRK2	None	Unknown
YP_006121193.1	+	+	-	-	-	9.B.30.1.1	e-46	P54176	Proteins	Hemolysin
YP_002404431.1	-	-	+	+	+	9.B.31.1.1	e-108	P60782	None	Unknown

Table S1, continued.

YP_002404986.1	+	+	+	+	+	9.B.32.1.1	e-68	P32108	None	Unknown
YP_002404971.1	-	-	-	+	+	9.B.32.1.2	e-59	P0ADK5	None	Unknown
YP_002403690.1	-	-	+	+	+	9.B.33.1.1	e-77	Q81JL2	None	Unknown
YP_002402694.1	-	-	-	+	+	9.B.34.1.1	e-21	Q1J0W6	None	Unknown
NP_414919.1	-	-	+	+	+	9.B.34.1.2	0	P0AAP1	None	Unknown
YP_002403242.1	-	-	+	+	+	9.B.35.2.1	e-15	O32142	None	Unknown
YP_002404887.1	+	+	+	+	+	9.B.36.1.1	e-85	P0AET5	None	Unknown
YP_026171.3	-	-	-	-	+	9.B.40.2.1	e-31	P54428	None	Unknown
NP_313223.1	-	-	+	+	-	9.B.40.2.2	e-35	Q0PBV6	Proteins	Hemolysin
YP_006107716.1	-	-	+	+	+	9.B.42.1.1	e-25	P45754	None	Unknown
YP_002403244.1	+	+	+	+	+	9.B.43.1.1	e-97	Q8XB73	Anions	Sulfite
YP_002404946.1	+	+	+	+	+	9.B.44.1.1	e-59	P11286	None	Unknown
YP_002404945.1	+	+	+	+	+	9.B.44.1.1	e-79	P0ADJ8	None	Unknown
NP_415097.1	+	+	+	+	+	9.B.50.1.1	0	P09169	Proteins	Proteins
YP_002401706.1	+	-	+	+	+	9.B.59.1.1	0	P15078	Electrons	Electrons
YP_002405859.1	-	-	+	+	+	9.B.59.1.1	0	P15078	None	Unknown
AID77766.1	-	+	-	-	-	9.B.59.1.1	e-51	P0AAV0	Electrons	Ubiquinol:O2
YP_002403073.1	+	+	+	+	+	9.B.62.1.2	e-19	P12377	Cations	Cu2+
YP_858992.1	+	+	+	+	+	9.B.65.1.1	0	P45804	None	Unknown
NP_416539.1	-	-	-	-	+	9.B.67.2.1	0	P37748	Polysaccharides	O-antigen
YP_006108029.1	+	+	+	-	+	9.B.67.5.1	e-37	P27243	Polysaccharides	O-antigen
YP_002401732.1	-	-	+	+	+	9.B.71.1.1	e-69	P37002	None	Unknown
YP_002402836.1	+	+	+	+	+	9.B.72.1.1	e-25	P52112	Carboxylates	Alginate
YP_002403753.1	+	+	+	+	+	9.B.75.2.1	e-131	P76555	Amines	Amines

Table S1, continued.

YP_002404944.1	+	+	+	+	+	9.B.97.1.1	e-177	P37669	Vitamins	Acetyl CoA
NP_752900.1	-	-	+	-	-	9.B.97.1.3	e-16	Q2NEN2	None	Unknown
NP_418041.1	-	-	-	+	+	9.B.99.1.1	e-144	P37681	None	Unknown
NP_416296.1	+	+	+	+	+	9.B.99.1.2	e-144	P0A908	None	Unknown
NP_415820.1	-	-	+	+	+	9.B.100.1.1	e-112	E8XKQ3	None	Unknown
YP_002403203.1	+	+	+	+	+	9.B.102.1.1	0	P31064	None	Unknown
YP_002403305.1	-	-	-	+	+	9.B.102.1.2	0	P33015	None	Unknown
YP_002403815.1	-	-	-	+	+	9.B.102.4.1	e-17	A0LFK9	None	Unknown
YP_002404773.1	+	+	+	+	+	9.B.104.1.1	e-162	P09391	Proteins	Proteins
AAN79214.1	-	+	+	-	-	9.B.104.1.4	0	E1PBX5	None	Unknown
NP_414568.1	-	-	+	+	+	9.B.105.1.1	e-22	Q58AJ7	None	Unknown
YP_002401982.1	-	-	+	+	+	9.B.105.1.3	e-12	P94571	None	Unknown
YP_002403422.1	+	+	+	+	+	9.B.114.1.1	e-126	P0AFY2	Drugs	Vancomycin
YP_002404724.1	+	+	+	-	+	9.B.118.1.1	0	P45546	None	Unknown
YP_002404231.1	+	+	+	+	+	9.B.120.1.1	e-114	Q46831	None	Unknown
YP_002404900.1	+	+	+	+	+	9.B.121.1.1	0	P37645	None	Unknown
YP_006105429.1	+	+	+	-	+	9.B.122.1.1	e-65	P75962	None	Unknown
YP_002272577.1	-	-	-	+	+	9.B.124.1.1	e-48	P64592	None	Unknown
YP_002404478.1	+	+	+	+	+	9.B.124.1.2	e-71	P64591	None	Unknown
YP_006104179.1	+	+	+	-	-	9.B.124.1.4	e-10	G2GUD4	None	Unknown
NP_418356.1	-	-	+	+	+	9.B.124.1.5	e-80	E4P4R7	None	Unknown
YP_002401244.1	+	+	+	+	+	9.B.125.1.1	e-158	P0AE14	None	Unknown
YP_002404898.1	+	+	+	+	+	9.B.126.1.1	0	P37642	Lipids	Lipids
YP_002405265.1	+	+	+	+	+	9.B.126.2.1	e-136	P0A8K8	Lipids	Lipids

Table S1, continued.

YP_002403735.1	+	+	+	+	+	9.B.127.1.1	e-66	P76538	None	Unknown
YP_002405179.1	+	+	+	+	+	9.B.128.1.1	0	B6I4D1	Polysaccharides	O-antigen
NP_418492.1	+	+	+	+	+	9.B.136.1.1	e-56	P0AF54	None	Unknown
NP_418231.1	+	+	+	+	+	9.B.146.1.4	e-24	R6S968	Sugar derviatives	Undecaprenyl-phosphate-N-acetylglucosaminyl
NP_418749.1	+	+	+	+	+	9.B.156.1.1	e-84	C8UN36	None	Unknown
YP_006121561.1	+	+	-	-	-	9.B.157.1.3	0	P0A9X4	None	Unknown
NP_417716.1	+	+	+	+	+	9.B.157.1.3	0	P16926	None	Unknown
YP_006121559.1	+	+	-	-	-	9.B.157.1.3	e-86	P0ABH4	None	Unknown
NP_416816.1	+	+	+	+	+	9.B.160.1.8	e-50	Q6LNU9	Proteins	Colicin
NP_416344.1	-	-	+	+	+	9.B.174.1.1	e-28	O35002	Proteins	Proteins

Table S2. Transport proteins unique to probiotic *E. coli* strains. Proteins that are present in both probiotic strains are marked in darker blue.

NCBI Acc. #	O83	Nissle 1917	K-12	TCID	E-Value	Acc #	General Substrate	Specific Substrate
YP_006120312.1	+	+	-	1.A.4.10.1	e-168	P0AA70	Cations	Ca2+ uptake
YP_006120378.1	+	-	-	1.A.8.1.1	e-105	P0AER0	Sugar alcohols	Glycerol
AID79903.1	-	+	-	1.A.34.1.2	e-50	B7LEG0	Proteins	Lipoprotein
YP_006118849.1	+	+	-	1.A.40.5.2	0	P77328	Nucleosides	Purines
AID79680.1	-	+	-	1.B.6.1.4	e-15	Q8KWW6	MDR	Cephalothin, cephaloridine
YP_006120938.1	+	-	-	1.B.6.1.4	e-15	Q8KWW6	MDR	Cephalothin, cephaloridine
YP_002401808.1	+	+	+	1.B.11.2.2	0	P75750	None	Unknown
YP_002401272.1	+	+	+	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_002402082.1	+	+	+	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
AID77359.1	-	+	-	1.B.12.4.5	0	Q7BS42	Proteins	Proteins
AID80026.1	-	+	-	1.B.12.4.6	0	Q8FDW4	Proteins	Proteins
AID77388.1	-	+	-	1.B.12.4.7	0	A1A7W8	Proteins	Proteins
YP_006118631.1	+	-	-	1.B.12.4.7	0	A1A7W8	Proteins	Proteins
AID78195.1	-	+	-	1.B.14.1.1	0	P16869	Siderophores	Fe3+-coprogen
AID81695.1	-	+	-	1.B.14.1.1	0	P16869	Siderophores	Fe3+-coprogen
AID81624.1	-	+	-	1.B.14.1.15	e-46	Q05202	Siderophores	Ferrichrome
NP_418711.1	-	+	+	1.B.14.1.20	0	P13036	Siderophores	Fe3+-citrate
AID78345.1	-	+	-	1.B.14.3.1	e-10	P06129	Vitamins	Vitamin B12
YP_006119583.1	+	-	-	1.B.14.10.1	e-9	P95494	Siderophores	Heme
AID80097.1	-	+	-	1.B.22.1.1	e-152	P15644	Proteins	Proteins
YP_006121284.1	+	-	-	1.B.22.1.1	e-152	P15644	Proteins	Proteins
AID80116.1	-	+	-	1.B.42.1.2	e-16	P0AF98	Polysaccharides	Murein
YP_006121302.1	+	-	-	1.B.42.1.2	e-17	P0AF98	Polysaccharides	LPS

Table S2, continued.

AID80115.1	-	+	-	1.B.42.1.2	e-30	P0ADC6	Polysaccharides	Murein
YP_006121301.1	+	-	-	1.B.42.1.2	e-31	P0ADC6	Polysaccharides	LPS
AID77913.1	-	+	-	1.B.46.1.1	e-118	P61316	Proteins	Lipoprotein
AID78362.1	-	+	-	1.B.46.1.1	e-119	P61320	Proteins	Lipoprotein
AID78138.1	-	+	-	1.B.48.1.1	e-73	P0AE95	Proteins	Proteins
YP_006119363.1	+	-	-	1.B.48.1.1	e-73	P0AE95	Proteins	Proteins
AID78137.1	-	+	-	1.B.48.1.1	e-77	P0AE98	Proteins	Proteins
YP_006119362.1	+	-	-	1.B.48.1.1	e-77	P0AE98	Proteins	Proteins
YP_026226.4	+	+	+	1.B.55.3.4	0	P37650	None	Unknown
AID81862.1	-	+	-	1.C.31.1.3	e-39	Q83TS1	Peptides	Microcin
YP_002401881.1	+	+	+	1.E.1.1.2	e-34	P77237	Proteins	Endolysin
YP_006119299.1	+	-	-	1.E.2.1.1	e-56	P03705	None	Unknown
YP_026229.1	+	+	+	1.E.53.1.2	e-23	P37305	Multiple substrates	Proteins, peptides, sugar derivatives
YP_006121047.1	+	+	-	1.E.53.1.9	e-19	K4WL31	Multiple substrates	Peptides, proteins, sugar derivatives
YP_006118891.1	+	-	-	1.E.53.1.9	e-23	K4WL31	Multiple substrates	Peptides, proteins, sugar derivatives
AID77864.1	-	+	-	2.A.1.2.18	0	P0AEY7	Oligosaccharides	Lactose, melibiose efflux
YP_006120458.1	+	+	-	2.A.6.2.12	0	P76398	MDR	Nalidixic acid, norfloxacin, cloxicillin, enoxacin, kanamycin, benzalkonium, bilte salts, SDS, deoxycholate
YP_006119690.1	+	+	-	2.A.6.2.19	0	Q8GC83	MDR	Chloramphenicol, ciprofloxacin, erythromycin, tetracycline, doxycycline
AID81729.1	-	+	-	2.A.6.4.1	e-180	P0AG90	Proteins	Proteins
AID81840.1	-	+	-	2.A.7.19.2	e-13	Q9ZPR7	Amines	Allantoin
YP_002415475.1	-	+	+	2.A.8.1.1	e-107	P12012	Carboxylates	Gluconate:H+ symporter

Table S2, continued.

YP_006122712.1	+	-	-	2.A.15.2.2	e-62	B4EY22	Amines	Carnitine:γ-butyrobetaine antiporter
YP_006120091.1	+	+	-	2.A.23.1.4	e-116	P54596	Amino acids	Cystine, selenocystine: H+ symporter
YP_006122719.1	+	-	-	2.A.35.1.1	e-61	P27611	Cations	Na+:H+ antiporter
YP_006122745.1	+	-	-	2.A.56.1.8	e-157	Q8FA78	Carboxylates	Sialic acid
YP_006122744.1	+	-	-	2.A.56.1.8	e-86	Q8FA79	Carboxylates	Sialic acid
YP_006120425.1	+	-	-	2.A.66.2.6	e-49	O32273	Carboxylates	Teichuronic acid exporter
YP_006119636.1	+	+	-	2.A.95.1.3	e-28	O32244	MDR	Unknown
YP_006119349.1	+	+	-	2.A.108.2.3	0	P31545	Cations	Fe2+ uptake
YP_006119347.1	+	+	-	2.A.108.2.3	e-151	P75901	Cations	Fe2+ uptake
YP_006120488.1	+	+	-	2.A.113.1.1	e-63	P64534	Cations	Ni2+, Co2+ export
AID77771.1	-	+	-	2.C.1.2.1	0	P0A855	Proteins	Colicin
YP_006119026.1	+	+	-	2.C.1.2.1	e-99	C6EJJ6	Proteins	Colicin
AID78461.1	-	+	-	3.A.1.1.25	e-36	Q72H67	Oligosaccharides	Trehalose, maltose, sucrose, palatinose
YP_006119707.1	+	+	-	3.A.1.1.28	e-12	Q00749	Oligosaccharides	Glucose uptake
YP_006119715.1	+	+	-	3.A.1.1.34	e-135	P94360	Monosaccharides	Arabinose
YP_006119709.1	+	+	-	3.A.1.1.41	e-45	G4FGN6	Oligosaccharides	Trehalose
YP_006119708.1	+	-	-	3.A.1.1.44	e-36	Q9KZ07	Oligosaccharides	Maltose
YP_002405646.1	+	+	+	3.A.1.2.14	e-137	Q0HIQ7	Monosaccharides	Arabinose
YP_002405647.1	+	+	+	3.A.1.2.14	e-59	Q0HIQ6	Monosaccharides	Arabinose
YP_002405648.1	+	+	+	3.A.1.2.14	e-75	Q0HIQ5	Monosaccharides	Arabinose
YP_002403972.1	+	+	+	3.A.1.2.14	e-98	Q0HIQ8	Monosaccharides	Arabinose
YP_006121570.1	+	+	-	3.A.1.2.20	e-116	G4FGN3	Monosaccharides	Ribose
AID80410.1	-	+	-	3.A.1.3.8	e-111	Q52815	Amino acids	Amines
AID80407.1	-	+	-	3.A.1.3.8	e-118	Q52812	Amino acids	Amines

Table S2, continued.

AID80408.1	-	+	-	3.A.1.3.8	e-94	Q52813	Amino acids	Amines
AID80409.1	-	+	-	3.A.1.3.8	e-98	Q52814	Amino acids	Amines
YP_006120509.1	+	+	-	3.A.1.12.4	e-73	O34992	Amino acids	Choline, carnitine, glycine betaine, proline betaine, crotonobetaine, γ-butyrobetaine, dimethylsulfonioacetate, dimethylsulfonionproprionate, ectoine, choline-O-sulfate
YP_006120510.1	+	+	-	3.A.1.12.10	e-26	Q87WH4	Amino acids	Glycine, betaine, choline uptake
YP_006120511.1	+	+	-	3.A.1.12.10	e-32	Q87WH3	Amino acids	Glycine betaine, choline, acetylcholine, carnitine, proline betaine
YP_006120508.1	+	+	-	3.A.1.12.14	e-34	Q8ZPK1	Amino acids	Glycine betaine, choline-O-sulfate uptake
YP_002405808.1	-	+	+	3.A.1.14.1	e-131	P15029	Siderophores	Fe3+-citrate
YP_002405806.1	-	+	+	3.A.1.14.1	e-137	P15031	Siderophores	Fe3+-citrate
YP_002405809.1	-	+	+	3.A.1.14.1	e-145	P15030	Siderophores	Fe3+-citrate
YP_002405810.1	-	+	+	3.A.1.14.1	e-166	P15028	Siderophores	Fe3+-citrate
YP_006121358.1	+	+	-	3.A.1.14.8	e-44	Q8GRB2	Siderophores	Fe3+-vibrioferrin
YP_006119586.1	+	+	-	3.A.1.14.11	e-34	Q57399	Anions	Molybdate, tungstate
YP_006119215.1	+	+	-	3.A.1.17.2	e-108	O85765	Anions	Aromatic sulfonates
YP_006119217.1	+	+	-	3.A.1.17.2	e-71	O85763	Anions	Aromatic sulfonates
YP_006119214.1	+	+	-	3.A.1.17.2	e-91	Q8KZQ6	Anions	Aromatic sulfonates
YP_006120115.1	+	+	-	3.A.1.19.4	0	B7L6M8	Anions	Sulfate, thiosulfate
YP_006120117.1	+	+	-	3.A.1.19.4	e-116	B7L6N0	Anions	Sulfate, thiosulfate
YP_006119038.1	+	+	-	3.A.1.26.1	e-27	A9WGB0	Vitamins	Vitamin B12
YP_006119073.1	+	+	-	3.A.1.105.4	e-135	Q4VWC9	Drugs	Pyoluteorin
YP_006119074.1	+	+	-	3.A.1.105.4	e-57	Q4VWD0	Drugs	Pyoluteorin

Table S2, continued.

YP_006119072.1	+	+	-	3.A.1.105.4	e-78	Q4VWC8	Drugs	Pyoluteorin
YP_006119071.1	+	+	-	3.A.1.105.4	e-78	Q4VWC7	Drugs	Pyoluteorin
YP_006118499.1	+	+	-	3.A.1.105.12	e-40	F8D412	MDR	Unknown
YP_006118498.1	+	+	-	3.A.1.105.12	e-62	F8D413	MDR	Unknown
YP_006118788.1	+	+	-	3.A.1.106.5	0	A7VN02	MDR	Norfloxacin, tetracycline, DAPI
YP_006118833.1	+	+	-	3.A.1.139.2	e-130	P77279	Cations	Iron efflux
YP_006121777.1	+	+	-	3.A.1.140.1	e-128	P0A9R7	Proteins	Proteins
YP_006122059.1	+	-	-	3.A.2.1.1	0	P0ABB4	Cations	H+
YP_006119669.1	+	-	-	3.A.7.7.1	e-27	Q07711	Nucleic acids	DNA
YP_006121115.1	+	+	-	3.A.7.9.1	e-11	Q5ZYB4	Nucleic acids	DNA
YP_006122512.1	+	-	-	3.A.7.11.1	0	Q5EPC8	Nucleic acids	DNA
AID78770.1	-	+	-	3.A.7.14.2	e-12	Q15HU4	Nucleic acids	DNA
AID77931.1	-	+	-	3.A.11.2.2	e-98	P44408	Nucleic acids	DNA
AID77537.1	-	+	-	3.A.11.2.3	e-14	A1EMW4	Nucleic acids	DNA
AID77912.1	-	+	-	3.A.12.1.2	0	P46889	Nucleic acids	DNA
YP_854398.1	+	+	+	3.A.15.1.1	e-12	P15752	Proteins	Pullulanase
YP_006121638.1	+	+	-	3.A.15.1.1	e-154	P15645	Proteins	Pullulanase
YP_006121283.1	+	+	-	3.A.15.1.1	e-164	P15645	Proteins	Pullulanase
YP_006121106.1	+	+	-	3.A.23.2.1	e-10	A8YQS0	Proteins	Proteins
YP_006118594.1	+	-	-	3.A.23.2.1	e-108	Q6EE20	Proteins	Proteins
AID78673.1	-	+	-	3.D.6.1.2	e-43	C4N8U1	Electrons	NADH:ferredoxin
YP_002415483.1	-	+	+	4.A.5.1.3	0	P39365	Sugar alcohols	Galactitol
YP_002415484.1	-	+	+	4.A.5.1.3	e-48	P58035	Sugar alcohols	Galactitol
YP_002415481.1	-	+	+	4.A.5.1.3	e-81	P39363	Sugar alcohols	Galactitol
AID77350.1	-	+	-	4.A.7.1.2	0	B7LDR9	Carboxylates	Ascorbate
AID77351.1	-	+	-	4.A.7.1.2	e-47	B7LDS2	Carboxylates	Ascorbate

Table S2, continued.

YP_859689.1	+	+	+	5.A.3.5.2	e-11	P31075	Electrons	Electrons
YP_006121147.1	+	+	-	8.A.5.1.3	e-28	P63144	None	Nontransport auxilliary
YP_006121717.1	+	+	-	9.A.8.1.1	e-39	P0AEL3	Cations	Fe2+
YP_006122635.1	+	+	-	9.A.40.2.2	e-35	Q0PBV6	Proteins	Hemolysin
YP_006121193.1	+	+	-	9.B.30.1.1	e-46	P54176	Proteins	Hemolysin
AID77766.1	-	+	-	9.B.59.1.1	e-51	P0AAV0	Electrons	Ubiquinol:O2
YP_006121561.1	+	+	-	9.B.157.1.3	0	P0A9X4	None	Unknown
YP_006121559.1	+	+	-	9.B.157.1.3	e-86	P0ABH4	None	Unknown

Table S3. Transport proteins unique to pathogenic *E. coli* strains. Proteins that are present in both pathogenic strains are marked in darker blue.

NCBI Acc. #	CFT073	O157	K-12	TCID	E-Value	Acc #	General Substrate	Specific Substrate
YP_002401926.1	+	+	+	1.A.14.2.2	e-118	P0AAC4	Carboxylates	Acetate
NP_308892.1	+	+	-	1.A.14.2.4	e-119	B7LC70	None	Unknown
YP_002403786.1	+	+	+	1.A.16.1.2	e-160	P77733	Carboxylates	Formate
YP_002329865.1	+	-	+	1.B.1.1.3	e-130	P06996	Cations	Cations
YP_002412976.1	-	+	-	1.B.1.1.3	e-29	P06996	Cations	Cations
YP_006105475.1	+	-	-	1.B.1.1.5	0	P07238	None	Unknown
NP_310730.1	-	+	-	1.B.1.1.20	e-54	J9VK71	None	Unknown
YP_002271473.1	-	+	-	1.B.6.2.1	e-19	P0A917	None	Unknown
YP_002270238.1	-	+	-	1.B.6.2.1	e-20	P0A917	None	Unknown
YP_002401907.1	-	+	-	1.B.6.2.1	e-20	P0A917	None	Unknown
YP_002271095.1	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002271189.1	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002271413.1	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002273579.1	-	+	-	1.B.6.2.1	e-21	P0A917	None	Unknown
YP_002269436.1	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002328284.1	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002328598.1	-	+	-	1.B.6.2.1	e-22	P0A917	None	Unknown
YP_002402169.1	+	-	-	1.B.6.2.1	e-22	P0A917	None	Unknown
NP_753376.1	+	-	-	1.B.6.2.1	e-23	P0A917	None	Unknown
YP_002401955.1	+	+	+	1.B.6.2.1	e-88	P0A917	None	Unknown
YP_002271766.1	-	+	-	1.B.6.2.2	e-19	Q0WCZ9	None	Unknown
YP_002330699.1	-	+	-	1.B.6.2.2	e-24	Q0WCZ9	None	Unknown
YP_006106711.1	+	-	-	1.B.9.1.1	0	P10384	Lipids	Fatty acids

Table S3, continued.

YP_006108762.1	+	-	-	1.B.11.2.1	0	P07110	Proteins	Fimbrial subunit
NP_755465.1	+	-	-	1.B.11.2.1	0	P07110	Proteins	Fimbrial subunit
YP_006106705.1	+	-	-	1.B.11.2.1	e-171	P07110	Proteins	Fimbrial subunit
YP_002269340.1	-	+	-	1.B.11.2.2	0	P75750	None	Unknown
YP_006107455.1	+	-	-	1.B.11.2.2	0	P75750	None	Unknown
YP_002271391.1	-	+	-	1.B.11.3.2	e-122	P21647	Proteins	Fimbrial subunit
YP_002268748.1	-	+	-	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_006104298.1	+	-	-	1.B.11.3.3	0	P33129	Proteins	Fimbrial subunit
YP_002404518.1	-	+	+	1.B.11.3.6	0	P42915	Proteins	Fimbrial subunit
NP_309305.1	-	+	-	1.B.11.3.7	e-130	Q9HWU4	Proteins	Proteins
YP_002402709.1	+	+	-	1.B.11.3.9	0	P30130	Proteins	Fimbrial subunit
YP_006105297.1	+	-	-	1.B.11.3.9	e-146	P30130	Proteins	Fimbrial subunit
YP_002273255.1	-	+	-	1.B.11.3.9	e-164	P30130	Proteins	Fimbrial subunit
YP_002401420.1	-	+	+	1.B.11.4.1	e-12	P25733	Proteins	Fimbrial subunit
YP_002401441.1	-	+	-	1.B.12.1.2	e-115	Q7BCK4	Proteins	Fimbrial subunit
NP_754776.1	+	-	-	1.B.12.1.3	e-85	Q9Z625	Proteins	Fimbrial subunit
AAN81229.1	+	-	-	1.B.12.5.4	e-27	Q9XCJ4	Proteins	Proteins
YP_002402354.1	+	+	-	1.B.12.8.3	e-13	Q9XD84	Proteins	Proteins
YP_006104536.1	+	-	-	1.B.12.8.3	e-31	Q9XD84	Proteins	Proteins
YP_002413240.1	-	+	-	1.B.12.8.3	e-93	Q9XD84	Proteins	Proteins
YP_006104308.1	+	-	-	1.B.14.1.2	0	P06971	Siderophores	Ferrichrome
YP_006106341.1	+	+	-	1.B.14.1.4	e-33	P17315	Siderophores	Fe3+-catecholate
AAN78782.1	+	-	-	1.B.14.1.11	e-55	P11461	Siderophores	Fe3+-coprogen
YP_006105316.1	+	-	-	1.B.14.2.2	e-144	P31499	Siderophore	Heme
YP_002411289.1	-	+	-	1.B.17.1.4	e-19	Q92Q38	Multiple substrates	Proteins, polysaccharides, drugs

Table S3, continued.

YP_002402183.1	-	+	+	1.B.18.3.1	e-145	P0A930	Polysaccharides	Capsular polysaccharide, colanic acid
NP_754476.1	+	-	+	1.B.18.3.1	e-92	P0A930	Polysaccharides	Capsular polysaccharide, colanic acid
YP_002269765.1	-	+	-	1.B.20.1.4	0	Q8XAN8	Proteins	Proteins
NP_309409.1	+	+	+	1.B.20.1.7	e-141	B5YV25	None	Unknown
YP_002413888.1	-	+	-	1.B.22.3.2	e-151	P35672	Proteins	Proteins
YP_002331417.1	-	+	-	1.B.22.3.3	e-72	Q01244	Proteins	Proteins
NP_312824.2	-	+	+	1.B.35.2.2	e-126	P76773	Oligosaccharides	Oligogalacturonate
YP_006108010.1	+	-	-	1.B.40.2.3	0	A8A667	Proteins	Proteins
YP_002273158.1	-	+	-	1.B.54.1.1	0	P43261	Proteins	Proteins
YP_006106838.1	+	-	-	1.B.54.1.2	e-71	P11922	Proteins	Proteins
YP_002413033.1	-	+	-	1.B.54.1.2	e-88	P11922	Proteins	Proteins
NP_308569.1	-	+	-	1.B.54.1.5	e-10	Q7W286	Proteins	Proteins
NP_308154.1	-	+	+	1.B.76.1.4	e-13	G9EQG6	Cations	Cu2+
YP_006105201.1	+	-	-	1.C.1.2.2	e-23	P02978	Proteins	Proteins
YP_002412216.1	-	+	+	1.C.10.1.1	e-159	P77335	Proteins	Proteins
YP_006105538.1	+	-	-	1.C.10.1.1	e-45	P77335	Proteins	Proteins
YP_006108796.1	+	-	-	1.C.11.1.3	e-72	P09983	Proteins	Proteins
YP_002273154.1	-	+	-	1.C.36.1.1	e-168	O69413	Proteins	Proteins
YP_002273153.1	-	+	-	1.C.36.1.1	e-80	Q8XC86	Proteins	Proteins
NP_312582.1	-	+	-	1.C.36.6.1	0	Q7DB81	Proteins	Proteins
YP_002271220.1	-	+	-	1.C.54.1.1	e-23	P69178	Proteins	Proteins
YP_002271796.1	-	+	-	1.C.54.1.1	e-24	P69178	Proteins	Proteins
YP_002270020.1	-	+	-	1.C.57.3.3	e-17	Q47107	Proteins	Proteins

Table S3, continued.

YP_002269764.1	-	+	-	1.C.75.1.1	e-34	P15320	Proteins	Proteins
YP_006104441.1	+	-	-	1.C.75.1.1	e-41	P15320	Proteins	Proteins
NP_757241.1	+	-	-	1.C.80.1.1	e-10	Q8KRT4	Proteins	Fimbrial subunit
YP_006107454.1	+	-	-	1.C.80.1.1	e-14	Q8KRT4	Proteins	Fimbrial subunit
NP_757036.1	+	-	-	1.C.80.1.1	e-15	Q8KRT4	Proteins	Fimbrial subunit
YP_006105224.1	+	-	-	1.C.80.1.1	e-20	Q8KRT4	Proteins	Fimbrial subunit
NP_415067.1	+	+	+	1.C.80.1.4	e-26	B7LAC5	Proteins	Proteins
YP_002402825.1	+	+	+	1.C.82.1.1	e-52	Q9ZK21	Proteins	Proteins
NP_417375.1	+	+	+	1.C.113.1.1	e-46	P54176	Proteins	Hemolysin
NP_755064.1	+	-	+	1.E.1.1.2	e-35	P77237	Proteins	Endolysin
YP_002269671.1	-	+	-	1.E.1.1.3	e-12	O48430	Proteins	Endolysin
YP_002270281.1	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002271496.1	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002271791.1	-	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002402144.1	+	+	-	1.E.1.1.3	e-20	O48430	Proteins	Endolysin
YP_002270568.1	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002270628.1	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002328258.1	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002328796.1	-	+	-	1.E.1.1.3	e-21	O48430	Proteins	Endolysin
YP_002269991.1	-	+	-	1.E.1.1.3	e-22	O48430	Proteins	Endolysin
YP_002271119.1	-	+	-	1.E.1.1.3	e-22	O48430	Proteins	Endolysin
YP_002328577.1	-	+	-	1.E.1.1.3	e-33	O48430	Proteins	Endolysin
NP_309675.1	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_309833.1	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_310017.1	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins
NP_310188.1	-	+	-	1.E.1.1.7	0	M8KG08	Proteins	Proteins

Table S3, continued.

AAN79429.1	+	-	-	1.E.25.2.2	e-30	B2VHA2	None	Unknown
NP_417570.1	+	+	+	1.E.34.2.1	e-71	P64585	None	Unknown
NP_309800.1	-	+	-	1.E.53.1.4	e-23	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_310781.1	-	+	-	1.E.53.1.4	e-27	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309107.1	-	+	-	1.E.53.1.4	e-28	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_944589.1	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_309272.1	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
NP_310225.1	-	+	-	1.E.53.1.4	e-29	L4XY02	Multiple substrates	Proteins, peptides, sugar derivatives
YP_002405405.1	-	+	+	2.A.1.1.3	0	P0AGF4	Monosaccharides	Xylose:H+ symporter
YP_002405261.1	+	-	-	2.A.1.1.95	e-16	Q46909	Monosaccharides	Xylose
YP_002270349.1	-	+	-	2.A.1.2.7	e-34	P28246	MDR	Biocyclomycin, sulfathiazole, tetracycline, fosfomycin, acriflavin:H+ antiporter
YP_006105663.1	+	-	-	2.A.1.2.7	e-35	P28246	MDR	Biocyclomycin, sulfathiazole, tetracycline, fosfomycin, acriflavin:H+ antiporter
YP_002411081.1	-	+	-	2.A.1.2.26	e-66	P0ADL1	Nucleosides	Purine:H+ antiporter
YP_002403545.1	+	+	+	2.A.1.3.17	e-31	P76269	Drugs	Trimethoprim
YP_852504.1	+	-	-	2.A.1.3.18	e-70	Q9KIH3	MDR	Phytoalexins, salicylate, drugs

Table S3, continued.

YP_854265.1	+	-	-	2.A.1.4.2	0	P12681	Anions	Phosphoglycerate:phosphate antiporter
YP_002269002.1	-	+	-	2.A.1.4.4	e-96	P09836	Monosaccharides	Hexose-P:Pi antiporter
NP_311268.1	-	+	-	2.A.1.5.3	0	P30000	Oligosaccharides	Sucrose:H+ symporter
YP_002405262.1	+	-	-	2.A.1.6.6	e-85	P76350	Carboxylates	Shikimate:H+ symporter
YP_006108502.1	+	-	-	2.A.1.6.9	e-60	P77228	Metabolites	Non-specific
YP_006107307.1	+	-	-	2.A.1.12.1	0	P41036	Carboxylates	Sialic acid:H+ symporter
NP_756357.1	+	-	-	2.A.1.14.2	e-103	P0AA78	Carboxylates	Glucuronate, galacturonate
YP_006108681.1	+	-	-	2.A.1.14.2	e-120	P0AA78	Carboxylates	Glucuronate, galacturonate
YP_002405343.1	+	-	-	2.A.1.14.33	e-132	P39398	Carboxylates	Galactonate
YP_002271658.1	-	+	+	2.A.1.14.35	e-95	P76470	Carboxylates	Rhamnonate
YP_001463490.1	-	+	-	2.A.1.15.1	e-82	Q51955	Carboxylates	4-hydroxybenzoate, protocatachuate
YP_002401484.1	-	+	+	2.A.1.15.2	e-180	P77589	Carboxylates	3-(3-hydroxyphenyl)propionate
YP_002401472.1	-	+	+	2.A.1.17.1	e-165	P17583	Anions	Cyanate
YP_002404099.1	+	+	+	2.A.1.42.2	e-176	Q89SS6	Lipids	Lysophospholipid
YP_002413287.1	-	+	-	2.A.1.46.5	e-52	C2UR80	MDR	Quinolone
YP_002273858.1	-	+	-	2.A.1.51.2	e-174	D6IHN4	Monosaccharides	Sugars
YP_002405489.1	-	+	+	2.A.2.1.1	0	A7ZUZ0	Oligosaccharides	Melibiose
YP_002414739.1	-	+	-	2.A.2.3.4	e-72	P31435	Monosaccharides	α-xyloside uptake
NP_312485.1	-	+	-	2.A.2.3.6	e-79	A1S5F2	Oligosaccharides	Cellobiose:Na+
YP_001465361.1	-	+	+	2.A.2.3.9	0	P32137	None	Unknown
YP_001465360.1	-	+	+	2.A.2.3.9	e-179	P32137	None	Unknown

Table S3, continued.

YP_006104421.1	+	-	-	2.A.2.5.1	e-153	Q93KC2	Oligosaccharides	Oligogalacturonide
YP_002402539.1	-	+	+	2.A.3.1.13	0	P76037	Amines	Putrescine
YP_859796.1	+	-	-	2.A.3.2.7	e-128	Q9Z6M8	Amino acids	Arginine:agmatine antiporter
YP_002402039.1	-	+	+	2.A.3.7.2	0	P75835	None	Unknown
YP_002404718.1	-	+	+	2.A.3.8.17	0	P45539	Sugar derivatives	Fructoselysine
YP_859756.1	+	-	-	2.A.6.2.6	e-138	P52002	MDR	N-(3-oxododecanoyl)-L-homoserine lactone autoinducer
YP_002401537.1	+	+	+	2.A.6.4.3	e-47	Q5SKE6	Proteins	Proteins
YP_002401872.1	+	+	+	2.A.7.1.3	e-61	P23895	MDR	Cationic lipophilic drugs
YP_002403230.1	+	+	+	2.A.7.3.22	e-131	p0aa70	None	Unknown
YP_002405830.1	+	+	+	2.A.8.1.3	0	P0AC94	Carboxylates	Fructuronate/gluconate:H+ symporter
YP_002403030.1	-	+	+	2.A.15.2.3	0	P0ABD2	Amines	Glycine betaine
YP_002405210.1	+	+	+	2.A.16.2.2	e-25	Q5EAK4	Carboxylates	Malate
NP_308785.1	-	+	-	2.A.23.1.6	e-70	P96603	Carboxylates	Dicarboxylate:H+ symporter
NP_416243.1	+	+	+	2.A.23.1.8	0	P77529	Amino acids	Cysteine
P0A8K2.1	+	-	-	2.A.25.1.6	e-45	B0SM05	Amino acids	Glycine
YP_006108896.1	+	-	-	2.A.36.3.1	e-160	P32703	Cations	Na+:H+ antiporter
NP_755569.1	+	-	-	2.A.38.4.5	e-10	P73948	Cations	K+
YP_006108271.1	+	-	-	2.A.39.1.1	e-26	P0AA82	Nucleosides	Cytosine
NP_415046.4	+	+	+	2.A.40.5.1	0	P77328	Nucleosides	Purines
YP_002404147.1	+	+	+	2.A.40.7.5	e-171	P0AF52	Nucleosides	Guanine, hypoxanthine, xanthine
YP_002403442.1	-	+	+	2.A.41.2.10	0	P33021	Nucleosides	Nucleosides

Table S3, continued.

YP_002403558.1	+	+	+	2.A.47.4.1	e-52	P72958	Cations	Na+:K+ symporter
AAN79230.1	+	-	-	2.A.47.4.7	0	E4P9F4	Ions	Na+:Sulfate symporter
YP_002404593.1	-	+	+	2.A.61.1.2	0	P45428	Carboxylates	C4-dicarboxylates
YP_002405419.1	+	+	+	2.A.66.1.4	0	P28303	Proteins	Proteins
NP_310869.1	-	+	-	2.A.66.10.1	0	F1XYT9	Polysaccharides	O-antigen
YP_026192.1	+	-	+	2.A.66.12.6	0	L8CW92	Polysaccharides	Polysaccharides
YP_002402577.1	-	+	+	2.A.68.1.1	0	P46133	Carboxylates	p-aminobenzoyl-glutamate uptake
YP_006108280.1	+	-	-	2.A.80.1.1	e-72	Q9FA44	Carboxylates	Tricarboxylates
NP_415758.1	+	+	+	2.A.95.1.7	e-121	P25743	Amino acids	Amino acids
NP_309381.1	-	+	-	2.A.109.1.1	0	Q7B1W8	Cations	Tellurium
NP_417620.1	+	-	+	2.A.119.1.2	e-12	A8VTI4	None	Unknown
YP_002402434.1	+	+	+	2.C.1.1.1	e-79	P02929	Proteins	Bacteriocin
YP_002402718.1	-	+	+	3.A.1.2.8	0	P77257	Amines	Autoinducer-2 uptake
YP_002402720.1	-	+	+	3.A.1.2.8	e-133	P0AFS1	Amines	Autoinducer-2 uptake
YP_002402719.1	-	+	+	3.A.1.2.8	e-156	P77672	Amines	Autoinducer-2 uptake
YP_002402721.1	-	+	+	3.A.1.2.8	e-174	P76142	Amines	Autoinducer-2 uptake
YP_002401453.1	-	+	-	3.A.1.2.9	e--87	Q7BSH4	Oligosaccharides	Rhamnose
YP_002401452.1	-	+	-	3.A.1.2.9	e-25	Q7BSH5	Oligosaccharides	Rhamnose
NP_416003.1	-	+	+	3.A.1.5.38	0	P77308	Peptides	Dialanine
NP_418000.1	-	+	+	3.A.1.5.39	e-127	W0WN20	Peptides	Di-, tri-peptides
YP_006104452.1	+	-	-	3.A.1.109.4	e-09	Q9I2M2	MDR	MDR
YP_002411291.1	-	+	-	3.A.1.109.4	e-115	Q9I2M1	MDR	MDR
YP_006104454.1	+	-	-	3.A.1.109.4	e-65	Q9I2M0	MDR	MDR
YP_002411292.1	-	+	-	3.A.1.109.4	e-73	Q9I2M0	MDR	MDR
YP_002402910.1	+	-	-	3.A.1.201.10	e-17	B0Y3B6	MDR	MDR

Table S3, continued.

YP_002402700.1	+	-	-	3.A.1.203.4	e-55	Q50614	MDR	MDR
YP_002331410.1	-	+	-	3.A.6.1.1	e-108	P40290	Proteins	Proteins
YP_002413886.1	-	+	-	3.A.6.1.1	e-126	P0C2V3	Proteins	Proteins
YP_002331411.1	-	+	-	3.A.6.1.1	e-133	P0C2V3	Proteins	Proteins
YP_001464196.1	-	+	-	3.A.6.1.1	e-14	Q7BFA7	Proteins	Proteins
YP_002405167.1	+	+	+	3.A.6.1.1	e-15	P40290	Proteins	Proteins
YP_002404120.1	-	+	-	3.A.6.1.1	e-22	Q7BFA4	Proteins	Proteins
YP_002331423.1	-	+	-	3.A.6.1.1	e-24	Q93KT5	Proteins	Proteins
YP_001464194.1	-	+	-	3.A.6.1.1	e-26	Q93KT4	Proteins	Proteins
YP_002331415.1	-	+	-	3.A.6.1.1	e-29	Q7BFA4	Proteins	Proteins
YP_002404126.1	-	+	-	3.A.6.1.1	e-32	Q9ZA77	Proteins	Proteins
YP_002331425.1	-	+	-	3.A.6.1.1	e-47	Q9ZA77	Proteins	Proteins
YP_002331422.1	-	+	-	3.A.6.1.1	e-57	Q93KT4	Proteins	Proteins
YP_002413885.1	-	+	-	3.A.6.1.1	e-99	P40290	Proteins	Proteins
YP_002270067.1	-	+	-	3.A.7.11.1	e-19	O30554	Nucleic acids	DNA
YP_002404645.1	+	+	+	3.A.11.1.3	e-33	Q8VRK4	Nucleic acids	DNA
YP_002401240.1	+	+	+	3.A.15.2.1	e-90	P22608	Proteins	Fimbrial subunit
YP_002403466.1	+	+	+	3.A.17.1.1	e-11	P08956	Nucleic acids	DNA
YP_002405855.1	+	+	-	3.A.17.1.1	e-40	P08956	Nucleic acids	DNA
YP_006107110.1	+	-	-	3.A.23.1.1	e-08	Q9KN44	Proteins	Proteins
YP_002401348.1	-	+	-	3.A.23.1.1	e-09	Q9KN44	Proteins	Proteins
YP_002401365.1	-	+	-	3.A.23.1.1	e-104	B2D7K2	Proteins	Proteins
YP_001461389.1	-	+	-	3.A.23.1.1	e-14	Q9KN47	Proteins	Proteins
YP_002401355.1	-	+	-	3.A.23.1.1	e-19	Q9KN52	Proteins	Proteins
YP_002402382.1	+	-	+	3.A.23.1.1	e-23	Q9KN48	Proteins	Proteins
YP_006107094.1	+	-	-	3.A.23.1.1	e-32	Q9KN51	Proteins	Proteins

Table S3, continued.

YP_002404771.1	+	+	+	3.A.23.1.1	e-33	Q9KN48	Proteins	Proteins
YP_002402565.1	+	+	+	3.A.23.1.1	e-41	Q9KN48	Proteins	Proteins
YP_002402546.1	+	+	+	3.A.23.1.1	e-44	Q9KN48	Proteins	Proteins
YP_002401353.1	-	+	-	3.A.23.1.1	e-45	Q9KN50	Proteins	Proteins
YP_002401356.1	-	+	-	3.A.23.1.1	e-45	Q9KN53	Proteins	Proteins
YP_002405248.1	+	+	+	3.A.23.1.1	e-48	Q9KN48	Proteins	Proteins
YP_002403967.1	+	+	+	3.A.23.1.1	e-49	Q9KN48	Proteins	Proteins
YP_002401461.1	+	+	+	3.A.23.1.1	e-50	Q9KN48	Proteins	Proteins
YP_002403992.1	+	+	+	3.A.23.1.1	e-51	Q9KN48	Proteins	Proteins
YP_002403785.1	-	+	+	3.A.23.1.1	e-52	Q9KN48	Proteins	Proteins
YP_002405379.1	+	+	+	3.A.23.1.1	e-56	Q9KN48	Proteins	Proteins
YP_006106593.1	+	-	+	3.A.23.1.1	e-58	Q9KN48	Proteins	Proteins
YP_002403848.1	+	+	+	3.A.23.1.1	e-59	Q9KN48	Proteins	Proteins
YP_002404132.1	+	+	+	3.A.23.1.1	e-61	Q9KN48	Proteins	Proteins
YP_002402023.1	+	+	+	3.A.23.1.1	e-69	Q9KN49	Proteins	Proteins
YP_006107106.1	+	-	-	3.A.23.1.1	e-76	Q9KN55	Proteins	Proteins
YP_002403884.1	+	+	+	3.A.23.2.1	e-144	Q6EE14	Proteins	Proteins
YP_002401362.1	-	+	-	3.A.23.2.1	e-15	Q6EE21	Proteins	Proteins
YP_006107092.1	+	-	-	3.A.23.2.1	e-20	Q6EE21	Proteins	Proteins
YP_006107099.1	+	-	-	3.A.23.2.1	e-35	A8YQR5	Proteins	Proteins
YP_002404621.1	+	+	+	3.B.1.1.5	e-09	Q9V0A6	Cations	Na+
YP_002403582.1	+	+	+	3.B.1.1.5	e-11	Q9V0A4	Cations	Na+
YP_002403781.1	-	+	+	3.D.1.9.1	0	P77329	Cations	H+
YP_002413502.1	-	+	+	3.D.1.9.1	0	P77416	Cations	H+
YP_002403778.1	-	+	+	3.D.1.9.1	0	P23482	Cations	H+
YP_002403780.1	-	+	+	3.D.1.9.1	0	P77437	Cations	H+

Table S3, continued.

YP_002403777.1	-	+	+	3.D.1.9.1	e-118	P23481	Cations	H+
YP_001463807.1	-	+	+	3.D.1.9.1	e-124	P77858	Cations	H+
YP_002403783.1	-	+	+	3.D.1.9.1	e-140	P77668	Cations	H+
YP_002403782.1	-	+	+	3.D.1.9.1	e-91	P77423	Cations	H+
YP_002403516.1	+	+	+	3.D.7.1.1	e-14	P96797	Cations	H+
NP_415493.1	+	+	+	3.D.7.2.3	e-66	T2K6Q3	Cations	H+
YP_002401814.1	+	+	+	3.D.10.1.1	0	Q65GF4	Electrons	Electrons
YP_002405572.1	+	+	+	3.D.10.1.1	e-24	Q65GF5	Electrons	Electrons
YP_006108267.1	+	-	-	4.A.1.1.9	e-116	P20166	Monosaccharides	Glucose
YP_002405072.1	-	+	-	4.A.1.1.10	0	Q9AGA7	Oligosaccharides	α-glucoside
YP_002405281.1	-	+	+	4.A.2.1.6	e-66	O31645	Monosaccharides	Mannose
YP_002404576.1	+	+	+	4.A.2.1.14	e-15	D2RXA7	Monosaccharides	Fructose
YP_002273416.1	-	+	+	4.A.2.1.14	e-16	D2RXA7	Monosaccharides	Fructose
NP_311713.1	-	+	-	4.A.2.1.17	e-85	Q9HY55	Monosaccharides	Fructose
YP_006107883.1	+	-	-	4.A.5.1.4	e-88	Q8FCM6	Sugar alcohols	Galactitol
YP_002404508.1	+	+	-	4.A.6.1.6	e-16	Q2QKM4	Monosaccharides	Glucose
YP_006108509.1	+	-	-	4.B.1.1.4	e-18	Q8EDN0	Nucleosides	Nicotinamide riboside
NP_417990.4	+	-	+	4.D.3.1.2	e-21	I7KBV6	Polysaccharides	Glycosyl residues
YP_002402899.1	+	+	+	5.A.3.5.1	e-56	P0A1I1	Electrons	Electrons
YP_002405448.1	+	+	+	5.A.3.5.2	e-58	P31076	Electrons	Electrons
YP_002404894.1	+	+	+	5.B.3.1.1	e-59	Q74FY6	Electrons	Electrons
YP_002405447.1	+	+	+	5.B.5.1.1	e-14	Q8EG35	Electrons	Electrons
YP_002404985.1	+	+	+	8.A.1.1.3	e-19	B1LPP9	None	Nontransport auxilliary
YP_002404970.1	-	+	+	8.A.1.1.3	e-22	B1LPP9	None	Nontransport auxilliary

Table S3, continued.

YP_006108793.1	+	-	-	8.A.1.3.1	0	P06739	None	Nontransport auxilliary
YP_002402874.1	+	+	+	8.A.1.7.1	e-53	P46482	None	Nontransport auxilliary
YP_002401335.1	+	+	+	8.A.5.1.4	e-16	P80874	None	Nontransport auxilliary
YP_006104523.1	+	+	-	8.A.5.1.4	e-17	P80874	None	Nontransport auxilliary
YP_002402877.1	+	-	+	8.A.5.1.4	e-18	P80874	None	Nontransport auxilliary
YP_002403007.1	+	+	+	8.A.5.1.4	e-23	P80874	None	Nontransport auxilliary
YP_002404097.1	+	+	+	8.A.5.1.4	e-27	P80874	None	Nontransport auxilliary
YP_006104522.1	+	-	-	8.A.5.1.4	e-37	P80874	None	Nontransport auxilliary
YP_002402997.1	+	+	+	8.A.5.1.4	e-47	P80874	None	Nontransport auxilliary
YP_002402931.1	+	+	+	8.A.7.1.4	e-36	D4GYE2	None	Nontransport auxilliary
YP_002405656.1	+	+	+	8.A.9.1.1	e-69	Q05839	None	Nontransport auxilliary
YP_002405591.1	+	+	+	8.A.21.2.1	e-08	O59180	None	Nontransport auxilliary
YP_002405590.1	+	+	+	8.A.21.2.1	e-09	O59180	None	Nontransport auxilliary
YP_002401618.1	+	+	+	8.A.21.2.1	e-37	O59180	None	Nontransport auxilliary
YP_002268839.1	-	+	-	8.A.28.1.1	e-14	Q01484	None	Nontransport auxilliary
YP_002401445.1	+	+	+	8.A.28.1.1	e-14	Q01484	None	Nontransport auxilliary
NP_416160.1	+	+	+	8.A.48.1.1	e-39	G4PZW1	None	Nontransport auxilliary

Table S3, continued.

NP_417709.2	+	+	+	8.A.48.1.2	e-32	D7XN98	None	Nontransport auxilliary
NP_752898.1	+	-	-	9.A.33.1.1	e-31	Q9KW03	None	Unknown
YP_002404867.1	+	+	+	9.B.4.1.1	e-63	P0A8S5	None	Unknown
YP_002403455.1	+	+	+	9.B.10.1.1	e-10	P94400	Cations	Zn2+
YP_002405857.1	+	+	+	9.B.10.1.1	e-20	P94400	Cations	Zn2+
YP_006105318.1	+	-	-	9.B.10.1.1	e-26	P94400	Cations	Zn2+
NP_311050.1	-	+	-	9.B.27.2.7	e-107	E4PCL6	None	Unknown
NP_416640.2	+	+	+	9.B.27.2.7	e-107	E4PCL6	None	Unknown
YP_002404431.1	+	+	+	9.B.31.1.1	e-108	P60782	None	Unknown
YP_002404971.1	-	+	+	9.B.32.1.2	e-59	P0ADK5	None	Unknown
YP_002403690.1	+	+	+	9.B.33.1.1	e-77	Q81JL2	None	Unknown
YP_002402694.1	-	+	+	9.B.34.1.1	e-21	Q1J0W6	None	Unknown
NP_414919.1	+	+	+	9.B.34.1.2	0	P0AAP1	None	Unknown
YP_002403242.1	+	+	+	9.B.35.2.1	e-15	O32142	None	Unknown
NP_313223.1	+	+	-	9.B.40.2.2	e-35	Q0PBV6	Proteins	Hemolysin
YP_006107716.1	+	+	+	9.B.42.1.1	e-25	P45754	None	Unknown
YP_002405859.1	+	+	+	9.B.59.1.1	0	P15078	None	Unknown
YP_002401732.1	+	+	+	9.B.71.1.1	e-69	P37002	None	Unknown
NP_752900.1	+	-	-	9.B.97.1.3	e-16	Q2NEN2	None	Unknown
NP_418041.1	-	+	+	9.B.99.1.1	e-144	P37681	None	Unknown
NP_415820.1	+	+	+	9.B.100.1.1	e-112	E8XKQ3	None	Unknown
YP_002403305.1	-	+	+	9.B.102.1.2	0	P33015	None	Unknown
YP_002403815.1	-	+	+	9.B.102.4.1	e-17	A0LFK9	None	Unknown
NP_414568.1	+	+	+	9.B.105.1.1	e-22	Q58AJ7	None	Unknown
YP_002401982.1	+	+	+	9.B.105.1.3	e-12	P94571	None	Unknown

Table S3, continued.

YP_002272577.1	-	+	+	9.B.124.1.1	e-48	P64592	None	Unknown
NP_418356.1	+	+	+	9.B.124.1.5	e-80	E4P4R7	None	Unknown
NP_416344.1	+	+	+	9.B.174.1.1	e-28	O35002	Proteins	Proteins

Table S4. Occurrence of carboxylate transporters and transport direction in *E. coli*. Transporters marked in yellow are present in all five strains, those in green are probiotic-exclusive, and those in red are pathogen-exclusive.

TCID	Substrate transported	Uptake	Efflux	O83	Nissle 1917	CFT073	O157	K-12
1.A.14.2.2	Acetate, other organic acids	X	X	1	1	2	1	1
1.A.16.1.1	Formate	X	X	1	1	1	1	1
1.A.16.1.2	Formate	X	X	0	0	1	1	1
2.A.1.6.1	Citrate	X		1	1	1	1	0
2.A.1.6.2	α-ketoglutarate	X		1	1	1	1	1
2.A.1.6.6	Shikimate	X		1	1	2	1	1
2.A.1.11.3	Oxalate, formate	X	X	1	1	1	1	1
2.A.1.12.1	Sialic acid	X		1	1	2	1	2
2.A.1.14.2	Hexuronate	X		1	1	3	1	1
2.A.1.14.7	Galactonate	X		1	1	1	0	1
2.A.1.14.14	Galactarate	X		1	1	1	1	1
2.A.1.14.33	Galactonate	X		1	1	1	1	1
2.A.1.14.35	Rhamnonate	X		1	1	1	2	2
2.A.1.14.40	Glucarate	X		1	1	1	1	1
2.A.1.15.1	4-hydroxybenzoate/protocatachuate	X		0	0	0	1	0
2.A.1.15.2	3-(3-hydroxyphenyl)propionate	X		0	0	0	1	1
2.A.1.15.12	Quinate, shikimate	X		1	1	1	1	1
2.A.1.15.13	Quinate, shikimate	X		1	1	1	1	1
2.A.1.27.1	Phenylproprionate	X		1	1	1	1	1
2.A.3.1.4	GABA	X		1	1	1	1	1
2.A.3.7.3	GABA	X		1	1	1	1	1
2.A.3.7.5	GABA	X		1	1	1	1	1
2.A.7.3.1	Acetate		X	1	1	1	1	1

Table S4, continued.

2.A.8.1.1	Gluconate	X		0	1	0	0	1
2.A.8.1.2	L-idonate, D-gluconate	X		1	0	1	0	1
2.A.8.1.3	D-fructuronate/D-gluconate	X		0	0	1	1	1
2.A.8.1.4	D-gluconate	X		1	1	1	1	1
2.A.8.1.7	Gluconate	X		1	1	1	0	1
2.A.8.1.8	Gluconate	X		1	1	1	1	1
2.A.10.1.2	2-keto-3-deoxygluconate	X		1	1	1	1	1
2.A.13.1.1	Fumarate	X	X	1	1	1	1	1
2.A.13.1.2	Fumarate, malate	X	X	1	1	1	1	1
2.A.14.1.1	L-lactate, D-lactate, glycolate	X		1	1	1	1	1
2.A.14.1.2	L-lactate, D-lactate, glycolate	X		1	1	1	0	1
2.A.16.2.2	Malate	X		0	0	1	1	1
2.A.21.1.1	Pantothenate	X		1	1	1	1	1
2.A.21.7.2	Acetate, glyoxylate	X		1	1	1	1	1
2.A.23.1.6	Dicarboxylates	X		0	0	0	1	0
2.A.23.1.7	Dicarboxylate	X		1	1	1	1	1
2.A.40.3.3	Urate	X		1	1	1	1	1
2.A.46.1.1	Benzoate	X		1	1	1	1	1
2.A.47.3.1	2-oxoglutarate, malate	X	X	1	1	1	1	1
2.A.47.3.2	Citrate, succinate	X	X	2	1	2	1	1
2.A.47.3.3	L-tartate, succinate	X	X	1	1	1	1	1
2.A.56.1.2	2,3-diketo-L-gulonate	X		3	3	3	0	0
2.A.56.1.8	Sialic acid	X		3	0	1	0	0
2.A.61.1.1	C4-dicarboxylates	X	X	1	1	1	1	1
2.A.61.1.2	C4-dicarboxylates	X	X	0	0	0	1	1

Table S4, continued.

2.A.68.1.1	ρ-aminobenzoyl-glutamate	X		0	0	0	1	1
2.A.69.3.5	Auxin		X	1	1	1	1	1
2.A.80.1.1	Tricarboxylate	X		1	1	2	0	0
2.A.80.1.3	Tricarboxylate	X		1	1	1	0	0
2.A.85.1.1	Fusaric acid		X	1	1	1	1	1
2.A.85.1.2	ρ-hydroxybenzoate		X	1	1	1	1	1
2.A.85.1.3	Fusaric acid		X	1	1	1	1	1
2.A.85.1.6	Fusaric acid		X	1	1	1	1	1
2.A.85.7.1	Fusaric acid		X	1	1	1	1	1
2.A.96.1.1	Acetate, succinate	X		1	1	1	1	1
2.A.118.1.2	C4-dicarboxylates	X		1	1	1	0	0
2.A.118.1.3	C4-dicarboxylates	X		1	1	1	0	1
4.A.2.1.3	2-O-α-mannosyl D-glycerate	X		0	0	0	0	1
4.A.7.1.1	Ascorbate	X		3	3	3	3	3
4.A.7.1.2	Ascorbate	X		0	2	0	0	0
9.B.72.1.1	Alginate		X	1	1	1	1	1

TABLES

Table 1. Overview of the five *E. coli* strains and their basic traits.

Strain designation	**O83:H1**	**Nissle 1917**	**CFT073**	**O157:H7**	**K-12 MG1655**
Accession no.	NC_017634.1	CP007799.1	AE014075.1	NC_002695.1	NC_000913.3
Genome size (Mbp)	4.75	5.44	5.23	5.50	4.64
Total proteins	4429	4821	5379	5204	4140
Total transport systems	589	581	649	640	591
Host location	Extracellular	Extracellular	Intracellular	Extracellular	Extracellular
Serovar type	Probiotic	Probiotic	UPEC	EHEC	Non-virulent

Table 2. Overview of the *E. coli* transporter analyses based on TC subclass. Numbers in parentheses represent amount of transport systems.

TC subclass and description	Transport proteins					%				
	O83	**Nissle 1917**	**CFT073**	**O157**	**K-12**	**O83**	**Nissle 1917**	**CFT 073**	**O157**	**K-12**
1.A, α-type channels	40 (40)	37 (36)	37 (33)	37 (34)	30 (27)	4.5	4.1	3.9	3.9	3.4
1.B, β-barrel porins	92 (92)	106 (105)	99 (99)	103 (92)	73 (63)	10.3	11.7	10.4	10.9	8.4
1.C, Pore-forming toxins	2 (2)	4 (4)	14 (14)	13 (11)	6 (6)	0.2	0.4	1.5	1.4	0.7
1.E, Holins	14 (14)	9 (9)	8 (8)	30 (30)	11 (11)	1.6	1.0	0.8	3.2	1.3
2.A, Porters (uniporters, symporters, antiporters)	271 (265)	271 (240)	293 (266)	273 (262)	282 (271)	30.4	29.9	30.9	28.9	32.3
2.C, Ion-gradient-driven energizers	5 (2)	4 (2)	5 (5)	3 (2)	4 (2)	0.6	0.4	0.5	0.3	0.5
3.A, P-P-bond-hydrolysis-driven transporters	265 (72)	263 (77)	240 (78)	240 (70)	218 (68)	29.9	29.1	25.3	25.4	24.9
3.B, Decarboxylation-driven transporters	0 (0)	0 (0)	2 (2)	2 (2)	2 (1)	0.0	0.0	0.2	0.2	0.2
3.D, Oxidoreduction-driven transporters	35 (7)	37 (8)	40 (10)	49 (11)	49 (11)	3.9	4.1	4.2	5.2	5.6
4.A, Phosphotransfer-driven group translocators	50 (15)	55 (16)	53 (26)	48 (27)	44 (23)	5.6	6.1	5.6	5.1	5.0
4.B Nicotinamide ribonucleoside uptake transporters	2 (1)	2 (1)	3 (2)	2 (1)	2 (1)	0.2	0.2	0.3	0.2	0.2
4.C, Acyl-CoA ligase-coupled transporters	2 (2)	2 (2)	2 (2)	2 (2)	2 (2)	0.2	0.2	0.2	0.2	0.2
4.D, Polysaccharide synthase exporters	3 (3)	3 (3)	4 (4)	3 (3)	4 (4)	0.3	0.3	0.4	0.3	0.5
5.A, Transmembrane two-electron transfer carriers	29 (12)	29 (12)	29 (12)	28 (10)	30 (12)	3.3	3.2	3.1	3.0	3.4
5.B, Transmembrane one-electron transfer carriers	0 (0)	0 (0)	2 (2)	2 (2)	4 (4)	0.0	0.0	0.2	0.2	0.5

Table 2, continued.

8.A, Auxiliary transport proteins	19 (0)	19 (0)	37 (0)	35 (0)	33 (0)	2.1	2.1	3.9	3.7	3.8
9.A, Recognized transporters of unknown biochemical mechanism	12 (11)	12 (11)	10 (10)	7 (7)	8 (8)	1.3	1.3	1.1	0.7	0.9
9.B, Putative transport proteins	51 (51)	54 (54)	71 (67)	69 (68)	72 (71)	5.5	5.8	7.5	7.3	8.2
Total	892 (589)	908 (581)	949 (649)	946 (640)	873 (591)	100	100	100	100	100

Table 3. Overview of transport systems in *E. coli* based on predicted substrate specificity.

Substrate category	Substrate subcategory	Transport systems					%				
		O83	Nissle 1917	CFT073	O157	K-12	O83	Nissle 1917	CFT073	O157	K-12
Organic	Amines	17	16	16	19	19	2.9	2.8	2.5	3.0	3.2
	Amino acids	60	58	56	55	57	10.2	10.0	8.6	8.6	9.6
	Carboxylates	56	54	57	52	57	9.5	9.3	8.8	8.1	9.6
	Drugs	38	37	43	38	33	6.5	6.4	6.6	5.9	5.6
	Nucleotides/nucleosides	20	20	21	20	21	3.4	3.4	3.2	3.1	3.6
	Mono/oligosaccharides	53	54	54	52	53	9.0	9.3	8.3	8.1	9.0
	Sugar derivatives	18	18	18	17	16	3.1	3.1	2.8	2.7	2.7
	Vitamins	6	7	6	6	6	1.0	1.2	0.9	0.9	1.0
	Sugar alcohols	10	10	10	9	8	1.7	1.7	1.5	1.4	1.4
	Siderophores	27	30	28	20	16	4.6	5.2	4.3	3.1	2.7
	Non-specific	5	7	9	8	9	0.8	1.2	1.4	1.3	1.5
Inorganic	Anions	37	39	39	37	27	6.3	6.7	6.0	5.8	4.6
	Cations	53	58	54	65	64	9.0	10.0	8.3	10.2	10.8
	Electrons	16	16	18	18	20	2.7	2.8	2.8	2.8	3.4
	Water	1	0	1	1	1	0.2	0.0	0.2	0.2	0.2
Macromolecule	DNA	3	2	11	11	10	0.5	0.3	1.7	1.7	1.7
	Polysaccharides	23	23	24	12	17	3.9	4.0	3.7	1.9	2.9
	Proteins/peptides	75	81	90	116	76	12.7	13.9	13.9	18.1	12.9
	Lipids	9	10	11	9	11	1.5	1.7	1.7	1.4	1.9
Unknown	Unknown	62	41	83	75	70	10.5	7.1	12.8	11.7	11.8
Total		589	581	649	640	591	100	100	100	100	100

Table 4. Occurrence of sugar transporters and transport direction in *E. coli*. Transporters marked in yellow are present in all five strains, while ones marked in green are probiotic-exclusive.

TCID	Substrate transported	Uptake	Efflux	O83	Nissle 1917	CFT073	O157	K-12
1.B.3.1.3	β-glucosides	X		2	2	2	0	1
1.B.15.1.1	Raffinose	X		1	1	1	1	0
1.B.35.2.2	Oligogalacturonate	X		0	0	0	1	1
2.A.1.1.1	Galactose		X	1	1	1	1	1
2.A.1.1.2	Arabinose		X	1	1	1	1	1
2.A.1.1.3	Xylose		X	0	0	0	1	1
2.A.1.1.92	Sugars		X	1	1	1	1	1
2.A.1.1.95	Xylose		X	1	1	2	0	1
2.A.1.1.114	Xylose		X	1	1	1	1	1
2.A.1.1.115	Xylose		X	1	1	1	1	1
2.A.1.2.14	Arabinose		X	1	1	1	1	1
2.A.1.2.15	Arabinose, isopropyl β-D-thio-galactopyranoside		X	1	1	1	1	1
2.A.1.2.18	Lactose, melibiose		X	0	1	0	0	0
2.A.1.2.65	Arabinose		X	1	1	1	1	1
2.A.1.4.1	Sugar-P	X		1	1	1	1	1
2.A.1.4.4	Hexose-P	X		1	1	1	2	1
2.A.1.5.1	Lactose	X		1	1	1	1	1
2.A.1.5.3	Sucrose	X		0	0	0	1	0
2.A.1.7.1	Fucose	X		1	1	1	1	1
2.A.1.7.5	Deoxyribose	X		0	1	1	0	0
2.A.1.7.14	Fucose	X		1	1	1	1	1

Table 4, continued.

2.A.1.20.1	Lactose, glucose, aromatic glucosides, galactosides		X	0	0	0	0	1
2.A.1.20.2	Lactose, glucose		X	1	1	1	1	1
2.A.1.20.3	Xylose		X	0	0	0	0	1
2.A.1.36.3	Arabinose	X	X	1	1	1	1	0
2.A.1.46.6	Arabinose		X	1	1	0	1	1
2.A.1.46.7	Arabinose		X	1	1	1	1	1
2.A.1.51.2	Sugars	X (?)		1	1	1	1	1
2.A.1.52.1	Sugars	X (?)		1	1	1	1	1
2.A.1.52.2	Sugars	X (?)		1	1	1	1	1
2.A.1.60.2	Sugars	X (?)		1	1	1	1	1
2.A.2.1.1	Melibiose	X		0	0	0	1	1
2.A.2.3.1	Glucuronide	X		1	1	1	1	1
2.A.2.3.4	α-xyloside	X		1	1	1	2	1
2.A.2.3.5	β-xyloside	X		0	0	0	0	1
2.A.2.3.6	Cellobiose	X		0	0	0	1	0
2.A.7.6.1	Rhamnose	X		1	1	1	0	1
2.A.21.3.9	Galactose	X		1	1	1	1	1
3.A.1.1.1	Maltooligosaccharides	X		4	4	4	4	4
3.A.1.1.25	Trehalose, maltose, sucrose, palatinose	X		0	1	0	0	0
3.A.1.1.28	Glucose	X		1	1	0	0	0
3.A.1.1.34	Arabinose	X		1	1	0	0	0
3.A.1.1.41	Trehalose	X		1	1	0	0	0
3.A.1.1.44	Maltose, maltodextrin	X		1	0	0	0	0

Table 4, continued.

3.A.1.2.1	Ribose	X		3	3	3	3	3
3.A.1.2.2	Arabinose	X		3	3	3	3	3
3.A.1.2.3	Galactose, glucose	X		3	3	3	3	3
3.A.1.2.4	Xylose	X		3	3	3	3	3
3.A.1.2.6	Allose	X		3	3	3	0	3
3.A.1.2.9	Rhamnose	X		0	0	0	2	0
3.A.1.2.14	Arabinose	X		4	4	0	0	4
3.A.1.2.20	Ribose	X		1	1	0	0	0
4.A.1.1.1	Glucose	X		2	2	2	2	2
4.A.1.1.3	Maltose	X		1	1	1	1	1
4.A.1.1.9	Glucose	X		0	0	1	0	0
4.A.1.1.10	α-glucoside	X		0	0	0	1	0
4.A.1.2.2	β-glucoside	X		1	1	1	0	1
4.A.1.2.3	β-glucoside	X		1	0	0	1	1
4.A.1.2.4	Trehalose	X		1	1	1	1	1
4.A.2.1.1	Fructose	X		2	2	2	2	2
4.A.2.1.6	Mannose	X		0	0	0	1	1
4.A.2.1.9	Fructose	X		3	3	3	0	0
4.A.2.1.11	Fructose	X		3	3	3	3	3
4.A.2.1.14	Fructose	X		0	0	1	2	2
4.A.6.1.1	Mannose	X		3	3	3	3	3
4.A.6.1.3	Sorbose	X		4	4	4	3	0
4.A.6.1.6	Glucose	X		0	0	1	1	0

Table 5. Occurrence of secretion system components in *E. coli*. Transporters marked in yellow are present in all five strains, those in green are probiotic-exclusive, and those in red are pathogen-exclusive.

Family	**TCID**	**Function**	**O83**	**Nissle 1917**	**CFT073**	**O157**	**K-12**
T1SS	3.A.1.105.4	Drug exporter 1 (4 components)	5	5	0	0	0
	3.A.1.109.4	Protein exporter 1 (4 components)	0	0	2	2	0
	3.A.1.110.1	Protein exporter 2 (4 components)	0	3	3	0	0
	3.A.1.113.3	Peptide 3 exporter (4 component)	1	1	1	1	1
T2SS GSP	3.A.5.1.1	SEC-SRP complex (7 components)	7	7	7	7	7
MTB	3.A.15.1.1	Pullulanase secretion system (12 components)	10	10	7	0	7
	3.A.15.2.1	Pilin secretion/fimbrial assembly system (9 components)	2	2	3	4	2
T3SS	3.A.6.1.1	Type III secretion system complex (22 components)	0	0	0	13	0
T4SS	3.A.7.7.1	Trs DNA transfer protein complex (15 components)	3	2	2	2	2
	3.A.7.9.1	Icm/Dot protein secretion system (26 components)	1	1	0	0	0
	3.A.7.11.1	Type IV betaproteobacterial DNA secretion system (20 components)	3	0	1	3	1
	3.A.7.14.1 and 2	Type IV (conjugal DNA-protein transfer) (15 components)	2	4	3	2	2
T6SS	3.A.23.1.1	T6SS VasA-L (14 components)	11	6	21	24	14
	3.A.23.2.1	T6SS EvpA-P (16 components)	4	3	5	2	1

Table 6. Occurrence of iron and iron-siderophore transporters and transport direction in *E. coli*. Transporters marked in yellow are present in all five strains, while ones marked in green are probiotic-exclusive.

TCID	Substrate transported	Uptake	Efflux	Unknown	O83	Nissle 1917	CFT073	O157	K-12
1.B.14.1.1	Fe3+-coprogen	X			1	3	1	1	1
1.B.14.1.2	Fe3+-ferrichrome	X			1	1	1	1	1
1.B.14.1.3	Fe3+-enterobactin	X			0	1	1	0	0
1.B.14.1.4	Fe3+-catecholate	X			1	2	3	2	1
1.B.14.1.9	Fe3+-catecholate	X			1	1	1	1	1
1.B.14.1.11	Fe3+-anguibactin	X			0	0	1	0	0
1.B.14.1.13	Fe3+	X			0	1	1	1	0
1.B.14.1.15	Fe3+-pseudobactin	X			0	1	0	0	0
1.B.14.1.20	Fe3+-ferrioxamine	X			0	1	0	0	1
1.B.14.1.22	Fe3+-enterobactin	X			1	1	1	1	1
1.B.14.1.24	Siderophores	X			1	1	1	1	0
1.B.14.2.2	Heme	X			0	1	2	0	0
1.B.14.2.14	Heme	X			1	1	1	1	0
1.B.14.7.2	Fe3+-yersiniabactin	X			1	1	1	0	0
1.B.14.9.3	Fe3+-ferrichrome, Fe3+-aerobactin	X			0	1	1	0	0
1.B.14.9.4	Heme	X			1	0	0	1	1
1.B.14.10.1	Heme	X			1	0	0	0	0
2.A.1.38.1	Enterobactin		X		1	1	1	1	1
2.A.1.57.3	Fe3+	X			1	1	1	0	0
2.A.4.7.1	Fe2+		X		1	1	1	1	1
2.A.5.5.1	Fe2+		X		1	1	0	1	1

Table 6, continued.

2.A.55.3.1	Fe2+		X		1	1	1	1	0
2.A.108.2.3	Fe2+		X		3	3	1	1	0
3.A.1.14.1	Fe3+-dicitrate	X			0	4	0	0	4
3.A.1.14.2	Fe3+-enterobactin	X			4	4	4	4	4
3.A.1.14.3	Fe3+-hydroxamate	X			3	3	3	3	3
3.A.1.14.6	Fe3+-vibriobactin/enterobactin	X			1	1	1	1	0
3.A.1.14.8	Fe3+-vibrioferrin	X			1	1	0	0	0
3.A.1.14.15	Bacillibactin	X			1	1	0	1	0
3.A.1.14.18	Heme	X			3	3	3	3	0
3.A.1.15.7	Fe2+	X			4	4	4	0	0
3.A.1.21.1	Fe3+-yersiniabactin	X			2	2	2	0	0
3.A.1.106.7	Salmochelin/enterobactin		X		0	1	1	0	0
3.A.1.107.3	Heme		X		3	3	3	3	3
3.A.1.120.6	Heme		X		1	1	2	2	2
3.A.1.139.2	Fe2+		X		1	1	0	1	1
9.B.14.1.3	Heme			X	1	1	1	1	1
9.B.14.2.3	Heme			X	1	1	1	1	1
9.B.15.1.1	Heme			X	1	1	1	1	1
9.B.21.2.1	Fe2+			X	1	1	1	1	1

Table 7. Occurrence of toxins in *E. coli*. Transporters marked in yellow are present in all five strains, while ones marked in green are probiotic-exclusive.

TCID	Family	Function	O83	Nissle 1917	CFT073	O157	K-12
1.C.1.2.2	Colicin	Colicin E1	0	0	1	0	0
1.C.10.1.1	HlyE	Hemolysin, HlyE	0	0	1	1	1
1.C.11.1.3	RTX toxin	Hemolysin, HlyA	0	0	1	0	0
1.C.31.1.3	Colicin V	Colicin V precursor, CeaV	0	1	0	0	0
1.C.36.1.1	IIITCP	T3SS: pore-forming complex EspBD	0	0	0	2	0
1.C.36.6.1	IIITCP	T3SS: pore-forming complex EspAD	0	0	0	1	0
1.C.54.1.1	Shiga toxin B	Shiga toxin B St-B	0	0	0	2	0
1.C.57.3.3	Clostridial cytotoxin	Pore formation; necrosis in host, Cnf	0	0	0	1	0
1.C.75.1.1	S-PFT	Hemolysin, ShlA	0	0	1	1	0
1.C.80.1.1	Cytotoxic major fimbrial subunit (MrxA)	Adhesive fimbriae (pore formation)	0	1	5	0	0
1.C.80.1.2	Cytotoxic major fimbrial subunit (MrxA)	Adhesive fimbriae (pore formation)	1	1	1	1	1
1.C.80.1.3	Cytotoxic major fimbrial subunit (MrxA)	Adhesive fimbriae (pore formation)	1	1	1	1	1
1.C.80.1.4	Cytotoxic major fimbrial subunit (MrxA)	Adhesive fimbriae (pore formation)	0	0	1	1	1
1.C.82.1.1	HP2-20	Pore formation	0	0	1	1	1
1.C.113.1.1	Hly III	Hemolysin, Hly III	0	0	1	1	1

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