Phylogenetic analysis reveals an ancient gene duplication as the origin of the MdtABC efflux pump.

Kamil Górecki¹, Megan M. McEvoy¹,²,³

¹Institute for Society & Genetics, ²Department of Microbiology, Immunology & Molecular Genetics, and ³Molecular Biology Institute, University of California, Los Angeles, CA 90095, United States of America

Corresponding author: mcevoymm@ucla.edu (M.M.M.)
Abstract

The efflux pumps from the Resistance-Nodulation-Division family, RND, are main contributors to intrinsic antibiotic resistance in Gram-negative bacteria. Among this family, the MdtABC pump is unusual by having two inner membrane components. The two components, MdtB and MdtC are homologs, therefore it is evident that the two components arose by gene duplication. In this paper, we describe the results obtained from a phylogenetic analysis of the MdtBC pumps in the context of other RNDs. We show that the individual inner membrane components (MdtB and MdtC) are conserved throughout the Proteobacterial species and that their existence is a result of a single gene duplication. We argue that this gene duplication was an ancient event which occurred before the split of Proteobacteria into Alpha-, Beta- and Gamma- classes. Moreover, we find that the MdtABC pumps and the MexMN pump from Pseudomonas aeruginosa share a close common ancestor, suggesting the MexMN pump arose by another gene duplication event of the original Mdt ancestor. Taken together, these results shed light on the evolution of the RND efflux pumps and demonstrate the ancient origin of the Mdt pumps and suggest that the core bacterial efflux pump repertoires have been generally stable throughout the course of evolution.

Keywords: efflux pumps, RND efflux pumps, gene duplication, antibiotic resistance
Introduction

The resistance-nodulation-division efflux pumps (RNDs) comprise a large family of proteins, widely distributed among bacterial species [1,2]. Their main function is to extrude superfluous or harmful substances, such as metabolites, antibiotics, toxins, or metal ions. Some RNDs are also believed to be involved in export of siderophores and quorum sensing molecules [3,4], and there may be additional functions to be discovered, given the fact that the vast majority of RND pumps have not been characterized [5]. In general, the RNDs are divided into two groups depending on the substrates they transport: hydrophobic and amphiphilic efflux (HAE) and heavy metal efflux (HME).

Virtually all bacteria contain multiple RND assemblies with often at least partially overlapping functions. For instance, *Escherichia coli* contains six RNDs in its genome (five HAEs, transporting a broad range of substrates, and one HME, transporting Cu and Ag) [6], while the opportunistic pathogen *Pseudomonas aeruginosa* can contain up to 13 different RND systems, depending on the strain [7]. This abundance remains a puzzle. While in *E. coli* deletion of all RNDs results in drastic changes in the phenotype and seriously decreased ability to grow, deletion of one or two RND systems does not seem to have a strong effect (with the exception of the HME Cu-transporting Cus system, which is required for Cu-resistance) [6]. These results suggest functional overlap between the RND systems, and the pumps may be expressed depending on circumstances like exponential/stationary phase or aerobic/anaerobic conditions.

Classically, the efflux system is formed as a tripartite assembly [8]. Most RND systems share the same architecture, with an RND homotrimer in the inner membrane bound to six protomers of a membrane fusion protein (MFP) in the periplasm, which in turn connect the assembly with a trimer of outer membrane proteins (OMP). However, there are exceptions. In the
MdtABC (multidrug transport) system from *E. coli* the inner membrane part is formed by a heterotrimer of MdtB$_2$C$_1$ stoichiometry [9]. A similar system called MuxABC was described in *P. aeruginosa*, with the MuxA, MuxB and MuxC proteins being homologous to MdtA, MdtB and MdtC, respectively (40, 65 and 61% sequence identity, and 78, 91 and 88% sequence similarity between the corresponding proteins) [10,11]. Other homologous systems were found and characterized in *Salmonella enterica* Serovar Typhimurium [12], *Serratia marcescens* [13], *Erwinia amylovora* [14], *Pseudomonas putida* [15], and *Photorhabdus luminescens* [16].

There are conflicting reports in the literature in regard to functional flexibility between the two subunits. Kim et al. reported that deletion of MdtC, but not MdtB, completely abolished the function of the Mdt system [9], while Da Wang and Fierke showed the opposite to be true [17]. It is possible there is a partial functional overlap between the two proteins, yet both subunits are needed for full function. Interestingly, the Mdt system has been shown to be able to facilitate both heavy metal and hydrophobic and amphiphilic efflux, and the heterogeneity of the inner membrane components may be a source of this promiscuity [17].

The evolutionary history of the two-RND subunit systems such as MdtBC remains unknown. While it may be hypothesized they arose originally through a gene duplication of the progenitor Mdt gene, both due to their high sequence similarity (e.g. 50% between MdtB and MdtC, compared to 25-30% between MdtB and other RNDs in *E. coli*) and their adjacent positions in genomes, it is not known if this gene duplication happens commonly in bacterial genomes or if it is rather an older phenomenon. The two-RND subunit systems from *E. coli* and *P. aeruginosa* are quite similar to each other, with higher homology between MdtB and MuxB, and between MdtC and MuxC, than between the proteins from the same organisms. *This* observation suggests
that the original RND gene duplication might indeed be an infrequent older phenomenon, and not a widespread feature happening frequently in bacterial genomes.

Within the highly diverse Proteobacteria, Epsilonproteobacteria separated earliest from the rest, in an event placed at around 2.8 bln years ago by Battistuzzi and Hedges [25]. Subsequently, Deltaproteobacteria split from the rest of the lineage around 2.6 bln years ago, and Alphaproteobacteria around 2.4 bln years ago. The split between the two last groups, Beta- and Gammaproteobacteria, happened the latest, around 1.6 bln years ago. We set out to investigate how the phylogenetics of the Mdt proteins compares to the evolution of the phylum, in order to shed light on the evolutionary history of the Mdt systems. We thus performed a number of phylogenetic analyses and present the results in this paper.

Materials and Methods

Phylogenetic analyses

In order to place the Mdt proteins in the context of other RNDs, the RND sequences from the work of Godoy et al. were used [5]. Out of over 2000 sequences there, 1106 were identified in UniProt (a full list is provided in the Supporting information). These sequences were aligned with MAFFT using the default settings [18]. The alignment was then used to construct a phylogenetic tree based on all non-gapped positions and using neighborhood joining. The heterogeneity among sites was estimated by the MAFFT algorithm and the bootstrap values were calculated from 100 replicates.

The sequences that clustered together with *E. coli* MdtB and MdtC (and *E. coli* AcrB as an outgroup) were aligned with MAFFT using G-INS-i, an iterative refinement method, and a phylogenetic tree was constructed using neighborhood joining (NJ) of all of gap-free sites (JTT
substitution model, the heterogeneity among sites was estimated by MAFFT, and bootstrap of 100 was used) [18]. The tree was then rooted on AcrB.

**Sequence similarity network and genomic neighborhood diagrams**

The sequence similarity network (SSN) was generated with the Enzyme Similarity Tool (ESI-EST) and visualized with Cytoscape [20-24], with an alignment score of 200. The genomic neighborhoods of the genes in Fig 2 were investigated with the Gene Neighborhood Tool (ESI-GNT) [20-23], and visualized together with the phylogenetic trees in iTOL [19].

The sequences for membrane fusion proteins and outer membrane proteins were identified with the help of the ESI-GNT, and the further analysis was done in the same way as for RND proteins, using *E. coli* AcrA and TolC as outgroups, respectively. The phylogenetic trees were visualized with iTOL.

**Results & Discussion**

**RNDs form a number of distinct clusters**

The comparison of over 1000 sequences of RND proteins, previously identified by Godoy et al. [5], was performed in order to divide them into functional groups, and thus clarify their possible evolutionary origins. In particular, we were interested in how the Mdt system is placed in relation to the better characterized efflux pumps like Acr, Mex (HAE) or Cus (HME). Since constructing reliable sequence alignments of large proteins containing both transmembrane helices and large periplasmic domains can be difficult, we also generated a sequence similarity network (SSN), to visualize direct relationships between the sequences [20-24].

There was a high similarity between the results obtained with the traditional phylogenetic analysis and the SSN. As seen in Fig 1, most proteins formed several large branches and clusters,
with a smaller number remaining separated. The largest cluster (cluster 1) encompassed most of
the characterized RNDs (all HAEs from \textit{E. coli}). The less studied RNDs from \textit{P. aeruginosa}
clustered as MexI/W (cluster 2) and TriC/MexK (cluster 5). As expected, the HME proteins
clustered together, with a further subdivision into mono- and di- valent transporting RNDs (cluster
3).

\textbf{Fig 1. Analysis of >1000 RND sequences.} Left, an unrooted phylogenetic tree, with bootstrap
values represented as branch colors. Leaves are labelled with colors corresponding to their clusters
(black represents proteins not belonging to the colored clusters, or singletons). Right, sequence
similarity network. Clusters containing more than 10 sequences are colored and given a number.
\textit{P. aeruginosa} and \textit{E. coli} proteins are marked with thick circles, black and white, respectively. On
both panels \textit{P. aeruginosa} and \textit{E. coli} proteins are additionally marked with their abbreviations (\textit{E.
coli} proteins underlined).

The Mdt proteins formed a distinct cluster (cluster 4), with one of the longest branches
from the middle in the phylogenetic tree. The MdtB-like and MdtC-like proteins split early in the
phylogenetic tree. The MdtB-like proteins, which are always directly adjacent to their respective
MFPs, clustered together into one branch. The MdtC-like protein, which are never directly
adjacent to their respective MFPs (i.e. there is always an MdtB-like protein in between), also
clustered together into one branch. The fact that the gene organization has been preserved
corroborates the notion that this heteromeric RND system is a result of an ancient gene duplication.
This relationship seems to be very old, since Alpha-, Beta- and Gammaproteobacterial MdtBs and
MdtCs form separate clusters, so that would put this duplication event to be older than the split between the major groups of *Proteobacteria* (over 2 billion years ago [25]).

Surprisingly, the branch/cluster containing Mdt-like proteins also included other RNDs, notably the MexN from *P. aeruginosa* and its homologues from other *Pseudomonodales*, as well as a number of other proteins. To investigate if this was an artefact caused by aligning a large number of sequences, we performed a new multiple sequence alignment with these 126 sequences, with *E. coli* AcrB as an outgroup. The results are shown in Fig 2, together with their genomic neighborhoods.

**Fig 2. A phylogenetic tree of the Mdt-like proteins.** The bootstrap values are represented by a branch color as in Fig 1 (the branches with bootstrap support lower than 50 were not collapsed, in order to show the genomic neighborhood of these genes). The taxonomy of each organism is represented with shading of the labels. To the right of the protein and organism names the genomic context is presented. The actual protein at the leaf tip is represented with a filled symbol: a dark red star for “progenitor-like” RNDs, a red star for “true” MexN-like proteins, a blue star for MdtB-like proteins and an orange star for MdtC-like proteins). The open symbols provide the genomic context for the RNDs. For example, in the second row, *Thiobacillus denitrificans*, the lack of symbols under “MdtABC” means there are no proteins from this group present in this organism. Further to the right under “MexMN”, an open green square means there is an OMP present, followed by an MFP (an open purple triangle), and an RND (a closed star). Lack of symbols under “OMP” and “MFS” means there are no further proteins in this set of genes.
A closer look into the Mdt cluster reveals the evolutionary history of the subfamily

As observed in the analysis of all RNDs (Fig 1), the MexN-like proteins clustered together with MdtB- and MdtC-like proteins (Fig 2). However, an interesting observation was that the MexN-like proteins were divided into two distinct groups. The first group was formed by MexN-like proteins from strains that also contained an MdtBC system. These MexN-like proteins clustered together with MdtB-like proteins, suggesting their common evolutionary origin (i.e. these MexN-like proteins and MdtB-like proteins are descendant from one of the originally duplicated genes). The second group was formed by MexN-like proteins from strains that did not contain an MdtBC system, and these MexN-like proteins separated from the rest of the tree before the split between MdtB- and MdtC-like proteins. Because this second group of RNDs split earliest from the rest, it is likely that they are directly descendant from the progenitor single RND, and no gene duplication occurred during their evolution. Since this subset of MexN-like proteins never underwent the gene duplication event, we subsequently named them “progenitor-like” RNDs in order to distinguish them from the “true” MexN-like proteins, with “true” meaning here “clustering together with P. aeruginosa MexN and therefore having the same evolutionary history”.

The “progenitor-like” RND group contained all Deltaproteobacterial sequences represented in our analysis, as well as the only sequence from a non-Proteobacterium, Gloeobacter violaceus, a Cyanobacterium (Fig 2). The fact that these “progenitor-like” RNDs did not cluster together with known MdtB- and MdtC-like proteins suggests they are direct descendants of the ancient common ancestor of the whole Mdt cluster, the progenitor gene. We also performed searches for MdtB- and MdtC-like proteins (i.e. having sequence similarity at least 40%) in Deltaproteobacteria and found only three hits, suggesting the MdtBC-like systems are virtually
absent in these two groups. A number of Alpha- and Betaproteobacterial orders contained the “progenitor-like” RNDs, but no Gammaproteobacteria did. Interestingly, all the Alpha- and Betaproteobacterial representants can fix nitrogen and/or reduce nitrate, suggesting a common habitat [26]. The fact that all the older bacterial lineages appeared in this group suggests that the original gene duplication that produced MdtB- and MdtC-like proteins occurred in the common ancestor of the Alpha-, Beta- and Gammaproteobacteria, around the end of the Archean Eon [25], and the sporadic occurrence of a “progenitor-like” RND in Alpha- and Betaproteobacteria is more likely a result of a horizontal gene transfer.

The rest of the RNDs formed two groups, with all the MdtB-like proteins in one and all the MdtC-like proteins in the other. Noticeably, the “true” MexN-like proteins clustered together with the MdtB-like proteins. This observation suggested the MexN separation happened after the original gene duplication that formed MdtB and MdtC from the progenitor RND gene. In general, the branching of both MdtB and MdtC groups was similar: Alphaproteobacteria separated earliest (with the exception of Gluconobacter oxydans and Zymomonas mobilis, see below), and then Beta- and Gammaproteobacteria. Surprisingly, the Gammaproteobacterial order Xanthomonodales separated together with Alphaproteobacteria (both in the MdtB- and the MdtC-like groups, with moderate to low bootstrap support, however). In Alphaproteobacteria, homologs of MdtBC/MexN were numerously found only in orders Rhizobiales and Rhodospirillales, and sporadically in a few other orders. In Betaproteobacteria, homologs of MdtBC/MexN were widespread and found in all major orders, and in Gammaproteobacteria homologs of MdtBC/MexN were found in most orders. In all three major Proteobacterial families there were examples of closely related species and strains where one contained MdtBC, MexN or both, and the other with no MdtBC/MexN homologs. In many organisms it was also suspected the process of losing the RND pumps was
ongoing. For instance, in *Shigella flexneri, Serratia marcescens, Pseudomonas syringae pv tomato* and *Magnetospirillum magneticum* an MdtB was missing; in *Salmonella paratyphi A* an MFP was missing; and in *Burkholderia mallei* the whole MdtABC operon was absent (see Supporting Information for details).

The genomic neighborhoods provided additional insights into the evolutionary history of the Mdt systems. Among the MdtBC systems, many contained OMP components, and the architecture was conserved in the main groups: in Alphaproteobacteria the OMP preceded the MFP, and in Beta- and Gammaproteobacteria it followed the MdtC protein. It is likely that the OMP components were acquired after the original gene duplication and this acquisition happened separately, once in Alphaproteobacteria, and once in a common ancestor to Beta- and Gammaproteobacteria, and in many cases it was subsequently lost (see Supporting information for details). Moreover, all *Enterobacterales* possessed an additional inner membrane protein from the Major Facilitator Superfamily (MFS), called MdtD in *E. coli*, an iron and citrate exporter [27], and no outer membrane proteins. The order *Enterobacterales* is an example of how the outer membrane channel function had converged on just one protein (e.g. TolC in *E. coli*), and the redundant outer membrane components of RND systems are removed from the genomes (with the exception of specialized functions, e.g. *E. coli* CusC as an outer membrane component for the Cu-exporting Cus system). The outer membrane proteins were also missing in the order *Xanthomonodales* and sporadically in other organisms. Notably, the *Burkholderia* MexMNs also contained an MFS, not related to other MFSs observed here.

**Horizontal gene transfers**

The exception to the observation that organisms containing a “progenitor-like” RND did not contain an MdtBC system occurred in *Cupriavidus pinatubonensis* (*Betaproteobacteria*, order
Burkholderiales, and one of two strains of *Rhodopseudomonas palustris*, namely strain HaA2 (Alphaproteobacteria, order Rhizobiales). These two organisms possessed both an MdtBC-like system, similar to other Proteobacteria in their respective groups, and a “progenitor-like” RND, likely a result of a horizontal gene transfer. The *C. pinatubonensis* RND showed close similarity to an RND from *Nitrosospira multiformis*, a distantly related Betaproteobacterium (order Nitrosomonadales), and their “progenitor-like” RNDs grouped together with other “progenitor-old” RNDs. The *R. palustris* HaA2 strain possibly lost the original MexN-like system and incorporated a “progenitor-like” RND, judging from its genomic contexts (see Supporting information). The other *R. palustris* strain, ATCC BAA-871, did not contain a “progenitor-like” RND system, and its other MdtBC- and MexN-like proteins behaved as its relatives in other Alphaproteobacteria.

A number of sequences originally clustering with other Mdts in Fig 1 did not align well and in consequence showed poor or unresolved phylogeny with low bootstrap values regardless of the methods used and were therefore removed from the analysis prior to the results shown in Fig 2. These sequences are described in the Supporting information.

Proteins from two Alphaproteobacteria, *Gluconobacter oxydans* and *Zymomonas mobilis*, did not cluster together with other Alphaproteobacterial Mdts, but were found closest to respective proteins from the order Burkholderia. While the long branches observed for all four proteins as well as moderate bootstrap values might render this clustering less reliable, it is possible those two organisms had lost their original Mdts and acquired new ones via horizontal gene transfer. Moreover, *G. oxydans* possesses a third protein with high sequence similarity to its own MdtC (not shown in Fig 2, see Supporting information). It is likely a result of a discrete gene duplication, particularly since this third gene does not possess an MFP.
As mentioned above, the order *Xanthomonadales* clustered somewhat reliably with Alphaproteobacteria, both in MdtB- and MdtC-like groups. They did not possess a third RND, either a “true” MexN-like protein or a “progenitor-like” RND. Since they separated the earliest from other Gammaproteobacteria, it is possible their ancestors lost both their original MdtABC and MexMN systems, and subsequently incorporated an MdtABC from an Alphaproteobacterium [28].

**Reconstructing the MdtABC/MexMN evolution**

The results described here, together with analysis of corresponding MFPs (see Supporting information) made it possible to propose an evolutionary scenario for the appearance of MdtBC and MexN pumps (Fig 3). The original RND progenitor gene underwent a duplication in the common ancestor to Alpha-, Beta- and Gammaproteobacteria, while remaining single in other bacterial groups (as “progenitor-like” RNDs). The MFP and the adjacent RND were duplicated, forming the “true” MexMN system. In the next step an OMP was acquired, and was inserted before the MFP in Alphaproteobacteria, or after the MdtC in the common ancestor to the Beta- and Gammaproteobacteria. From these points many organisms lost the MexMN system. In Alphaproteobacteria only two orders represented in Figs 1 and 2 retained the original genes. Many Betaproteobacteria retained the OMPs (occurring always after the MdtCs) but lost the duplicated MexMN, with the exception of the *Burkholderia* genus, which lost the OMPs, but retained the MexMN and also gained an MFS next to it. In Gammaproteobacteria the configuration was generally kept intact, with the exception of *Enterobacteriales*, which lost the MexMN and incorporated an MFS into its MdtABC operon.
Fig 3. The proposed evolutionary scenario. The evolution within the Alpha-, Beta- and Gamma-proteobacteria groups is shown, as deduced from the phylogenetic tree in Fig 2 and a timeline of evolution of Proteobacteria (Battistuzzi, Feijao and Hedges 2004). The cladograms lengths and timepoints of evolutionary events are not to scale. As an example of horizontal gene transfer, Cupriavidus pinatubonensis is also shown.
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**Supporting information**

S1 File. Supporting information containing the list of used sequences, as well as detailed discussion, is available.
Figure 3
Supplementary material

**Horizontal Gene Transfer**

*Rhodopseudomonas palustris* strains

As described in the main text, the two *Rhodopseudomonas palustris* strains differ in their single subunit RND systems. The CGA009 strain looks like its close relatives from other Alphaproteobacteria (an MdtBC and an MexN), and the HaA2 strain contains a “progenitor-like” RND. The Supplementary Figure 1 below shows the two locations in their genomes where the corresponding deletion and insertion occurred.

Supplementary Figure 1. Alignment of genomes of the two strains of *Rhodopseudomonas palustris*. Upper panel, a spot where the MexN was lost in the strain HaA2. Lower panel, an insertion point of the “progenitor-like” RND.
Supplementary Figure 2. Sequence alignment of the translated DNA between the MdtA and MdtC in the P. aeruginosa strain lacking MdtB, and the MdtB from the most closely related P. aeruginosa (PSEU2).
Loss of MdtABC in Some Organisms

Some organisms are in the process of losing one of the Mdt components. As an example, in Supplementary Figure 2 we show the translated DNA from between the mdtA and mdtC from *Pseudomonas syringae pv tomato* strain ATCC BAA-87, compared to the MdtB sequence from the most closely related *Pseudomonas syringae pv syringae* strain B728a. Up until amino acid 318 the sequences are practically identical, and afterwards they differ radically. Interestingly, the lost component was always an MdtB, suggesting the MdtC alone can retain some of the function, as suggested in the literature.

Removed Sequences

Sequences that were removed prior to obtaining results shown in Figure 2 are: *Acinetobacter baylyi* Q6FD21, Q6FD22, Q6F786, Q6F787; *Gluconobacter oxydans* Q5FSC3; *Mesorhizobium japonicum* Q98B06; *Bradyrhizobium diaeofficiens* Q89XN1. They proved to be difficult to align to other RNDs, and thus their positions in the trees were highly sensitive to the methods used, and it is therefore possible these proteins are fusions of distantly related RNDs. Rerunning the analysis without these seven sequences significantly improved the bootstrap values of the tree, therefore we decided to exclude them from the main analysis.

*Acinetobacter baylyi* contains two sets of RND protein pairs, Q6FD21 & Q6FD22, and Q6F786 & Q6F787. Judging just by their genomic neighborhood they are both two RND subunit containing systems of similar architecture: MFP-RND1-RND2-OMP. The sequence identity and similarity values between the two systems in *A. baylyi* are low (52/69% and 40/57% for the corresponding B and C-like proteins), however, the Q6F786/Q6F787 system is most closely related to the MdtBC system from *Chromobacterium violaceum*, a Betaproteobacterium (67% and 63% sequence
identity and 79% and 76% sequence similarity between the corresponding B and C-like proteins). This observation, together with the fact that no close homologues of the Q6F786/Q6F787 system were found in other Acinetobacter while it is abundant in Chromobacteriaceae suggests a horizontal gene transfer from C. violaceum or a close relative. The other pair, Q6FD21/Q6FD22, clustered together with other Gammaproteobacteria, however its actual placement was strongly sensitive to even the smallest variations in the sequence alignments. The other two sequences (from M. japonicum and B. diazoefficiens) usually clustered together with “true” MexN-like proteins, yet with low bootstrap values and long branches. They are most likely results of a gene duplication of their respective “true” MexN-like proteins.

**Outer Membrane Proteins**

It is particularly difficult to do phylogenetic analyses of outer membrane proteins due to their unique architecture: the outwards facing transmembrane residues are never strongly conserved, seriously decreasing the number of residues available for alignment. Moreover, most outer membrane proteins have similar 3D structure despite high divergence in sequences. Nevertheless, our analysis of the outer membrane factors from the Mdt/Mex systems supports the evolutionary scenario proposed in Figure 3. As shown in Supplementary Figure 3, the OMFs of the “progenitor-like” RNDs separate first from the rest, followed by Alpha OMFs. The rest was Beta and Gammaproteobacteria, and the branching follows the one seen in Figure 2.
Supplementary Figure 3. A phylogenetic tree of outer membrane factors from the Mdt/Mex systems, rooted on distantly related TolC from E. coli.

Membrane Fusion Proteins

As a complement to the analysis of the RND proteins, their corresponding MFPs were aligned, and phylogeny reconstructed (Supplementary Figure 4). However, due to their shorter lengths and lower conservation levels the results were less reliable and therefore excluded from the main text. Nevertheless, the general conclusion is similar to the one obtained by comparing RNDs: the “progenitor-like” RNDs separate earliest from the rest.
Supplementary Figure 4. A phylogenetic tree of membrane fusion proteins, rooted on distantly related E. coli AcrA. The annotations are the same as in Fig. 2.
### Sequences used for the analysis

| Name        | Organism                                           | Description                                           |
|-------------|----------------------------------------------------|-------------------------------------------------------|
| A0A0F7RLT4  | Bacillus anthracis.                               | Transporter | AcrB/AcrD/AcrF family                      |
| A0A0H2UYQ5  | Shigella flexnerii.                               | Efflux pump membrane transporter                      |
| A0A0H2V123  | Shigella flexnerii.                               | Efflux pump membrane transporter                      |
| A0A0H2V4W9  | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Efflux pump membrane transporter                      |
| A0A0H2V703  | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Efflux pump membrane transporter                      |
| A0A0H2V9F8  | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Efflux pump membrane transporter                      |
| A0A0H2VBM4  | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Efflux pump membrane transporter                      |
| A0A0H2VIZ4  | Staphylococcus epidermidis (strain ATCC 12228)     | Acriflavin resistance protein                        |
| A0A0H2W6E0  | Yersinia pestis.                                   | Efflux pump membrane transporter                      |
| A0A0H2WBD9  | Burkholderia mallei (strain ATCC 23344)           | Heavy metal efflux pump CzcA                         |
| A0A0H2WCV6  | Burkholderia mallei (strain ATCC 23344)           | Hydrophobe/amphiphile efflux family protein          |
| A0A0H2WD52  | Burkholderia mallei (strain ATCC 23344)           | Efflux pump membrane transporter                      |
| A0A0H2WG76  | Burkholderia mallei (strain ATCC 23344)           | AcrB/AcrD/AcrF family protein                        |
| A0A0H2WHE9  | Burkholderia mallei (strain ATCC 23344)           | Heavy metal efflux pump CzcA family                  |
| A0A0H2WHU3  | Burkholderia mallei (strain ATCC 23344)           | Efflux pump membrane transporter                      |
| A0A0H2WIU9  | Burkholderia mallei (strain ATCC 23344)           | AcrB/AcrD/AcrF family protein                        |
| A0A0H2WN05  | Salmonella paratyphi A (strain ATCC 9150 / SARB42) | Efflux pump membrane transporter                      |
| A0A0H2WS58  | Salmonella paratyphi A (strain ATCC 9150 / SARB42) | Efflux pump membrane transporter                      |
| A0A0H2WTM3  | Salmonella paratyphi A (strain ATCC 9150 / SARB42) | Efflux pump membrane transporter                      |
| A0A0H2WW53  | Staphylococcus aureus (strain COL)                 | AcrB/AcrD/AcrF family protein                        |
| A0A0H2X3D6  | Xanthomonas campestris pv. campestris (strain 8004) | Cation efflux system protein                         |
| A0A0H2X4R2  | Xanthomonas campestris pv. campestris (strain 8004) | Acriflavin resistance protein                        |
| A0A0H2X699  | Xanthomonas campestris pv. campestris (strain 8004) | Efflux pump membrane transporter                      |
| A0A0H2X729  | Xanthomonas campestris pv. campestris (strain 8004) | Transport protein                                    |
| A0A0H2X7G8  | Xanthomonas campestris pv. campestris (strain 8004) | Efflux pump membrane transporter                      |
| A0A0H2X8U8  | Xanthomonas campestris pv. campestris (strain 8004) | Transport protein                                    |
| A0A0H2XAS3  | Xanthomonas campestris pv. campestris (strain 8004) | Efflux pump membrane transporter                      |
| Accession | Organism/Microorganism and Strain | Protein Description |
|-----------|----------------------------------|---------------------|
| A0A0H2XBS4 | Xanthomonas campestris pv. campestris (strain 8004) | Acriflavin resistance protein |
| A0A0H2XE02 | Xanthomonas campestris pv. campestris (strain 8004) | Cation efflux system protein |
| A0A0H3G1R6 | Brucella suis biovar 1 (strain 1330) | AcrB/AcrD/AcrF multidrug efflux protein |
| A0A0H3G714 | Brucella suis biovar 1 (strain 1330) | AcrB/AcrD/AcrF multidrug efflux protein |
| A0A0H3GFZ4 | Brucella suis biovar 1 (strain 1330) | AcrB/AcrD/AcrF multidrug efflux protein |
| A0A0H3JMN8 | Escherichia coli O157:H7. | Efflux pump membrane transporter |
| A0A0H3JN48 | Staphylococcus aureus (strain N315) | SA2056 protein |
| A0A0H3K0N2 | Staphylococcus aureus (strain Mu50 / ATCC 700699) | Similar to acriflavin resistance protein |
| A0A0H3K3Z1 | Synechococcus sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1) | RND multidrug efflux transporter |
| A0A0H3K464 | Staphylococcus aureus (strain MW2) | MW2179 protein |
| A0A0H3K4S1 | Synechococcus sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1) | Probable cation efflux system protein |
| A0A0H3LLX7 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | Efflux pump membrane transporter |
| A0A0H3LQU0 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | Efflux pump membrane transporter |
| A0A0H3LQV1 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | AcrB/AcrD/AcrF family protein |
| A0A0H3LT18 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | Efflux pump membrane transporter |
| A0A0H3LT9 | Bartonella quintana (strain Toulouse) | Acriflavin resistance protein d |
| A0A0H3LUJ4 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | Integral membrane component of multidrug efflux system |
| A0A0H3LWT2 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | Probable membrane protein |
| A0A0H3LZH6 | Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) | AcrB/AcrD/AcrF family protein |
| A0A0H3M8G5 | Ehrlichia ruminantium (strain Welgevonden) | Probable aminoglycoside efflux pump (Acriflavine resistance protein D) |
| A0A0R4J7B3 | Bartonella henselae (strain ATCC 49882 / DSM 28221 / Houston 1) | Acriflavin resistance protein d |
| O06471 | Burkholderia cepacia | Efflux pump membrane transporter |
| O25328 | Helicobacter pylori (strain ATCC 700392 / 26695) | Acriflavin resistance protein (AcrB) |
| O25622 | Helicobacter pylori (strain ATCC 700392 / 26695) | Cation efflux system protein (CzcA) |
| O25887 | Helicobacter pylori (strain ATCC 700392 / 26695) | Cation efflux system protein (CzcA) |
| O31100 | Pseudomonas putida | Solvent-resistant pump membrane transporter SrpB |
| O31501 | Bacillus subtilis (strain 168) | Swarming motility protein SwrC |
| O52248 | Pseudomonas putida (strain DOT-T1E) | Toluene efflux pump membrane transporter TtgB |
| O66770 | Aquifex aeolicus (strain VFS) | Cation efflux system (AcrB/AcrD/AcrF family) |
| Accession | Organism                                      | Description                                      |
|-----------|----------------------------------------------|--------------------------------------------------|
| O66916    | Aquifex aeolicus (strain VF5)                | Cation efflux system (AcrB/AcrD/AcrF family)    |
| O66977    | Aquifex aeolicus (strain VF5)                | Cation efflux (AcrB/AcrD/AcrF family)           |
| O68962    | Helicobacter pylori                          | RND pump protein                                 |
| O87936    | Burkholderia pseudomallei                   | Efflux pump membrane transporter                 |
| POC070    | Pseudomonas putida                           | Multidrug/solvent efflux pump membrane transporter MepB |
| P13511    | Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34) | Cobalt-zinc-cadmium resistance protein CzcA |
| P24177    | Escherichia coli (strain K12)                | Probable aminoglycoside efflux pump              |
| P24181    | Escherichia coli (strain K12)                | Multidrug export protein AcrF                    |
| P25197    | Rhizobium meliloti (strain 1021)             | Nodulation protein NoL G                         |
| P31224    | Escherichia coli (strain K12)                | Multidrug efflux pump subunit AcrB               |
| P37637    | Escherichia coli (strain K12)                | Multidrug resistance protein MdtF                |
| P37972    | Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34) | Nickel and cobalt resistance protein CnrA        |
| P38054    | Escherichia coli (strain K12)                | Cation efflux system protein CusA                |
| P52002    | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 /JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Multidrug resistance protein MexB                |
| P69340    | Shigella flexneri.                           | Multidrug resistance protein MdtB                |
| P73998    | Synechocystis sp. (strain PCC 6803 / Kazusa) | Cation or drug efflux system protein             |
| P74461    | Synechocystis sp. (strain PCC 6803 / Kazusa) | Cation or drug efflux system protein             |
| P76398    | Escherichia coli (strain K12)                | Multidrug resistance protein MdtB                |
| P76399    | Escherichia coli (strain K12)                | Multidrug resistance protein MdtC                |
| P94177    | Alcaligenes sp. (strain CT14)                | Cation efflux system protein CusA                |
| P95422    | Pseudomonas aeruginosa.                      | Efflux pump membrane transporter                 |
| Q2IGB6    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Heavy metal efflux pump CzcA                     |
| Q2IGC8    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2IGK2    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2IHW6    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2JG5     | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2IK25    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2IMH0    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein                    |
| Q2INB4    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Efflux pump membrane transporter                 |
| Q2IPR5    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Heavy metal efflux pump CzcA                     |
| Accession | Organism/Strain | Protein Function |
|-----------|----------------|-----------------|
| Q2IQ78    | Anaeromyxobacter dehalogenans (strain 2CP-C) | Acriflavin resistance protein |
| Q2IS23    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IS29    | Rhodopseudomonas palustris (strain HaA2) | Heavy metal efflux pump CzcA |
| Q2IS98    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2ISU1    | Rhodopseudomonas palustris (strain HaA2) | Efflux pump membrane transporter |
| Q2ITW6    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IU06    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IU55    | Rhodopseudomonas palustris (strain HaA2) | Heavy metal efflux pump CzcA |
| Q2IUUK7   | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IW07    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IW08    | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IWLF2   | Rhodopseudomonas palustris (strain HaA2) | Acriflavin resistance protein |
| Q2IWZ0    | Rhodopseudomonas palustris (strain HaA2) | Efflux pump membrane transporter |
| Q2IXW6    | Rhodopseudomonas palustris (strain HaA2) | Efflux pump membrane transporter |
| Q2J147    | Rhodopseudomonas palustris (strain HaA2) | Heavy metal efflux pump CzcA |
| Q2JZ12    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable efflux transporter protein| acriflavin resistance protein family |
| Q2K1A4    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable efflux cation transporter protein |
| Q2K3Z4    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable multidrug efflux transporter protein |
| Q2K4R7    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Efflux pump membrane transporter |
| Q2K4W2    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Efflux pump membrane transporter |
| Q2K4X5    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Efflux pump membrane transporter |
| Q2K6F6    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable acriflavin resistance (Multidrug efflux transporter) protein |
| Q2K7A2    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable cation efflux system protein (Heavy metal efflux pump) | CzcA family |
| Q2KAM7    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable multidrug efflux transporter protein| AcrB/AcrD/AcrF family |
| Q2KCU0    | Rhizobium etli (strain CFN 42 / ATCC 51251) | Probable cation/multidrug efflux transport protein |
| Q2KUN1    | Bordetella avium (strain 197N) | Multidrug efflux system transmembrane protein |
| Q2KUN3    | Bordetella avium (strain 197N) | Multidrug efflux system transmembrane protein |
| Q2KV59    | Bordetella avium (strain 197N) | Multidrug efflux system transmembrane protein |
| Q2KKM0    | Bordetella avium (strain 197N) | Efflux pump membrane transporter |
| Q2K2R5    | Bordetella avium (strain 197N) | Efflux pump membrane transporter |
| Q2L1H0    | Bordetella avium (strain 197N) | Efflux pump membrane transporter |
| Q2LDR7    | Syntrophus aciditrophicus (strain SB) | Efflux pump membrane transporter |
| Q2LY61    | Syntrophus aciditrophicus (strain SB) | Efflux pump membrane transporter |
| Accession | Organism / Strain | Function |
|-----------|-------------------|----------|
| Q2NBE8   | Erythrobacter litoralis (strain HTCC2594) | Heavy metal RND efflux transporter | CzcA family protein |
| Q2NBG2   | Erythrobacter litoralis (strain HTCC2594) | Metal ion efflux RND protein family protein |
| Q2NV66   | Sodalis glossinidius (strain morisitans) | Efflux pump membrane transporter |
| Q2RFY8   | Moorella thermoacetica (strain ATCC 39073 / JCM 9320) | Acriflavin resistance protein |
| Q2RN02   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Acriflavin resistance protein |
| Q2RQ71   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Acriflavin resistance protein |
| Q2RSK1   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Acriflavin resistance protein |
| Q2RSP4   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Efflux pump membrane transporter |
| Q2RVC6   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Efflux pump membrane transporter |
| Q2RW08   | Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1) | Efflux pump membrane transporter |
| Q2RYR4   | Salinibacter ruber (strain DSM 13855 / M31) | Cation efflux system protein czcA |
| Q2S141   | Salinibacter ruber (strain DSM 13855 / M31) | Transporter | AcrB/D/F family |
| Q2S3C4   | Salinibacter ruber (strain DSM 13855 / M31) | Acriflavine resistance protein (Cation efflux system) |
| Q2S4L8   | Salinibacter ruber (strain DSM 13855 / M31) | Multidrug resistance protein | putative |
| Q2SSB3   | Salinibacter ruber (strain DSM 13855 / M31) | Multidrug efflux transporter | AcrB/AcrD/AcrF family |
| Q2SSQS   | Salinibacter ruber (strain DSM 13855 / M31) | Cation-multidrug efflux pump |
| Q2S6E3   | Salinibacter ruber (strain DSM 13855 / M31) | Transporter | AcrB/D/F family |
| Q2S716   | Hahella chejuensis (strain KCTC 2396) | Efflux pump membrane transporter |
| Q2S728   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SB32   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SET3   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SF27   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SFQ4   | Hahella chejuensis (strain KCTC 2396) | Efflux pump membrane transporter |
| Q2SFT2   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SHT7   | Hahella chejuensis (strain KCTC 2396) | Putative silver efflux pump |
| Q2SJY0   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SM00   | Hahella chejuensis (strain KCTC 2396) | Cation-multidrug efflux pump |
| Q2SUM0   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | AcrB/AcrD/AcrF family protein |
| Accession | Organism                                      | Protein Description                                      |
|-----------|-----------------------------------------------|----------------------------------------------------------|
| Q2S9T4   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Efflux pump membrane transporter                          |
| Q2S9W90  | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | AcrB/AcrD/AcrF family protein                            |
| Q2S9X70  | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | AcrB/AcrD/AcrF family protein                            |
| Q2T9R2   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Efflux pump membrane transporter                          |
| Q2T3F6   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Efflux pump membrane transporter                          |
| Q2T5H8   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Heavy metal efflux pump CzcA                              |
| Q2T5R6   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Hydrophobe/amphiphile efflux family protein              |
| Q2T618   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Heavy metal efflux pump CzcA| putative                                    |
| Q2T989   | Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264) | Transporter | AcrB/D/F family                                   |
| Q2W1N8   | Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) | Cation/multidrug efflux pump                             |
| Q2W1P6   | Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) | Efflux pump membrane transporter                          |
| Q2W1Q9   | Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) | Cation/multidrug efflux pump                             |
| Q2W646   | Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) | Efflux pump membrane transporter                          |
| Q2W7X3   | Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) | Putative silver efflux pump                              |
| Q2Y770   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Cobalt-zinc-cadmium resistance protein CzcA               |
| Q2Y7K6   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Acriflavin resistance protein                             |
| Q2Y896   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Efflux pump membrane transporter                          |
| Q2Y8I2   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Cobalt-zinc-cadmium resistance protein CzcA               |
| Q2Y962   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Cu(I)/Ag(I) efflux system membrane protein CusA/SilA      |
| Q2Y9A05  | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Cobalt-zinc-cadmium resistance protein CzcA               |
| Q2YAR7   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Efflux pump membrane transporter                          |
| Q2YB73   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Efflux pump membrane transporter                          |
| Q2YB76   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Efflux pump membrane transporter                          |
| Q2YD19   | Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849 / C 71) | Efflux pump membrane transporter                          |
| Q2YIU1   | Brucella abortus (strain 2308)                 | Acriflavin resistance protein                             |
| Q2YPC8   | Brucella abortus (strain 2308)                 | Acriflavin resistance protein                             |
| Accession | Organism/Genotype | Function/Description |
|-----------|-------------------|---------------------|
| Q2YPE6    | Brucella abortus (strain 2308) | Efflux pump membrane transporter |
| Q2YPZ1    | Brucella abortus (strain 2308) | Acriflavin resistance protein |
| Q2Z053    | uncultured bacterium. | Heavy metal efflux pump |
| Q30B59    | Acinetobacter sp. 4365. | Efflux pump membrane transporter |
| Q30NZ6    | Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) | Resistance-Nodulation-Cell Division Superfamily transporter |
| Q30QL4    | Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) | Resistance-Nodulation-Cell Division Superfamily transporter |
| Q30S70    | Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) | Resistance-Nodulation-Cell Division Superfamily transporter |
| Q30T66    | Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) | Efflux pump membrane transporter |
| Q311N6    | Desulfovibrio alaskensis (strain G20) | Acriflavin resistance protein |
| Q313Y0    | Desulfovibrio alaskensis (strain G20) | Acriflavin resistance protein |
| Q315C5    | Desulfovibrio alaskensis (strain G20) | Acriflavin resistance protein |
| Q315P7    | Desulfovibrio alaskensis (strain G20) | Acriflavin resistance protein |
| Q316E4    | Desulfovibrio alaskensis (strain G20) | Efflux pump membrane transporter |
| Q31DT9    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31E33    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31EH5    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31EQ3    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31EX8    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31FE9    | Hydrogenovibrio crunogenus (strain XCL-2) | Efflux pump membrane transporter |
| Q31FQ2    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31J34    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31JL9    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily transporter |
| Q31JR8    | Hydrogenovibrio crunogenus (strain XCL-2) | Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter |
| Q31KM0    | Synechococcus elongatus (strain PCC 7942) | Hydrophobe/amphiphile efflux-1 HAE1 |
| Q31M20    | Synechococcus elongatus (strain PCC 7942) | Probable cation efflux system protein |
| Q31VB1    | Shigella boydii serotype 4 (strain Sb227) | Efflux pump membrane transporter |
| Q31W02    | Shigella boydii serotype 4 (strain Sb227) | Efflux pump membrane transporter |
| Q323D9    | Shigella boydii serotype 4 (strain Sb227) | Multidrug resistance protein MdtC |
| Q323E0    | Shigella boydii serotype 4 (strain Sb227) | Multidrug resistance protein MdtB |
| Q324W8    | Shigella boydii serotype 4 (strain Sb227) | Putative inner membrane component for iron transport |
| Q325D4    | Shigella boydii serotype 4 (strain Sb227) | Efflux pump membrane transporter |
| Accession | Organism & Strain | Function & Description |
|-----------|------------------|-----------------------|
| Q32AZ2    | Shigella dysenteriae serotype 1 (strain Sd197) | Efflux pump membrane transporter |
| Q32DA0    | Shigella dysenteriae serotype 1 (strain Sd197) | Efflux pump membrane transporter |
| Q32GN8    | Shigella dysenteriae serotype 1 (strain Sd197) | Efflux pump membrane transporter |
| Q32J42    | Shigella dysenteriae serotype 1 (strain Sd197) | Efflux pump membrane transporter |
| Q392S4    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Heavy metal efflux pump | CzcA family |
| Q395M1    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Acriflavin resistance protein |
| Q397Q3    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q398J2    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39AU9    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39DD3    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39FY6    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Acriflavin resistance protein |
| Q39G27    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39GQ3    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39I14    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Acriflavin resistance protein |
| Q39NU6    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39PF8    | Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB9086 / R18194 / 383) | Efflux pump membrane transporter |
| Q39PW0    | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump | RND family | inner membrane protein |
| Q39QY3    | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump | RND family | inner membrane protein |
| Q39SN5    | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump | RND family | inner membrane protein |
| Q39V29 | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump membrane transporter |
| Q39V41 | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump | RND family | inner membrane protein | AcrB/AcrD/AcrF family |
| Q39VE3 | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Metal ion efflux pump | RND family | inner membrane protein |
| Q39XH2 | Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) | Efflux pump membrane transporter |
| Q39X7 | Pelobacter carbinolicus (strain DSM 2380 / NBRC 103641 / GraBd1) | Efflux pump membrane transporter |
| Q3A2C4 | Pelobacter carbinolicus (strain DSM 2380 / NBRC 103641 / GraBd1) | Efflux pump | RND family | inner membrane protein | AcrB/AcrD/AcrF family |
| Q3A5K8 | Pelobacter carbinolicus (strain DSM 2380 / NBRC 103641 / GraBd1) | Efflux pump membrane transporter |
| Q3A6S9 | Pelobacter carbinolicus (strain DSM 2380 / NBRC 103641 / GraBd1) | Efflux pump membrane transporter |
| Q3A7U6 | Pelobacter carbinolicus (strain DSM 2380 / NBRC 103641 / GraBd1) | Efflux pump membrane transporter |
| Q3AR80 | Chlorobium chlorochromatii (strain CaD3) | Hydrophobe/amphiphile efflux-1 HAE1 |
| Q3ARZ1 | Chlorobium chlorochromatii (strain CaD3) | NolG efflux transporter |
| Q3AUC4 | Chlorobium chlorochromatii (strain CaD3) | AcrB/AcrD/AcrF family protein |
| Q3B1E0 | Chlorobium luteolum (strain DSM 273 / 2530) | AcrB/AcrD/AcrF family protein |
| Q3B4Q3 | Chlorobium luteolum (strain DSM 273 / 2530) | Hydrophobe/amphiphile efflux-1 HAE1 |
| Q3B4Z4 | Chlorobium luteolum (strain DSM 273 / 2530) | RND family efflux transporter |
| Q3BMM3 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BNG5 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BPY9 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BR79 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | Efflux pump membrane transporter |
| Q3BRC2 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BS5S | Xanthomonas campestris pv. vesicatoria (strain 85-10) | Efflux pump membrane transporter |
| Q3BSU9 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | Efflux pump membrane transporter |
| Q3BTF0 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BF01 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BTSS | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein |
| Q3BVE1 | Xanthomonas campestris pv. vesicatoria (strain 85-10) | Efflux pump membrane transporter |
| Accession | Organism                                      | Function                                      |
|-----------|-----------------------------------------------|-----------------------------------------------|
| Q3BYG6    | Xanthomonas campestris pv. vesicatoria (strain 85-10) | RND superfamily protein                        |
| Q3BYU5    | Xanthomonas campestris pv. vesicatoria (strain 85-10) | Efflux pump membrane transporter              |
| Q3ER77    | Bacillus thuringiensis serovar israelensis ATCC 35646. | Acriflavin resistance plasma membrane protein |
| Q3IBZ0    | Pseudoalteromonas haloplanktis (strain TAC 125) | Efflux pump membrane transporter              |
| Q3IC20    | Pseudoalteromonas haloplanktis (strain TAC 125) | Efflux pump membrane transporter              |
| Q3IC5     | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative metabolite exporter| AcrB/D/F family |
| Q3ICE4    | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative metabolite exporter| AcrB/D/F family |
| Q3IC5     | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative acrB/acrD.acrF acriflavin resistance family protein |
| Q3IK01    | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative multidrug resistance protein| AcrB/AcrD/AcrF family |
| Q3IK50    | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative transport protein                    |
| Q3ILD1    | Pseudoalteromonas haloplanktis (strain TAC 125) | Cation efflux system protein cusA             |
| Q3ILG7    | Pseudoalteromonas haloplanktis (strain TAC 125) | Cobalt-zinc-cadmium resistance protein czcA (Cation efflux system protein czcA) |
| Q3ILI6    | Pseudoalteromonas haloplanktis (strain TAC 125) | Putative multidrug resistance protein(AcrB/AcrD/AcrF family) |
| Q3IX11    | Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158) | Efflux pump membrane transporter              |
| Q3J0Q2    | Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158) | AcrB/AcrD/AcrF family cation/multidrug efflux pump |
| Q3J2H3    | Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158) | Multidrug/cation efflux pump| RND superfamily |
| Q3J2M9    | Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158) | Cation/multidrug efflux pump| RND superfamily |
| Q3J4A5    | Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158) | AcrB/AcrD/AcrF multidrug efflux pump          |
| Q3J715    | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Acriflavin resistance protein                 |
| Q3J9P1    | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Acriflavin resistance protein                 |
| Q3J451    | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Efflux pump membrane transporter              |
| Q3JX7     | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Heavy metal efflux pump                      |
| Q3JC12    | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Efflux pump membrane transporter              |
| Q3JEC3    | Nitrosococcus oceanii (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107) | Heavy metal efflux pump                      |
| Accession | Organism                                      | Function/Description                                                                 |
|-----------|-----------------------------------------------|-------------------------------------------------------------------------------------|
| Q3JEL4    | Nitrosococcus oceani (strain ATCC 19707 /    | Acriflavin resistance protein                                                        |
|           | BCRC 17464 / NCIMB 11848 / C-107)             |                                                                                     |
| Q3JER0    | Nitrosococcus oceani (strain ATCC 19707 /    | Heavy metal efflux pump                                                             |
|           | BCRC 17464 / NCIMB 11848 / C-107)             |                                                                                     |
| Q3JHF5    | Burkholderia pseudomallei (strain 1710b)     | Efflux pump membrane transporter                                                    |
| Q3JMG5    | Burkholderia pseudomallei (strain 1710b)     | Hydrophobe/amphiphile efflux family protein                                         |
| Q3JML3    | Burkholderia pseudomallei (strain 1710b)     | Heavy metal efflux pump CzcA                                                        |
| Q3JQU5    | Burkholderia pseudomallei (strain 1710b)     | AcrB/AcrD/AcrF family protein                                                       |
| Q3JRW2    | Burkholderia pseudomallei (strain 1710b)     | AcrB/AcrD/AcrF family protein                                                       |
| Q3JSK0    | Burkholderia pseudomallei (strain 1710b)     | Efflux pump membrane transporter                                                    |
| Q3JU49    | Burkholderia pseudomallei (strain 1710b)     | AcrB/AcrD/AcrF family protein                                                       |
| Q3JVH2    | Burkholderia pseudomallei (strain 1710b)     | Efflux pump membrane transporter                                                    |
| Q3JWX5    | Burkholderia pseudomallei (strain 1710b)     | Heavy metal efflux pump | CzcA family                            |
| Q3K755    | Pseudomonas fluorescens (strain Pf0-1)        | Putative AcrB/AcrD/AcrF family membrane protein                                     |
| Q3K7M4    | Pseudomonas fluorescens (strain Pf0-1)        | Integral membrane component of membrane efflux system                               |
| Q3KA45    | Pseudomonas fluorescens (strain Pf0-1)        | Cobalt-zinc-cadmium resistance membrane protein                                      |
| Q3KC70    | Pseudomonas fluorescens (strain Pf0-1)        | Efflux pump membrane transporter                                                    |
| Q3CK7     | Pseudomonas fluorescens (strain Pf0-1)        | Efflux pump membrane transporter                                                    |
| Q3CV6     | Pseudomonas fluorescens (strain Pf0-1)        | Efflux pump membrane transporter                                                    |
| Q3KD91    | Pseudomonas fluorescens (strain Pf0-1)        | Multidrug efflux system transmembrane protein                                       |
| Q3KD92    | Pseudomonas fluorescens (strain Pf0-1)        | Multidrug efflux system transmembrane protein                                       |
| Q3KDC9    | Pseudomonas fluorescens (strain Pf0-1)        | Putative efflux protein                                                             |
| Q3KDL7    | Pseudomonas fluorescens (strain Pf0-1)        | Heavy metal RND efflux transporter | CzcA family                            |
| Q3KGT4    | Pseudomonas fluorescens (strain Pf0-1)        | Efflux pump membrane transporter                                                    |
| Q3KH3     | Pseudomonas fluorescens (strain Pf0-1)        | Putative transport-related membrane protein                                         |
| Q3KIF5    | Pseudomonas fluorescens (strain Pf0-1)        | Integral membrane component of multidrug efflux system                              |
| Q3KJT0    | Pseudomonas fluorescens (strain Pf0-1)        | Putative transport-related membrane protein                                         |
| Q3M3V4    | Anabaena variabilis (strain ATCC 29413 /    | Acriflavin resistance protein                                                        |
|           | PCC 7937)                                     |                                                                                     |
| Q3M6E3    | Anabaena variabilis (strain ATCC 29413 /    | Hydrophobe/amphiphile efflux-1 HAE1                                                |
|           | PCC 7937)                                     |                                                                                     |
| Q3MA27    | Anabaena variabilis (strain ATCC 29413 /    | Acriflavin resistance protein                                                        |
|           | PCC 7937)                                     |                                                                                     |
| Q3RC69    | Xylella fastidiosa Dixon.                    | Efflux pump membrane transporter                                                    |
| Q3RC79    | Xylella fastidiosa Dixon.                    | Acriflavin resistance protein                                                        |
| Q3RDM8    | Xylella fastidiosa Dixon.                    | Acriflavin resistance protein                                                        |
| Q3SFX2    | Thiobacillus denitrificans (strain ATCC 25259)| Probable transmembrane drug efflux protein                                         |
| Accession | Organism | Function | Remarks |
|-----------|----------|----------|---------|
| Q3SGA0    | Thiobacillus denitrificans (strain ATCC 25259) | Acriflavin resistance protein |         |
| Q3SGH8    | Thiobacillus denitrificans (strain ATCC 25259) | Probable RND efflux transporter |         |
| Q3SI34    | Thiobacillus denitrificans (strain ATCC 25259) | Heavy metal efflux pump CzcA |         |
| Q3SJ00    | Thiobacillus denitrificans (strain ATCC 25259) | Efflux pump membrane transporter |         |
| Q3SJ81    | Thiobacillus denitrificans (strain ATCC 25259) | Heavy metal efflux pump CzcA |         |
| Q3SJ87    | Thiobacillus denitrificans (strain ATCC 25259) | Heavy metal efflux pump CzcA |         |
| Q3SKD0    | Thiobacillus denitrificans (strain ATCC 25259) | Heavy metal efflux pump CzcA |         |
| Q3SJ81    | Thiobacillus denitrificans (strain ATCC 25259) | Heavy metal efflux pump CzcA |         |
| Q3SMW3    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Heavy metal efflux pump CzcA |         |
| Q3SN60    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Acriflavin resistance protein |         |
| Q3SNI0    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Heavy metal efflux pump CzcA |         |
| Q3SNZ7    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Efflux pump membrane transporter |         |
| Q3SQA4    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Acriflavin resistance protein |         |
| Q3SSF8    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Acriflavin resistance protein |         |
| Q3SSF9    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Acriflavin resistance protein |         |
| Q3SSM3    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Heavy metal efflux pump CzcA |         |
| Q3ST65    | Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255) | Acriflavin resistance protein |         |
| Q3YRZ9    | Ehrlichia canis (strain Jake) | Acriflavin resistance protein |         |
| Q3YWI8    | Shigella sonnei (strain Ss046) | Efflux pump membrane transporter |         |
| Q3YZ83    | Shigella sonnei (strain Ss046) | Efflux pump membrane transporter |         |
| Q3ZOC8    | Shigella sonnei (strain Ss046) | Multidrug resistance protein MdtC |         |
| Q3ZOC9    | Shigella sonnei (strain Ss046) | Multidrug resistance protein MdtB |         |
| Q3Z4L7    | Shigella sonnei (strain Ss046) | Putative inner membrane component for iron transport |         |
| Q3Z4T7    | Shigella sonnei (strain Ss046) | Efflux pump membrane transporter |         |
| Q44586    | Alcaligenes xylosoxydans xylosoxydans | Nickel-cobalt-cadmium resistance protein NccA |         |
| Q46MN5    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Efflux pump membrane transporter |         |
| Accession | Organism                      | Protein Description                        |
|-----------|-------------------------------|-------------------------------------------|
| Q46PD4    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Heavy metal efflux pump CzcA               |
| Q46PF0    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q46T47    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Efflux pump membrane transporter           |
| Q46TT9    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Efflux pump membrane transporter           |
| Q46U60    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Heavy metal efflux pump CzcA               |
| Q46UM2    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Heavy metal efflux pump CzcA               |
| Q46VH3    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Heavy metal efflux pump CzcA               |
| Q46VN5    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Efflux pump membrane transporter           |
| Q46VQ1    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q46WR1    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Efflux pump membrane transporter           |
| Q470K2    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q472E0    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q474Q1    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q475I0    | Cupriavidus necator (strain JMP 134 / LMG 1197) | Acriflavin resistance protein              |
| Q479C5    | Dechloromonas aromatica (strain RCB)             | Efflux pump membrane transporter           |
| Q479J1    | Dechloromonas aromatica (strain RCB)             | Acriflavin resistance protein              |
| Q47AQ9    | Dechloromonas aromatica (strain RCB)             | Acriflavin resistance protein              |
| Q47BU3    | Dechloromonas aromatica (strain RCB)             | Acriflavin resistance protein              |
| Q47CA0    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47CS5    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47CT4    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47D66    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47DS9    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47DU2    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47E30    | Dechloromonas aromatica (strain RCB)             | Efflux pump membrane transporter           |
| Q47E0W    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47GU7    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47I6W    | Dechloromonas aromatica (strain RCB)             | Acriflavin resistance protein              |
| Q47IC6    | Dechloromonas aromatica (strain RCB)             | Heavy metal efflux pump CzcA               |
| Q47MJ1    | Thermobifida fusca (strain YX)                   | Putative integral membrane efflux protein  |
| Q47U52    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein              |
| Accession | Organism/Strain                                      | Description                                                                 |
|-----------|-----------------------------------------------------|------------------------------------------------------------------------------|
| Q47UM5    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | Cation efflux system protein CusA                                             |
| Q47V77    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q47VA5    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q47VP1    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q47X86    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q480E7    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | Heavy metal efflux pump | CzcA family                  |
| Q480Y8    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q483S5    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q483S7    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | Putative RND efflux system protein                                           |
| Q484D7    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q485I6    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | Efflux pump membrane transporter                                             |
| Q486B7    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | Efflux pump membrane transporter                                             |
| Q48815    | Legionella pneumophila.                              | Protein HelA                                                                 |
| Q488L9    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q48A59    | Colwellia psychrerythraea (strain 34H / ATCC BAA-681) | AcrB/AcrD/AcrF family protein                                               |
| Q48CG6    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Cation efflux family protein                                               |
| Q48EP3    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Efflux pump membrane transporter                                             |
| Q48HB1    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Transporter | AcrB/AcrD/AcrF family       |
| Q48HP4    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Efflux pump membrane transporter                                           |
| Q48IE8    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Multidrug RND efflux transporter | permease protein MdtC       |
| Q48IE9    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Multidrug RND efflux transporter | permease protein MdtB       |
| Q48J50    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Efflux pump membrane transporter                                           |
| Q48JE7    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | Efflux pump membrane transporter                                           |
| Q48MA9    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | RND efflux transporter | AcrB/AcrD/AcrF family       |
| Q48NJ4    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6) | RND efflux transporter | hydrophobe/amphiphile efflux-1 (HAE1) family   |
| Accession | Species                                                                 | Description                                                                                           |
|-----------|--------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|
| Q48PN7    | Pseudomonas savastanoi pv. phaseolicola (strain 1448A / Race 6)          | RND efflux transporter| hydrophobe/amphiphile efflux-1 (HAE1) family                                                        |
| Q49ZH9    | Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41) | Putative cation multidrug efflux pump                                                                 |
| Q4BYX0    | Crocosphaera watsonii WH 8501.                                            | Hydrophobe/amphiphile efflux-1 HAE1                                                                      |
| Q4C067    | Crocosphaera watsonii WH 8501.                                            | Hydrophobe/amphiphile efflux-1 HAE1                                                                      |
| Q4ECJ9    | Wolbachia endosymbiont of Drosophila ananassae.                          | MMPL family protein                                                                                      |
| Q4FP77    | Pelagibacter ubique (strain HTCC1062)                                    | RND superfamily multidrug efflux pump                                                                    |
| Q4FPX8    | Psychrobacter arcticus (strain DSM 17307 / 273-4)                        | Efflux pump membrane transporter                                                                            |
| Q4FRD4    | Psychrobacter arcticus (strain DSM 17307 / 273-4)                        | Efflux pump membrane transporter                                                                            |
| Q4K638    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Cobalt/zinc/cadmium resistance protein CzcA                                                                 |
| Q4K6K5    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| heavy metal efflux (HME) family| permease protein                                    |
| Q4KAL4    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| HAE1 family                                                    |
| Q4KBK7    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Efflux pump membrane transporter                                                                            |
| Q4KBN7    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Efflux pump membrane transporter                                                                            |
| Q4KCR6    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Multidrug RND efflux transporter| permease protein MdtC                                    |
| Q4KCR7    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Multidrug RND efflux transporter| permease protein MdtB                                    |
| Q4KDL8    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| heavy metal efflux (HME) family| permease protein                                    |
| Q4KH23    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | Efflux pump membrane transporter                                                                            |
| Q4KHJ4    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| hydrophobe/amphiphile efflux-1 (HAE1) family| permease protein                                    |
| Q4KHX4    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| HAE1 family                                                    |
| Q4KK49    | Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / PF-5)      | RND transporter| hydrophobe/amphiphile efflux-1 (HAE1) family| permease protein                                    |
| Q4L8C5    | Staphylococcus haemolyticus (strain JSC1435)                             | Uncharacterized protein                                                                                   |
| Q4LDT6    | Pseudomonas aeruginosa.                                                  | Efflux pump membrane transporter                                                                            |
| Q4LDT8    | Pseudomonas aeruginosa.                                                  | RND multidrug efflux transporter MexN                                                                    |
| Q4QM13    | Haemophilus influenzae (strain 86-028NP)                                  | Predicted cation/multidrug efflux pump                                                                  |
| Q4UKH1    | Rickettsia felis (strain ATCC VR-1525 / URRWxCal2)                       | Hydrophobe/amphiphile efflux-1 HAE1 family protein                                                      |
| Q4VSJ4    | Burkholderia glumae                                                     | Probable RND efflux transporter                                                                        |
| Accession | Species and Strain Information | Protein Type |
|-----------|--------------------------------|--------------|
| Q4ZLZ2    | Pseudomonas syringae pv. syringae (strain B728a) | Heavy metal efflux pump CzcA |
| Q4ZP84    | Pseudomonas syringae pv. syringae (strain B728a) | Efflux pump membrane transporter |
| Q4ZRQ8    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZS70    | Pseudomonas syringae pv. syringae (strain B728a) | Efflux pump membrane transporter |
| Q4ZSH1    | Pseudomonas syringae pv. syringae (strain B728a) | Efflux pump membrane transporter |
| Q4ZJ61    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZT99    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZTK0    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZU47    | Pseudomonas syringae pv. syringae (strain B728a) | Efflux pump membrane transporter |
| Q4ZUD5    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZXE0    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q4ZZK4    | Pseudomonas syringae pv. syringae (strain B728a) | Acriflavin resistance protein |
| Q51073    | Neisseria gonorrhoeae. | Efflux pump membrane transporter |
| Q51396    | Pseudomonas aeruginosa. | Efflux pump membrane transporter |
| Q55584    | Synechocystis sp. (strain PCC 6803 / Kazusa) | Cation or drug efflux system protein |
| Q55935    | Synechocystis sp. (strain PCC 6803 / Kazusa) | Cation or drug efflux system protein |
| Q57124    | Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) | Uncharacterized transporter HI_0895 |
| Q579D3    | Brucella abortus biovar 1 (strain 9-941) | AcrB/AcrD/AcrF multidrug efflux protein |
| Q57D49    | Brucella abortus biovar 1 (strain 9-941) | AcrB/AcrD/AcrF multidrug efflux protein |
| Q57F66    | Brucella abortus biovar 1 (strain 9-941) | Efflux pump membrane transporter |
| Q57F78    | Brucella abortus biovar 1 (strain 9-941) | AcrB/AcrD/AcrF multidrug efflux protein |
| Q57J78    | Salmonella choleraesuis (strain SC-B67) | Efflux pump membrane transporter |
| Q57LN0    | Salmonella choleraesuis (strain SC-B67) | Efflux pump membrane transporter |
| Q57MM4    | Salmonella choleraesuis (strain SC-B67) | Multidrug resistance protein MdtC |
| Q57MM5    | Salmonella choleraesuis (strain SC-B67) | Multidrug resistance protein MdtB |
| Q57S88    | Salmonella choleraesuis (strain SC-B67) | Efflux pump membrane transporter |
| Q58AF4    | Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34) | SilA| pump of the three components proton antiporter cation efflux system involved in silver| copper resistance |
| Q58AG2    | Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34) | NccA| three components proton antiporter cation efflux system| cation efflux pump |
| Q5DYC7    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Efflux pump membrane transporter |
| Accession | Species                                      | Description                                           |
|-----------|----------------------------------------------|-------------------------------------------------------|
| QSDZ19    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Efflux pump membrane transporter                      |
| QSE0D1    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Copper/silver efflux system | membrane component |
| QSE0L9    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSE1S7    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSE2W9    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSE4H0    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSE5L7    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSE8S3    | Aliivibrio fischeri (strain ATCC 700601 / ES114) | Acriflavin resistance plasma membrane protein         |
| QSF725    | Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090) | Efflux pump membrane transporter                      |
| QSGFX1    | Ehrlichia ruminantium (strain Gardel)        | Probable aminoglycoside efflux pump (Acriflavine resistance protein D) |
| QSGA83    | Gluconobacter oxydans (strain 621H)         | Cation efflux system protein CzcA                     |
| QST29     | Gluconobacter oxydans (strain 621H)         | Efflux pump membrane transporter                      |
| QSF7G4    | Gluconobacter oxydans (strain 621H)         | Heavy-metal ion transporter HelA                      |
| QSTX0     | Gluconobacter oxydans (strain 621H)         | Putative transport transmembrane protein             |
| QSFU14    | Gluconobacter oxydans (strain 621H)         | Acriflavin resistance protein D                       |
| QSG7J3    | Rhizobium etli.                              | Efflux pump membrane transporter                      |
| QSGV29    | Xanthomonas oryzae pv. oryzae (strain KACC10331 / KX085) | Acriflavin resistance protein                     |
| QSGC3     | Xanthomonas oryzae pv. oryzae (strain KACC10331 / KX085) | Acriflavin resistance protein                     |
| QSGZ12    | Xanthomonas oryzae pv. oryzae (strain KACC10331 / KX085) | Acriflavin resistance protein                     |
| QSH2K4    | Xanthomonas oryzae pv. oryzae (strain KACC10331 / KX085) | Acriflavin resistance protein                     |
| QSHLY7    | Staphylococcus epidermidis (strain ATCC 35984 / RP62A) | AcrB/AcrD/AcrF family protein               |
| QSI5O2    | Morganella morganii                          | Efflux pump membrane transporter                      |
| QSKWT2    | Geobacillus kaustophilus (strain HTA426)     | Hypothetical conserved protein                        |
| QSL7H0    | Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) | Putative transmembrane AcrB/D/F-family transporter |
| QSL8F0    | Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) | Putative transmembrane Acr-type transport protein |
| QSL8Q3    | Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) | Putative transport related membrane protein         |
| QSL990    | Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) | Putative transport-related membrane protein         |
| QSL9M7    | Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) | Putative metal resistance related transport membrane protein |
| Accession  | Organism                          | Strain Details                                    | Function Description                                                                 |
|-----------|-----------------------------------|--------------------------------------------------|---------------------------------------------------------------------------------------|
| Q5LA33    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative multidrug resistance/siderophore transport related | membrane protein |
| Q5LA16    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative transport-related membrane protein |
| Q5LB81    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative aminoglycoside efflux pump |
| Q5LC18    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative drug resistance transport-related membrane protein |
| Q5LD76    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative cation efflux-related membrane protein |
| Q5LDG2    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative cation transport related membrane protein |
| Q5LHM2    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative AcrB/AcrD/AcrF family efflux transporter |
| Q5LIU3    | Bacteroides fragilis              | (strain ATCC 25285 / DSM 2151 / JCM 11019/ NCTC 9343) | Putative AcrB/AcrD family RND transport protein |
| Q5LT89    | Ruegeria pomeroyi                 | (strain ATCC 700808 / DSM 15171 / DSS-3)          | Transporter | AcrB/AcrD/AcrF family |
| Q5LTL7    | Ruegeria pomeroyi                 | (strain ATCC 700808 / DSM 15171 / DSS-3)          | Efflux pump membrane transporter |
| Q5LUY1    | Ruegeria pomeroyi                 | (strain ATCC 700808 / DSM 15171 / DSS-3)          | Transporter | AcrB/AcrD/AcrF family |
| Q5LX87    | Ruegeria pomeroyi                 | (strain ATCC 700808 / DSM 15171 / DSS-3)          | Transporter | AcrB/AcrD/AcrF family |
| Q5NIG7    | Francisella tularensis subsp. tularensis | (strain SCHU S4 / Schu 4)                                    | Transporter AcrB/AcrD/AcrF family |
| Q5NMA8    | Zymomonas mobilis subsp. mobilis  | (strain ATCC 31821 / ZM4 / CP4)                    | Acriflavin resistance protein |
| Q5NQU7    | Zymomonas mobilis subsp. mobilis  | (strain ATCC 31821 / ZM4 / CP4)                    | Efflux pump membrane transporter |
| Q5NXR2    | Aromatoleum aromaticum           | (strain EbN1)                                      | Cation/multidrug efflux pump protein |
| Q5P2W3    | Aromatoleum aromaticum           | (strain EbN1)                                      | Probable cation efflux system protein CZCA |
| Q5P2Z3    | Aromatoleum aromaticum           | (strain EbN1)                                      | Predicted acriflavin resistance protein |
| Q5P649    | Aromatoleum aromaticum           | (strain EbN1)                                      | Cation efflux system protein |
| Q5P6P0    | Aromatoleum aromaticum           | (strain EbN1)                                      | Probable RND efflux transporter |
| Q5PDW7    | Salmonella paratyphi A            | (strain ATCC 9150 / SARB42)                        | Multidrug resistance protein MdtB |
| Q5PDW8    | Salmonella paratyphi A            | (strain ATCC 9150 / SARB42)                        | Multidrug resistance protein MdtC |
| Q5QVF0    | Idiomarina loihiensis            | (strain ATCC BAA-735 / DSM 15497 / L2-TR)          | Co/Zn/Cd efflux system membrane component |
| Q5QV8     | Idiomarina loihiensis            | (strain ATCC BAA-735 / DSM 15497 / L2-TR)          | RND family efflux transporter |
| Q5WW28    | Idiomarina loihiensis            | (strain ATCC BAA-735 / DSM 15497 / L2-TR)          | RND family efflux transporter |
| Q5YY6     | Idiomarina loihiensis            | (strain ATCC BAA-735 / DSM 15497 / L2-TR)          | RND family efflux transporter |
| Q5R021 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | Probable Co/Zn/Cd efflux system membrane component |
| Q5R024 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | RND family efflux transporter |
| QSR0E7 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | Efflux pump membrane transporter |
| QSR0R1 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | RND family efflux transporter |
| QSR0W3 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | Metal efflux system membrane component (Silver efflux pump related) |
| QSR0W8 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | Metal efflux system membrane component (Silver efflux pump related) |
| QSR138 | Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) | Co/Zn/Cd efflux system membrane component |
| QSWCH2 | Bacillus clausii (strain KSM-K16) | AcrB/AcrD/AcrF family cation/multidrug efflux pump |
| QSWTT9 | Legionella pneumophila (strain Lens) | Efflux pump membrane transporter |
| QSWU4 | Legionella pneumophila (strain Lens) | Efflux pump membrane transporter |
| QSWUV4 | Legionella pneumophila (strain Lens) | Chemiosmotic efflux system protein A-like protein |
| QSWXP7 | Legionella pneumophila (strain Lens) | HeLa protein |
| QSWYH9 | Legionella pneumophila (strain Lens) | Uncharacterized protein |
| QSZSK5 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Efflux pump membrane transporter |
| QSZTI4 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Efflux pump membrane transporter |
| QSZTM7 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Chemiosmotic efflux system protein A (CzcA) |
| QSZWI9 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Chemiosmotic efflux system B protein A |
| QSZWQ6 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Chemiosmotic efflux system protein A-like protein |
| QSZWR5 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Chemiosmotic efflux system B protein A |
| QSZWS7 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Cobalt/zinc/cadmium efflux RND transporter | permease protein HeLa |
| QSZXL1 | Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /ATCC 33152 / DSM 7513) | Multidrug resistance protein |
| Q603J0 | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q603S9 | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Accession | Organism (strain) | Description |
|-----------|------------------|-------------|
| Q605G0    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q605L6    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q605P8    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Efflux pump membrane transporter |
| Q605X2    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q605Z1    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q606T0    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q607J2    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q607N7    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q608A0    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Efflux pump membrane transporter |
| Q608X6    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Efflux pump membrane transporter |
| Q609D7    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q609J5    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q60A90    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | Heavy metal efflux pump | CzcA family |
| Q60CD0    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q60CM7    | Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) | AcrB/AcrD/AcrF family protein |
| Q630G7    | Bacillus cereus (strain ZK / E33L) | Conserved transporter possible acriflavin resistance protein |
| Q63FS7    | Bacillus cereus (strain ZK / E33L) | Acriflavin resistance protein |
| Q63L89    | Burkholderia pseudomallei (strain K96243) | Putative RND efflux transporter |
| Q63LH4    | Burkholderia pseudomallei (strain K96243) | Putative cation efflux system protein |
| Q63NK6    | Burkholderia pseudomallei (strain K96243) | Efflux pump membrane transporter |
| Q63ST6    | Burkholderia pseudomallei (strain K96243) | Putative AcrB/AcrD/AcrF family membrane protein |
| Q63U14    | Burkholderia pseudomallei (strain K96243) | Efflux pump membrane transporter |
| Q63UM9    | Burkholderia pseudomallei (strain K96243) | Putative drug-resistance cell envelope-related protein |
| Q63VH8    | Burkholderia pseudomallei (strain K96243) | Putative transport system | membrane protein |
| Q63WS7    | Burkholderia pseudomallei (strain K96243) | Efflux pump membrane transporter |
| Q63Y79    | Burkholderia pseudomallei (strain K96243) | Putative cation efflux system protein |
| Q64MM9    | Bacteroides fragilis (strain YCH46) | AcrB/D/F family transporter |
| Q64NQ0    | Bacteroides fragilis (strain YCH46) | Putative cation efflux transporter |
| Accession  | Organism                                      | Description                                                                 |
|-----------|-----------------------------------------------|----------------------------------------------------------------------------|
| Q64PF1    | *Bacteroides fragilis* (strain YCH46)        | AcrB/AcrD/AcrF family cation efflux system protein                         |
| Q64PW6    | *Bacteroides fragilis* (strain YCH46)        | AcrB/AcrD/AcrF family cation efflux system protein                         |
| Q64QE5    | *Bacteroides fragilis* (strain YCH46)        | AcrB/AcrD family multidrug resistance protein                             |
| Q64RM7    | *Bacteroides fragilis* (strain YCH46)        | Putative aminoglycoside efflux pump                                        |
| Q64TN7    | *Bacteroides fragilis* (strain YCH46)        | Putative cation efflux pump                                               |
| Q64U98    | *Bacteroides fragilis* (strain YCH46)        | Cation efflux system protein CzcA                                           |
| Q64YJ6    | *Bacteroides fragilis* (strain YCH46)        | Multidrug efflux membrane fusion protein                                   |
| Q64Z27    | *Bacteroides fragilis* (strain YCH46)        | AcrB/AcrD family multidrug resistance protein                             |
| Q65MP2    | *Bacillus licheniformis* (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) | Swarming and motility protein SwrC                                        |
| Q65QR6    | *Mannheimia succiniciproducens* (strain MBEL55E) | AcrB protein                                                               |
| Q65VE8    | *Mannheimia succiniciproducens* (strain MBEL55E) | AcrB protein                                                               |
| Q662M2    | *Borrelia bavariensis* (strain ATCC BAA-2496 / DSM 23469 / P8i) | Acriflavine resistance protein                                              |
| Q666F2    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Efflux pump membrane transporter                                           |
| Q668C5    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Multidrug resistance protein MdtC                                           |
| Q668C6    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Multidrug resistance protein MdtB                                           |
| Q668H5    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Efflux pump membrane transporter                                           |
| Q66DR0    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Efflux pump membrane transporter                                           |
| Q66EX5    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Putative heavy metal/multi-drug efflux protein| RND family                   |
| Q66F48    | *Yersinia pseudotuberculosis* serotype I (strain IP32953) | Efflux pump membrane transporter                                           |
| Q67J93    | *Symbiobacterium thermophilum* (strain T / IAM 14863) | AcrB family membrane transport protein                                      |
| Q68XJ7    | *Rickettsia typhi* (strain ATCC VR-144 / Wilmington) | Acriflavin resistance protein D                                             |
| Q69HW2    | *Escherichia coli.* | Efflux pump membrane transporter                                           |
| Q6AJB4    | *Desulfotalea psychrophila* (strain LSv54 / DSM 12343) | Related to cobalt-zinc-cadmium resistance protein (CzcA)                   |
| Q6ALC4    | *Desulfotalea psychrophila* (strain LSv54 / DSM 12343) | Related to multidrug-efflux transport protein                              |
| Q6AMJ9    | *Desulfotalea psychrophila* (strain LSv54 / DSM 12343) | Efflux pump membrane transporter                                           |
| Q6ARC4    | *Desulfotalea psychrophila* (strain LSv54 / DSM 12343) | Probable cation efflux system protein (CzcA)                               |
| Accession | Species/Microbial Name | Description |
|-----------|-----------------------|-------------|
| Q6CZM0    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Efflux pump membrane transporter |
| Q6D1J9    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Efflux pump membrane transporter |
| Q6D2B0    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Multidrug resistance protein MdtC |
| Q6D2B1    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Multidrug resistance protein MdtB |
| Q6D315    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Putative efflux protein |
| Q6D7E2    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Cation efflux system protein |
| Q6D806    | Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) | Efflux pump membrane transporter |
| Q6EMD9    | Escherichia coli. | Cu(+)/Ag(+) efflux RND transporter permease subunit SilA |
| Q6F6Q9    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Putative efflux transporter causing drug resistance (Acr family) |
| Q6F786    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Multidrug transport protein (RND family) |
| Q6F787    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Multidrug transport protein| outer membrane (RND family) |
| Q6F7C5    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | RND divalent metal cation efflux transporter |
| Q6F8F6    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Efflux pump membrane transporter |
| Q6F8P8    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Efflux pump membrane transporter |
| Q6FD21    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Putative multidrug transporter |
| Q6FD22    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Putative RND efflux transporter |
| Q6FE22    | Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) | Nodulation protein |
| Q6HAK2    | Bacillus thuringiensis subsp. konkukian (strain 97-27) | Conserved transporter possible acriflavin resistance protein |
| Q6HN96    | Bacillus thuringiensis subsp. konkukian (strain 97-27) | Acriflavin resistance protein |
| Q6IVS4    | uncultured gamma proteobacterium eBACHOT4E07. | Predicted cation efflux system |
| Q6KAY1    | Stenotrophomonas maltophilia | Efflux pump membrane transporter |
| Q6KAZ0    | Stenotrophomonas maltophilia | Efflux pump membrane transporter |
| Q6KAZ6    | Stenotrophomonas maltophilia | Efflux pump membrane transporter |
| Q6LGP3    | Photobacterium profundum (strain SS9) | Putative transporter| AcrB/D/F family |
| Q6LGT2    | Photobacterium profundum (strain SS9) | Efflux pump membrane transporter |
| Q6LI4Y    | Photobacterium profundum (strain SS9) | Efflux pump membrane transporter |
| Q6LNK7    | Photobacterium profundum (strain SS9) | Putative multidrug resistance protein |
| Q6LPI6    | Photobacterium profundum (strain SS9) | Putative AcrB| Cation/multidrug efflux pump |
| Accession | Organism                                              | Description                                           |
|-----------|-------------------------------------------------------|-------------------------------------------------------|
| Q6LPS3    | Photobacterium profundum (strain SS9)                 | Hypothetical transporter | AcrB/D/F family                                      |
| Q6LTG2    | Photobacterium profundum (strain SS9)                 | Putative cation efflux system transmembrane protein   |
| Q6LV21    | Photobacterium profundum (strain SS9)                 | Putative Cation/multidrug efflux pump                 |
| Q6LVZ3    | Photobacterium profundum (strain SS9)                 | Putative multidrug resistance protein                  |
| Q6MDJ2    | Protochlamydia amoebophila (strain UWE25)            | Uncharacterized protein                                |
| Q6MDS4    | Protochlamydia amoebophila (strain UWE25)            | Uncharacterized protein                                |
| Q6MEI7    | Protochlamydia amoebophila (strain UWE25)            | Uncharacterized protein                                |
| Q6MIU0    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | Efflux transporter                                    |
| Q6ML00    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | Cation efflux system protein | AcrB/AcrD/AcrF family protein                        |
| Q6MM46    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | NoLG efflux transporter                               |
| Q6MM88    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | NoLG efflux transporter                               |
| Q6MNU1    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | Acriflavin resistance protein                         |
| Q6MP63    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | Acriflavin resistance protein                         |
| Q6MPG6    | Bdellovibrio bacteriovorus (strain ATCC 15536 / DSM 50701 / NCIB 9529/ HD100) | Acriflavin resistance protein                         |
| Q6MXQ0    | Serratia marcescens.                                  | Putative cation efflux system protein (Silver resistance) |
| Q6N0T1    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Putative efflux transporter                           |
| Q6N1C7    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Putative heavy metal cation efflux system protein     |
| Q6N1J1    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Putative RND efflux transporter                       |
| Q6N2F5    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter                      |
| Q6N2Z4    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter                      |
| Q6N3B9    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Putative RND efflux transporter                       |
| Q6N457    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | RND efflux transporter                                |
| Q6N5L8    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter                      |
| Q6N682    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter                      |
| Q6N6N9    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Possible RND efflux transporter                       |
| Q6N6P0    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Possible RND efflux transporter                       |
| Q6N787    | Rhodopseudmonas palustris (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter                      |
| Accession | Organism | Description |
|-----------|----------|-------------|
| Q6N848    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | RND divalent metal cation efflux transporter CzcA |
| Q6N8D5    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | RND efflux transporter |
| Q6N8E2    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | RND efflux transporter |
| Q6N8U5    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Putative RND divalent metal cation efflux transporter CzcA |
| Q6N8Z7    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Putative cation efflux system protein |
| Q6N9P2    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter |
| Q6N9W6    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Putative inner membrane component for iron transport |
| Q6NB09    | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Putative transporter | AcrB/D/F family Cation efflux system protein |
| Q6NK9     | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | Efflux pump membrane transporter |
| Q6PKZ7    | *Campylobacter coli.* | Efflux pump membrane transporter |
| Q6Q918    | uncultured marine gamma proteobacterium EBAC20E09 | Predicted cation efflux system |
| Q6SGZ1    | uncultured marine bacterium 443. | Efflux transporter | RND family | outer membrane subunit | putative |
| Q6SH26    | uncultured marine bacterium 442. | Multidrug efflux transporter | AcrB/AcrD/AcrF family |
| Q6U5N9    | *Klebsiella pneumoniae* CG43. | SlIA |
| Q6V6X8    | *Pseudomonas fluorescens.* | Efflux pump membrane transporter |
| Q6VW68    | *Burkholderia pseudomallei* | Efflux pump membrane transporter |
| Q6W1F3    | *Sinorhizobium fredii* (strain NBRC 101917 / NGR234) | Acriflavin resistance plasma membrane protein |
| Q6YRW1    | *Synechocystis sp.* (strain PCC 6803 / Kazusa) | Slr6043 protein |
| Q71UZ6    | *Pseudomonas stutzeri* | Efflux pump membrane transporter |
| Q72S1     | *Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / DSM 644 /NCIMB 8303) | Efflux pump membrane transporter |
| Q727N9    | *Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / DSM 644 /NCIMB 8303) | Efflux pump membrane transporter |
| Q72EY0    | *Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / DSM 644 /NCIMB 8303) | AcrB/AcrD/AcrF family protein |
| Q72G02    | *Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / DSM 644 /NCIMB 8303) | Efflux pump membrane transporter |
| Q72MQ9    | *Leptospira interrogans* serogroup Icterohaemorrhagiae serovarcopenhagenii (strain Fiocruz L1-130) | Acriflavin resistance |
| Q72MU9    | *Leptospira interrogans* serogroup Icterohaemorrhagiae serovarcopenhagenii (strain Fiocruz L1-130) | Acriflavin resistance |
| Q72MW5    | *Leptospira interrogans* serogroup Icterohaemorrhagiae serovarcopenhagenii (strain Fiocruz L1-130) | Acriflavin resistance |
| ID  | Organism                                                                 | Protein/Transporter                                                                 |
|-----|--------------------------------------------------------------------------|----------------------------------------------------------------------------------|
| Q72Q8 | Leptospira interrogans serogroup Icterohaemorrhagiae serovargopenhageni (strain Fiocruz L1-130) | Heavy metal efflux pump                                                          |
| Q72V12 | Leptospira interrogans serogroup Icterohaemorrhagiae serovargopenhageni (strain Fiocruz L1-130) | Acriflavin resistance                                                             |
| Q72X10 | Bacillus cereus (strain ATCC 10987 / NRS 248) | Transporter | AcrB/AcrD/AcrF family |
| Q73DC5 | Bacillus cereus (strain ATCC 10987 / NRS 248) | Transporter | AcrB/AcrD/AcrF family |
| Q73FK8 | Wolbachia pipiens wMel. | Multidrug resistance protein D                                                   |
| Q746W8 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Heavy metal efflux pump | RND family | inner membrane protein | CzcA family |
| Q749G1 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner membrane protein | AcrB/AcrD/AcrF family |
| Q749P6 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump membrane transporter                                                  |
| Q749S8 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner and outer membrane proteins |
| Q748A6 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner membrane protein |
| Q74CR1 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner membrane protein | AcrB/AcrD/AcrF family |
| Q74DI4 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Metal ion efflux pump | RND family | inner membrane protein |
| Q74EX9 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner membrane protein |
| Q74G55 | Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) | Efflux pump | RND family | inner membrane protein |
| Q79MP3 | Serratia marcescens subsp. marcescens. | Multidrug resistance protein MdtC                                                 |
| Q7ACM1 | Escherichia coli O157:H7. | Multidrug resistance protein MdtC                                                 |
| Q7B054 | Cupriavidus metallidurans. | CnrA protein                                                                       |
| Q7M912 | Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 /NCTC 11488 / FDC 602W) | RND PUMP PROTEIN                                                                  |
| Q7M9I0 | Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 /NCTC 11488 / FDC 602W) | Efflux pump membrane transporter                                                  |
| Q7M9P9 | Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 /NCTC 11488 / FDC 602W) | Efflux pump membrane transporter                                                  |
| Q7MCH1 | Vibrio vulnificus (strain YJ016) | Putative multidrug resistance protein                                              |
| Q7MCR8 | Vibrio vulnificus (strain YJ016) | Putative silver efflux pump                                                      |
| Q7MDF8 | Vibrio vulnificus (strain YJ016) | Efflux pump membrane transporter                                                  |
| Q7MDY8 | Vibrio vulnificus (strain YJ016) | Transporter | AcrB/D/F family |
| Q7MEG9 | Vibrio vulnificus (strain YJ016) | Transporter | AcrB/D/F family |
| Q7MEY5 | Vibrio vulnificus (strain YJ016) | Transporter | AcrB/D/F family |
| Q7MG13 | Vibrio vulnificus (strain YJ016) | Uncharacterized protein                                                           |
| PDB ID  | Organism                             | Function Description                              |
|---------|--------------------------------------|--------------------------------------------------|
| Q7MHZ2  | Vibrio vulnificus (strain YJ016)     | Putative multidrug resistance protein             |
| Q7MLN0  | Vibrio vulnificus (strain YJ016)     | Transporter | AcrB/D/F family                               |
| Q7MME3  | Vibrio vulnificus (strain YJ016)     | Putative multidrug resistance protein             |
| Q7MQH1  | Vibrio vulnificus (strain YJ016)     | Putative multidrug resistance protein             |
| Q7MWQ6  | Porphyromonas gingivalis (strain ATCC BAA-308 / W83) | AcrB/AcrD/AcrF family protein                  |
| Q7MXU3  | Porphyromonas gingivalis (strain ATCC BAA-308 / W83) | Heavy metal efflux pump | CzcA family                                 |
| Q7N0N0  | Photorehbus luminescens subsp. laumondii (strain DSM 15139 / CIP105565 / TT01) | Efflux pump membrane transporter                |
| Q7N3E1  | Photorehbus luminescens subsp. laumondii (strain DSM 15139 / CIP105565 / TT01) | Multidrug resistance protein MdtC               |
| Q7N3E2  | Photorehbus luminescens subsp. laumondii (strain DSM 15139 / CIP105565 / TT01) | Multidrug resistance protein MdtB               |
| Q7N8G7  | Photorehbus luminescens subsp. laumondii (strain DSM 15139 / CIP105565 / TT01) | Uncharacterized protein                          |
| Q7NCY7  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | RND multidrug efflux transporter                |
| Q7NDR2  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Gll4170 protein                                  |
| Q7NE52  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Glr4028 protein                                  |
| Q7NE92  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | RND multidrug efflux transporter                |
| Q7NFA7  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Gll3619 protein                                  |
| Q7NHP1  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | AcrB/AcrD/AcrF family protein                   |
| Q7NJ01  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Cation efflux system protein                     |
| Q7NL29  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | AcrB/AcrD/AcrF family protein                   |
| Q7NM91  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Gll0876 protein                                  |
| Q7NMG0  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | AcrB/AcrD/AcrF family protein                   |
| Q7NNM9  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | Glr0382 protein                                  |
| Q7NNZ4  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | AcrB/AcrD/AcrF family protein                   |
| Q7NP24  | Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) | AcrB/AcrD/AcrF family protein                   |
| Q7NR60  | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCMIB 9131 / NCTC 9757) | Probable transmembrane drug efflux protein     |
| Q7NRE6  | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCMIB 9131 / NCTC 9757) | Probable multidrug efflux membrane protein     |
| Accession | Organism Description                                      | Function                                      |
|-----------|-----------------------------------------------------------|-----------------------------------------------|
| Q7NUG4    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | Probable drug efflux pump transmembrane protein |
| Q7NUG5    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | Probable drug efflux pump transmembrane protein |
| Q7NVV1    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | Efflux pump membrane transporter               |
| Q7NWL0    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | NolG efflux transporter                        |
| Q7NXK0    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | Probable multidrug efflux protein              |
| Q7POY1    | Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) | Efflux pump membrane transporter               |
| Q7UDI0    | Shigella flexneri.                                        | Efflux pump membrane transporter               |
| Q7UEM8    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Cation efflux system protein CZCA              |
| Q7UH35    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Predicted cation efflux system (AcrB/AcrD/AcrF family) |
| Q7UJP2    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Probable multidrug resistance protein          |
| Q7UJT6    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Acriflavine resistance protein B               |
| Q7ULF2    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | RND multidrug efflux transporter MexF          |
| Q7USF5    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Cation efflux system protein czcA-1            |
| Q7UZ48    | Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) | Cation efflux system | AcrB/AcrD/AcrF family |
| Q7VII0    | Helicobacter hepaticus (strain ATCC 51449 / 3B1)          | Uncharacterized protein                        |
| Q7VIM1    | Helicobacter hepaticus (strain ATCC 51449 / 3B1)          | SSD domain-containing protein                  |
| Q7VJR9    | Helicobacter hepaticus (strain ATCC 51449 / 3B1)          | Efflux pump membrane transporter               |
| Q7VLE5    | Haemophilus ducreyi (strain 35000HP / ATCC 700724)        | Acriflavine resistance protein                 |
| Q7VSV8    | Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) | AcrB/AcrD/AcrF family protein                 |
| Q7VSV9    | Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) | AcrB/AcrD/AcrF family protein                 |
| Q7VWW1    | Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) | Efflux pump membrane transporter               |
| Q7VZD3    | Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) | Efflux pump membrane transporter               |
| Q7VZR4    | Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) | Integral membrane component of multidrug efflux system |
| Accession | Organism                                      | Description                                                   |
|-----------|-----------------------------------------------|---------------------------------------------------------------|
| Q7W3S1    | *Bordetella parapertussis* (strain 12822 / ATCC BAA-587 / NCTC 13253) | AcrB/AcrD/AcrF family protein                                |
| Q7W3S2    | *Bordetella parapertussis* (strain 12822 / ATCC BAA-587 / NCTC 13253) | AcrB/AcrD/AcrF family protein                                |
| Q7W438    | *Bordetella parapertussis* (strain 12822 / ATCC BAA-587 / NCTC 13253) | Probable membrane protein                                    |
| Q7WAC5    | *Bordetella parapertussis* (strain 12822 / ATCC BAA-587 / NCTC 13253) | Efflux pump membrane transporter                             |
| Q7WC93    | *Bordetella parapertussis* (strain 12822 / ATCC BAA-587 / NCTC 13253) | Efflux pump membrane transporter                             |
| Q7WSD5    | *Serratia marcescens.*                        | Efflux pump membrane transporter                             |
| Q7WTQ9    | *Erwinia amylovora*                           | Efflux pump membrane transporter                             |
| Q7X364    | uncultured Acidobacteria bacterium.           | Putative multidrug resistance pump                           |
| Q814J5    | *Bacillus cereus* (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) | Acriflavin resistance plasma membrane protein                |
| Q81HR8    | *Bacillus cereus* (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) | Acriflavin resistance plasma membrane protein                |
| Q81JL8    | *Bacillus anthracis.*                         | Transporter | AcrB/AcrD/AcrF family protein                                |
| Q820K8    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Acriflavin resistance protein:Heavy metal efflux pump CzcA |
| Q820R2    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Acriflavin resistance protein:Heavy metal efflux pump CzcA |
| Q820R6    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Acriflavin resistance protein:Heavy metal efflux pump CzcA |
| Q82AL7    | *Streptomyces avermitilis* (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) | Putative cation/multidrug efflux protein                     |
| Q82T82    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Acriflavin resistance protein                                |
| Q82VH6    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Efflux pump membrane transporter                             |
| Q82WK5    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Acriflavin resistance protein                                |
| Q82XT4    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Efflux pump membrane transporter                             |
| Q82XU2    | *Nitrosomonas europaea* (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) | Efflux pump membrane transporter                             |
| Q83CM1    | *Coxiella burnetii* (strain RSA 493 / Nine Mile phase I) | Acriflavin resistance plasma membrane protein                |
| Q83DD4    | *Coxiella burnetii* (strain RSA 493 / Nine Mile phase I) | Acriflavin resistance plasma membrane protein                |
| Q83DH8    | *Coxiella burnetii* (strain RSA 493 / Nine Mile phase I) | Acriflavin resistance plasma membrane protein                |
| Q83Ki4    | *Shigella flexneri.*                          | Multidrug resistance protein MdtC                             |
| Q83SC3    | *Shigella flexneri.*                          | Putative inner membrane component for iron transport         |
| Q840D3    | *Acinetobacter baumannii.*                   | Efflux pump membrane transporter                             |
| ID  | Organism                                      | Description                                                                 |
|-----|-----------------------------------------------|-----------------------------------------------------------------------------|
| Q84R0 | Pseudomonas putida (strain ATCC 700007 / DSM 6899 / BCRC 17059 / F1) | Probable efflux pump membrane transporter SepB                              |
| Q84GI9 | Serratia marcescens subsp. marcescens.       | Efflux pump membrane transporter                                             |
| Q87BP4 | Xylella fastidiosa (strain Temecula1 / ATCC 700964) | Acriflavin resistance protein                                                |
| Q87DA3 | Xylella fastidiosa (strain Temecula1 / ATCC 700964) | Efflux pump membrane transporter                                             |
| Q87EU7 | Xylella fastidiosa (strain Temecula1 / ATCC 700964) | Acriflavin resistance protein                                                |
| Q87GX5 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Efflux pump membrane transporter                                             |
| Q87HZ7 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Transporter AcrB/D/F family                                                |
| Q87IX6 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative cation efflux system transmembrane protein                         |
| Q87IY5 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Efflux pump membrane transporter                                             |
| Q87J90 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative efflux protein                                                     |
| Q87JA9 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative multidrug resistance protein                                       |
| Q87LY6 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative multidrug resistance protein                                       |
| Q87QH1 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Transporter AcrB/D/F family                                                |
| Q87QQ7 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Efflux pump membrane transporter                                             |
| Q87R57 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative multidrug resistance protein                                       |
| Q87TN1 | Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) | Putative multidrug resistance protein                                       |
| Q87UV1 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | AcrB/AcrD/AcrF family protein                                               |
| Q87X84 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | Efflux pump membrane transporter                                             |
| Q87ZX0 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | AcrB/AcrD/AcrF family protein                                               |
| Q880Q4 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | Efflux pump membrane transporter                                             |
| Q881X7 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | AcrB/AcrD/AcrF family protein                                               |
| Q882N4 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | Efflux pump membrane transporter                                             |
| Q887I4 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | AcrB/AcrD/AcrF family protein                                               |
| Q889D0 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | AcrB/AcrD/AcrF family protein                                               |
| Q88AL5 | Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) | Cation efflux family protein                                                |
| Q88BZ6 | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Probable copper efflux transporter CzcA family                             |
| Accession | Organism (strain) | Function |
|-----------|------------------|----------|
| Q88CK7    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | RND efflux transporter |
| Q88GY2    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Multidrug efflux transport system-membrane subunit |
| Q88HA4    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Efflux pump membrane transporter |
| Q88HD4    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Efflux pump membrane transporter |
| Q88HQ1    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | RND efflux transporter |
| Q88I31    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Efflux pump membrane transporter |
| Q88K81    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Cation membrane transporter |
| Q88L70    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Multidrug efflux RND transporter |
| Q88MQ3    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | RND efflux transporter |
| Q88N31    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Probable efflux pump membrane transporter TtgB |
| Q88PE4    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Putative Multidrug efflux RND transporter |
| Q88RT6    | Pseudomonas putida (strain ATCC 47054 / DSM 6125 / NCIMB 11950 / KT2440) | Cation efflux system protein |
| Q89DV7    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89DX5    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family protein |
| Q89EQ3    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family protein |
| Q89FH4    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89I68    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family cation efflux protein |
| Q89K38    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89KG8    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Blr4937 protein |
| Q89KH2    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Blr4933 protein |
| Q89LT5    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Blr4458 protein |
| Q89LT6    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family protein |
| Q89M74    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Blr4319 protein |
| Q89MT0    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Probable cation efflux system protein |
| Q89NE0    | Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family protein |
| Accession | Organism | Protein Description |
|-----------|----------|---------------------|
| Q89NG9    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89QU2    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Cation efflux system protein |
| Q89R38    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | RagC protein |
| Q89RB1    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Blr2861 protein |
| Q89SH7    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Cation efflux system protein |
| Q89TZ3    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Multidrug resistance protein |
| Q89UA1    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89VP8    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Efflux pump membrane transporter |
| Q89XF8    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Acr family transport protein |
| Q89KK8    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | Cation efflux protein |
| Q89YN1    | Bradyrhizobium diaeoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110) | AcrB/AcrD/AcrF family protein |
| Q89YN7    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Cation efflux system protein |
| Q8AOQ2    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Cation efflux system protein | AcrB/AcrD/AcrF family protein |
| Q8A2G7    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | AcrB/AcrD family multidrug resistance protein |
| Q8A3L3    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Multidrug resistance protein mexB (Multidrug-efflux protein) |
| Q8A4B7    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Putative cation efflux transporter |
| Q8A5I7    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Multidrug efflux membrane fusion protein |
| Q8A647    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Cation efflux system protein | AcrB/AcrD/AcrF family protein |
| Q8A6B8    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Multidrug resistance protein | AcrB/AcrD family |
| Q8A899    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Transporter | AcrB/D/F family |
| Accession | Organism                                      | Description                                                                 |
|-----------|----------------------------------------------|----------------------------------------------------------------------------|
| Q8A9C9    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Putative cation efflux pump                                               |
| Q8A9Y5    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Cation efflux system protein czcA                                           |
| Q8AB07    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Putative aminoglycoside efflux pump (Acriflavine resistance protein)      |
| Q8AB13    | Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) | Cation efflux system (AcrB/AcrD/AcrF family)                             |
| Q8CK05    | Streptomyces coelicolor (strain ATCC BAA-471 / A3(2)) | Putative integral membrane efflux protein                                 |
| Q8CX78    | Oceanobacillus iheyensis (strain DSM 14371 / CIP 107618 / JCM 11309 / KCTC 3954 / HTE831) | Acriflavine resistance protein (Cation efflux system)                     |
| Q8DIH0    | Thermosynechococcus elongatus (strain BP-1)  | Multidrug efflux transporter                                               |
| Q8DJR3    | Thermosynechococcus elongatus (strain BP-1)  | AcrB/AcrD/AcrF family protein                                              |
| Q8E808    | Shewanella oneidensis (strain MR-1)          | Copper/silver efflux pump permease component CusA                         |
| Q8E8B2    | Shewanella oneidensis (strain MR-1)          | Efflux pump membrane transporter                                           |
| Q8E8R3    | Shewanella oneidensis (strain MR-1)          | Copper/silver efflux pump permease component CusA                         |
| Q8EA94    | Shewanella oneidensis (strain MR-1)          | HAE1 family efflux pump permease component                                |
| Q8EBL9    | Shewanella oneidensis (strain MR-1)          | Efflux pump membrane transporter                                           |
| Q8EBM6    | Shewanella oneidensis (strain MR-1)          | HAE1 family efflux pump permease component                                |
| Q8EC65    | Shewanella oneidensis (strain MR-1)          | RND superfamily efflux pump permease component                            |
| Q8ECN3    | Shewanella oneidensis (strain MR-1)          | Thiophosphate efflux pump permease component                              |
| Q8EFP6    | Shewanella oneidensis (strain MR-1)          | RND superfamily efflux pump permease component 2                          |
| Q8EFP7    | Shewanella oneidensis (strain MR-1)          | RND superfamily efflux pump permease component 1                          |
| Q8EFT4    | Shewanella oneidensis (strain MR-1)          | HAE1 family efflux pump permease component                                |
| Q8EI98    | Shewanella oneidensis (strain MR-1)          | RND superfamily efflux pump permease component                            |
| Q8EJE7    | Shewanella oneidensis (strain MR-1)          | Heavy metal efflux pump permease component CzcA family                    |
| Q8EYC8    | Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) | Cation/multidrug efflux pump                                              |
| Q8EZI2    | Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) | Acriflavine resistance protein                                             |
| Accession  | Organism                                      | Function                                |
|------------|-----------------------------------------------|-----------------------------------------|
| Q8EZK7     | Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) | Cation/multidrug efflux pump            |
| Q8EZW3     | Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) | Acriflavine resistance protein          |
| Q8F5X3     | Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) | Heavy metal efflux pump                 |
| Q8FC18     | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Multidrug resistance protein MdtF       |
| Q8FG03     | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Multidrug resistance protein MdtC       |
| Q8FG04     | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Multidrug resistance protein MdtB       |
| Q8FK36     | Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | Cation efflux system protein CusA       |
| Q8FWVV9    | Brucella suis biovar 1 (strain 1330) | Efflux pump membrane transporter BepG    |
| Q8G2M6     | Brucella suis biovar 1 (strain 1330) | Efflux pump membrane transporter BepE    |
| Q8GC83     | Klebsiella aerogenes | Efflux pump membrane transporter        |
| Q8GKU1     | Acinetobacter sp. 4365. | Efflux pump membrane transporter        |
| Q8KAV4     | Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 /TLS) | AcrB/AcrD/AcrF family protein           |
| Q8KCX0     | Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 /TLS) | Multidrug resistance protein | AcrB/AcrD family |
| Q8P3N5     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Cation efflux system protein            |
| Q8P4C1     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Acriflavin resistance protein           |
| Q8P613     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Acriflavin resistance protein           |
| Q8P7C9     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Efflux pump membrane transporter        |
| Q8P875     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Efflux pump membrane transporter        |
| Q8P8U2     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Transport protein                       |
| Q8P8U3     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Transport protein                       |
| Q8PAN9     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 /NCPPB 528 / LMG 568 / P 25) | Efflux pump membrane transporter        |
| Accession  | Organism                                      | Function                              |
|------------|-----------------------------------------------|---------------------------------------|
| Q8PDB8     | Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25) | Cation efflux system protein          |
| Q8PF28     | Xanthomonas axonopodis pv. citri (strain 306) | Cation efflux system protein          |
| Q8PFX2     | Xanthomonas axonopodis pv. citri (strain 306) | Acriflavin resistance protein         |
| Q8PHD3     | Xanthomonas axonopodis pv. citri (strain 306) | Acriflavin resistance protein         |
| Q8PIQ2     | Xanthomonas axonopodis pv. citri (strain 306) | Efflux pump membrane transporter      |
| Q8PIU6     | Xanthomonas axonopodis pv. citri (strain 306) | Acriflavin resistance protein         |
| Q8PJN1     | Xanthomonas axonopodis pv. citri (strain 306) | Efflux pump membrane transporter      |
| Q8PKM4     | Xanthomonas axonopodis pv. citri (strain 306) | Cation efflux system protein          |
| Q8PKU6     | Xanthomonas axonopodis pv. citri (strain 306) | Transport protein                     |
| Q8PKU7     | Xanthomonas axonopodis pv. citri (strain 306) | Transport protein                     |
| Q8PME6     | Xanthomonas axonopodis pv. citri (strain 306) | Efflux pump membrane transporter      |
| Q8PQ89     | Xanthomonas axonopodis pv. citri (strain 306) | Cation efflux system protein          |
| Q8PQJ5     | Xanthomonas axonopodis pv. citri (strain 306) | Efflux pump membrane transporter      |
| Q8RE51     | Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131) | Acriflavin resistance protein B       |
| Q8RG07     | Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131) | Acriflavin resistance protein D       |
| Q8RG44     | Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131) | Acriflavin resistance protein B       |
| Q8RNP2     | Legionella pneumophila.                       | Chemiosmotic efflux system B protein A|
| Q8RNQ8     | Legionella pneumophila.                      | AcrB/AcrD/AcrF family protein         |
| Q8RSM1     | uncultured bacterium.                        | MexD protein                          |
| Q8RTE4     | Campylobacter jejuni.                        | Efflux pump membrane transporter      |
| Q8VPA8     | Proteus mirabilis.                           | Efflux pump membrane transporter      |
| Q8X3J5     | Escherichia coli O157:H7.                    | Multidrug resistance protein MdtF     |
| Q8X7E2     | Escherichia coli O157:H7.                    | Efflux pump membrane transporter      |
| Q8X7J4     | Escherichia coli O157:H7.                    | Multidrug resistance protein MdtB     |
| Q8XBY1     | Escherichia coli O157:H7.                    | Cation efflux system protein CusA     |
| Q8XD55     | Escherichia coli O157:H7.                    | Efflux pump membrane transporter      |
| Q8XEH2     | Escherichia coli O157:H7.                    | Efflux pump membrane transporter      |
| Accession  | Organism                                      | Description                                    |
|-----------|-----------------------------------------------|-----------------------------------------------|
| Q8XPP1    | Ralstonia solanacearum (strain GMI1000)       | Probable transport transmembrane protein      |
| Q8XQ28    | Ralstonia solanacearum (strain GMI1000)       | Probable transporter transmembrane protein    |
| Q8XQM3    | Ralstonia solanacearum (strain GMI1000)       | Probable drug efflux transmembrane protein    |
| Q8XQM4    | Ralstonia solanacearum (strain GMI1000)       | Probable drug efflux pump transmembrane protein |
| Q8XQV5    | Ralstonia solanacearum (strain GMI1000)       | Efflux pump membrane transporter               |
| Q8XR28    | Ralstonia solanacearum (strain GMI1000)       | Putative cation efflux system transmembrane protein |
| Q8XRD0    | Ralstonia solanacearum (strain GMI1000)       | Probable cation efflux system transmembrane protein |
| Q8XR3L3   | Ralstonia solanacearum (strain GMI1000)       | Efflux pump membrane transporter               |
| Q8XSE6    | Ralstonia solanacearum (strain GMI1000)       | Putative cation efflux system transmembrane protein |
| Q8XSI1    | Ralstonia solanacearum (strain GMI1000)       | Probable cation efflux system transmembrane protein |
| Q8XT05    | Ralstonia solanacearum (strain GMI1000)       | Efflux pump membrane transporter               |
| Q8XUJ3    | Ralstonia solanacearum (strain GMI1000)       | Probable transmembrane drug efflux protein    |
| Q8XYV2    | Ralstonia solanacearum (strain GMI1000)       | Probable transmembrane drug efflux protein    |
| Q8Y3H0    | Ralstonia solanacearum (strain GMI1000)       | Efflux pump membrane transporter               |
| Q8YCW5    | Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) | Acriflavin resistance protein f |
| Q8YCZ5    | Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) | Acriflavin resistance protein d |
| Q8YF77    | Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) | Acriflavin resistance protein b |
| Q8YF93    | Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) | Efflux pump membrane transporter               |
| Q8YHA9    | Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) | Acriflavin resistance protein b |
| Q8YLK4    | Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) | Alr5294 protein |
| Q8YSE5    | Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) | RND multidrug efflux transporter               |
| Q8YWF7    | Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) | Alr1656 protein |
| Q8Z4S4    | Salmonella typhi.                              | Efflux pump membrane transporter               |
| Q8Z5F6    | Salmonella typhi.                              | Multidrug resistance protein MdtC              |
| Q8Z5F7    | Salmonella typhi.                              | Multidrug resistance protein MdtB              |
| Q8Z8T8    | Salmonella typhi.                              | Efflux pump membrane transporter               |
| Q8ZCV9    | Yersinia pestis.                               | Multidrug resistance protein MdtC              |
| Q8ZCW0    | Yersinia pestis.                               | Multidrug resistance protein MdtB              |
| Q8ZLN4    | Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) | Efflux pump membrane transporter               |
| Q8ZN77    | Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) | Efflux pump membrane transporter               |
| Accession  | Organism                                      | Description                                      |
|------------|-----------------------------------------------|--------------------------------------------------|
| Q8ZNQ1     | *Salmonella typhimurium* (strain LT2 / SGSC1412 / ATCC 700720) | Multidrug resistance protein MdtC               |
| Q8ZNQ2     | *Salmonella typhimurium* (strain LT2 / SGSC1412 / ATCC 700720) | Multidrug resistance protein MdtB               |
| Q8ZRA7     | *Salmonella typhimurium* (strain LT2 / SGSC1412 / ATCC 700720) | Efflux pump membrane transporter                 |
| Q8ZRG9     | *Salmonella typhimurium* (strain LT2 / SGSC1412 / ATCC 700720) | Efflux pump membrane transporter                 |
| Q8ZS81     | Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) | Cation efflux system protein                    |
| Q8ZS94     | Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) | Cation efflux system protein                    |
| Q92J58     | *Rickettsia conorii* (strain ATCC VR-613 / Malish 7) | Acriflavin resistance protein D                  |
| Q92M87     | *Rhizobium meliloti* (strain 1021)             | Efflux pump membrane transporter                 |
| Q92NP7     | *Rhizobium meliloti* (strain 1021)             | Probable acriflavine resistance protein          |
| Q92SH0     | *Rhizobium meliloti* (strain 1021)             | Efflux pump membrane transporter                 |
| Q92T03     | *Rhizobium meliloti* (strain 1021)             | Efflux pump membrane transporter                 |
| Q92U15     | *Rhizobium meliloti* (strain 1021)             | Efflux pump membrane transporter                 |
| Q92WK8     | *Rhizobium meliloti* (strain 1021)             | Probable acriflavine family protein              |
| Q92Y52     | *Rhizobium meliloti* (strain 1021)             | Cation/multidrug efflux protein                 |
| Q92YH0     | *Rhizobium meliloti* (strain 1021)             | Efflux pump membrane transporter                 |
| Q93E19     | *Acinetobacter baumannii.*                    | Efflux pump membrane transporter                 |
| Q93K40     | *Klebsiella pneumoniae.*                      | Efflux pump membrane transporter                 |
| Q93PU4     | *Pseudomonas putida* (strain DOT-T1E)          | Toluene efflux pump membrane transporter TtgH   |
| Q93SR9     | *Pseudomonas putida*                          | Membrane-bound cation-proton-antiporter CzrA    |
| Q986H1     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Efflux pump membrane transporter                 |
| Q986L9     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Component of multidrug efflux system            |
| Q988I4     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Efflux pump membrane transporter                 |
| Q98B06     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | RND efflux transporter                          |
| Q98BL7     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | RND efflux transporter                          |
| Q98FD0     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Multidrug resistance protein                    |
| Q98FR6     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | RND efflux transporter                          |
| Q98GK4     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Efflux pump membrane transporter                 |
| Q98IH3     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Probable RND efflux transporter                 |
| Q98KL0     | *Mesorhizobium japonicum* (strain LMG 29417 / CECT 9101 / MAFF 303099) | Probable RND efflux transporter                 |
| Accession   | Organism                          | Function                                      |
|-------------|-----------------------------------|-----------------------------------------------|
| Q9A3K6      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | AcrB/AcrD/AcrF family protein                 |
| Q9A4V1      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | Metal ion efflux RND protein family           |
| Q9A5Q7      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | AcrB/AcrD/AcrF family protein                 |
| Q9A7D5      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | AcrB/AcrD/AcrF family protein                 |
| Q9A8Z1      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | AcrB/AcrD/AcrF family protein                 |
| Q9AA04      | Caulobacter vibrioides (strain ATCC 19089 / CB15) | Efflux pump membrane transporter              |
| Q9AEG1      | Klebsiella aerogenes               | Efflux pump membrane transporter              |
| Q9AG05      | Wolbachia sp. subsp. Drosophila simulans (strain wRi) | Multidrug resistance protein D               |
| Q9ALR2      | Pseudomonas fluorescens.           | CztA                                          |
| Q9CLS7      | Pasteurella multocida (strain Pm70) | AcrB                                          |
| Q9F240      | Stenotrophomonas maltophilia       | Efflux pump membrane transporter              |
| Q9F7M0      | Gamma-proteobacterium EBAC31A08.   | Predicted cation efflux system (AcrB/AcrD/AcrF family) |
| Q9F8V7      | Rhizobium radiobacter              | Efflux pump membrane transporter              |
| Q9HV9       | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Efflux pump membrane transporter              |
| Q9HW27      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9HW4       | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9HXW4      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9HY87      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Efflux pump membrane transporter              |
| Q9I0V6      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9I0V7      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9I0W2      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Resistance-Nodulation-Cell Division (RND) divalent metal cation efflux transporter CzcA |
| Q9I0Y8      | Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Efflux pump membrane transporter              |
| Accession Number | Organism and Strain Information                                                                 | Functional Description |
|------------------|--------------------------------------------------------------------------------------------------|------------------------|
| Q9I3R1           | *Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9I6X4           | *Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | Probable Resistance-Nodulation-Cell Division (RND) efflux transporter |
| Q9JY67           | *Neisseria meningitidis* serogroup B (strain MC58)                                               | Efflux pump membrane transporter |
| Q9K6B3           | *Bacillus halodurans* (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM9153 / C-125)         | Cation efflux system     |
| Q9KJC2           | *Pseudomonas putida*                                                                             | Antibiotic efflux pump membrane transporter ArpB |
| Q9KLV3           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Transporter | AcrB/D/F family |
| Q9KR85           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Transporter | AcrB/D/F family |
| Q9KRG9           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Transporter | AcrB/D/F family |
| Q9KTI8           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Multidrug resistance protein | putative |
| Q9KU94           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Multidrug resistance protein | putative |
| Q9KV12           | *Vibrio cholerae* serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)                          | Multidrug resistance protein | putative |
| Q9KW65           | *Pseudomonas syringae*                                                                           | ORFF protein            |
| Q9KWV4           | *Pseudomonas putida* (strain DOT-T1E)                                                           | Toluene efflux pump membrane transporter TtgE |
| Q9PAV9           | *Xylella fastidiosa* (strain 9a5c)                                                              | Acriflavin resistance protein |
| Q9PB6            | *Xylella fastidiosa* (strain 9a5c)                                                               | Efflux pump membrane transporter |
| Q9PBQ7           | *Xylella fastidiosa* (strain 9a5c)                                                               | Cation efflux system protein |
| Q9PGQ5           | *Xylella fastidiosa* (strain 9a5c)                                                               | Acriflavin resistance protein |
| Q9RBY8           | *Stenotrophomonas maltophilia*                                                                  | Efflux pump membrane transporter |
| Q9RG59           | *Pseudomonas aeruginosa*                                                                         | Efflux pump membrane transporter |
| Q9RLI8           | *Pseudomonas aeruginosa*                                                                         | CzrA protein            |
| Q9RQG6           | *Staphylococcus aureus*                                                                         | AcrB/AcrD/AcrF family protein |
| Q9WYK5           | *Thermotoga maritima* (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)                          | Cation efflux system protein | putative |
| Q9ZDZ3           | *Rickettsia prowazekii* (strain Madrid E)                                                       | ACRIFLAVIN RESISTANCE PROTEIN D (AcrD) |
| Q9ZH24           | *Pseudomonas aeruginosa*                                                                         | Efflux pump membrane transporter |
| Q9ZHC9           | *Salmonella typhimurium*                                                                        | Putative cation efflux system protein SilA |
| Q9ZJO5           | *Helicobacter pylori* (strain J99 / ATCC 700824)                                                | CATION EFFLUX SYSTEM PROTEIN |
| Q9ZKN2           | *Helicobacter pylori* (strain J99 / ATCC 700824)                                                | Putative cation efflux system protein |
| Q9ZLM5           | *Helicobacter pylori* (strain J99 / ATCC 700824)                                                | Putative efflux transporter |
| Q9ZNG8           | *Pseudomonas aeruginosa*                                                                         | Efflux pump membrane transporter |
