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

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9

10 **Abstract**

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

25

26 **Keywords:** efflux pumps, RND efflux pumps, gene duplication, antibiotic resistance

27

28 **Introduction**

29 The resistance-nodulation-division efflux pumps (RNDs) comprise a large family of
30 proteins, widely distributed among bacterial species [1,2]. Their main function is to extrude
31 superfluous or harmful substances, such as metabolites, antibiotics, toxins, or metal ions. Some
32 RNDs are also believed to be involved in export of siderophores and quorum sensing molecules
33 [3,4], and there may be additional functions to be discovered, given the fact that the vast majority
34 of RND pumps have not been characterized [5]. In general, the RNDs are divided into two groups
35 depending on the substrates they transport: hydrophobic and amphiphilic efflux (HAE) and heavy
36 metal efflux (HME).

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

47 Classically, the efflux system is formed as a tripartite assembly [8]. Most RND systems
48 share the same architecture, with an RND homotrimer in the inner membrane bound to six
49 protomers of a membrane fusion protein (MFP) in the periplasm, which in turn connect the
50 assembly with a trimer of outer membrane proteins (OMP). However, there are exceptions. In the

51 MdtABC (multidrug transport) system from *E. coli* the inner membrane part is formed by a
52 heterotrimer of MdtB₂C₁ stoichiometry [9]. A similar system called MuxABC was described in *P.*
53 *aeruginosa*, with the MuxA, MuxB and MuxC proteins being homologous to MdtA, MdtB and
54 MdtC, respectively (40, 65 and 61% sequence identity, and 78, 91 and 88% sequence similarity
55 between the corresponding proteins) [10,11]. Other homologous systems were found and
56 characterized in *Salmonella enterica* Serovar Typhimurium [12], *Serratia marcescens* [13],
57 *Erwinia amylovora* [14], *Pseudomonas putida* [15], and *Photobacterium luminescens* [16].

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

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

73 that the original RND gene duplication might indeed be an infrequent older phenomenon, and not
74 a widespread feature happening frequently in bacterial genomes.

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

83 **Materials and Methods**

84 **Phylogenetic analyses**

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

92 The sequences that clustered together with *E. coli* MdtB and MdtC (and *E. coli* AcrB as an
93 outgroup) were aligned with MAFFT using G-INS-i, an iterative refinement method, and a
94 phylogenetic tree was constructed using neighborhood joining (NJ) of all of gap-free sites (JTT

95 substitution model, the heterogeneity among sites was estimated by MAFFT, and bootstrap of 100
96 was used) [18]. The tree was then rooted on AcrB.

97 **Sequence similarity network and genomic neighborhood diagrams**

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

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

106 **Results & Discussion**

107 **RNDs form a number of distinct clusters**

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

115 There was a high similarity between the results obtained with the traditional phylogenetic
116 analysis and the SSN. As seen in Fig 1, most proteins formed several large branches and clusters,

117 with a smaller number remaining separated. The largest cluster (cluster 1) encompassed most of
118 the characterized RNDs (all HAEs from *E. coli*). The less studied RNDs from *P. aeruginosa*
119 clustered as MexI/W (cluster 2) and TriC/MexK (cluster 5). As expected, the HME proteins
120 clustered together, with a further subdivision into mono- and di- valent transporting RNDs (cluster
121 3).

122

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

130

131 The Mdt proteins formed a distinct cluster (cluster 4), with one of the longest branches
132 from the middle in the phylogenetic tree. The MdtB-like and MdtC-like proteins split early in the
133 phylogenetic tree. The MdtB-like proteins, which are always directly adjacent to their respective
134 MFPs, clustered together into one branch. The MdtC-like protein, which are never directly
135 adjacent to their respective MFPs (i.e. there is always an MdtB-like protein in between), also
136 clustered together into one branch. The fact that the gene organization has been preserved
137 corroborates the notion that this heteromeric RND system is a result of an ancient gene duplication.
138 This relationship seems to be very old, since Alpha-, Beta- and Gammaproteobacterial MdtBs and

139 MdtCs form separate clusters, so that would put this duplication event to be older than the split
140 between the major groups of *Proteobacteria* (over 2 billion years ago [25]).

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

147

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

160

161 **A closer look into the Mdt cluster reveals the evolutionary history of**
162 **the subfamily**

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

177 The “progenitor-like” RND group contained all Deltaproteobacterial sequences
178 represented in our analysis, as well as the only sequence from a non-Proteobacterium, *Gloeobacter*
179 *violaceus*, a Cyanobacterium (Fig 2). The fact that these “progenitor-like” RNDs did not cluster
180 together with known MdtB- and MdtC-like proteins suggests they are direct descendants of the
181 ancient common ancestor of the whole Mdt cluster, the progenitor gene. We also performed
182 searches for MdtB- and MdtC-like proteins (i.e. having sequence similarity at least 40%) in
183 Deltaproteobacteria and found only three hits, suggesting the MdtBC-like systems are virtually

184 absent in these two groups. A number of Alpha- and Betaproteobacterial orders contained the
185 “progenitor-like” RNDs, but no Gammaproteobacteria did. Interestingly, all the Alpha- and
186 Betaproteobacterial representants can fix nitrogen and/or reduce nitrate, suggesting a common
187 habitat [26]. The fact that all the older bacterial lineages appeared in this group suggests that the
188 original gene duplication that produced MdtB- and MdtC-like proteins occurred in the common
189 ancestor of the Alpha-, Beta- and Gammaproteobacteria, around the end of the Archean Eon [25],
190 and the sporadic occurrence of a “progenitor-like” RND in Alpha- and Betaproteobacteria is more
191 likely a result of a horizontal gene transfer.

192 The rest of the RNDs formed two groups, with all the MdtB-like proteins in one and all the
193 MdtC-like proteins in the other. Noticeably, the “true” MexN-like proteins clustered together with
194 the MdtB-like proteins. This observation suggested the MexN separation happened after the
195 original gene duplication that formed MdtB and MdtC from the progenitor RND gene. In general,
196 the branching of both MdtB and MdtC groups was similar: Alphaproteobacteria separated earliest
197 (with the exception of *Gluconobacter oxydans* and *Zymomonas mobilis*, see below), and then Beta-
198 and Gammaproteobacteria. Surprisingly, the Gammaproteobacterial order *Xanthomonadales*
199 separated together with Alphaproteobacteria (both in the MdtB- and the MdtC-like groups, with
200 moderate to low bootstrap support, however). In Alphaproteobacteria, homologs of MdtBC/MexN
201 were numerous found only in orders *Rhizobiales* and *Rhodospirillales*, and sporadically in a few
202 other orders. In Betaproteobacteria, homologs of MdtBC/MexN were widespread and found in all
203 major orders, and in Gammaproteobacteria homologs of MdtBC/MexN were found in most orders.
204 In all three major Proteobacterial families there were examples of closely related species and
205 strains where one contained MdtBC, MexN or both, and the other with no MdtBC/MexN
206 homologs. In many organisms it was also suspected the process of losing the RND pumps was

207 ongoing. For instance, in *Shigella flexneri*, *Serratia marcescens*, *Pseudomonas syringae* pv *tomato*
208 and *Magnetospirillum magneticum* an MdtB was missing; in *Salmonella paratyphi A* an MFP was
209 missing; and in *Burkholderia mallei* the whole MdtABC operon was absent (see Supporting
210 Information for details).

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

227 **Horizontal gene transfers**

228 The exception to the observation that organisms containing a “progenitor-like” RND did
229 not contain an MdtBC system occurred in *Cupriavidus pinatubonensis* (*Betaproteobacteria*, order

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

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

245 Proteins from two Alphaproteobacteria, *Gluconobacter oxydans* and *Zymomonas mobilis*,
246 did not cluster together with other Alphaproteobacterial Mdts, but were found closest to respective
247 proteins from the order *Burkholderia*. While the long branches observed for all four proteins as
248 well as moderate bootstrap values might render this clustering less reliable, it is possible those two
249 organisms had lost their original Mdts and acquired new ones via horizontal gene transfer.
250 Moreover, *G. oxydans* possesses a third protein with high sequence similarity to its own MdtC (not
251 shown in Fig 2, see Supporting information). It is likely a result of a discrete gene duplication,
252 particularly since this third gene does not possess an MFP.

253 As mentioned above, the order *Xanthomonadales* clustered somewhat reliably with
254 Alphaproteobacteria, both in MdtB- and MdtC-like groups. They did not possess a third RND,
255 either a “true” MexN-like protein or a “progenitor-like” RND. Since they separated the earliest
256 from other Gammaproteobacteria, it is possible their ancestors lost both their original MdtABC
257 and MexMN systems, and subsequently incorporated an MdtABC from an Alphaproteobacterium
258 [28].

259 **Reconstructing the MdtABC/MexMN evolution**

260 The results described here, together with analysis of corresponding MFPs (see Supporting
261 information) made it possible to propose an evolutionary scenario for the appearance of MdtBC
262 and MexN pumps (Fig 3). The original RND progenitor gene underwent a duplication in the
263 common ancestor to Alpha-, Beta- and Gammaproteobacteria, while remaining single in other
264 bacterial groups (as “progenitor-like” RNDs). The MFP and the adjacent RND were duplicated,
265 forming the “true” MexMN system. In the next step an OMP was acquired, and was inserted before
266 the MFP in Alphaproteobacteria, or after the MdtC in the common ancestor to the Beta- and
267 Gammaproteobacteria. From these points many organisms lost the MexMN system. In
268 Alphaproteobacteria only two orders represented in Figs 1 and 2 retained the original genes. Many
269 Betaproteobacteria retained the OMPs (occurring always after the MdtCs) but lost the duplicated
270 MexMN, with the exception of the *Burkholderia* genus, which lost the OMPs, but retained the
271 MexMN and also gained an MFS next to it. In Gammaproteobacteria the configuration was
272 generally kept intact, with the exception of *Enterobacterales*, which lost the MexMN and
273 incorporated an MFS into its MdtABC operon.

274

275 **Fig 3. The proposed evolutionary scenario.** The evolution within the Alpha-, Beta- and Gamma-
276 proteobacteria groups is shown, as deduced from the phylogenetic tree in Fig 2 and a timeline of
277 evolution of Proteobacteria (Battistuzzi, Feijao and Hedges 2004). The cladograms lengths and
278 timepoints of evolutionary events are not to scale. As an example of horizontal gene transfer,
279 *Cupriavidus pinatubonensis* is also shown.

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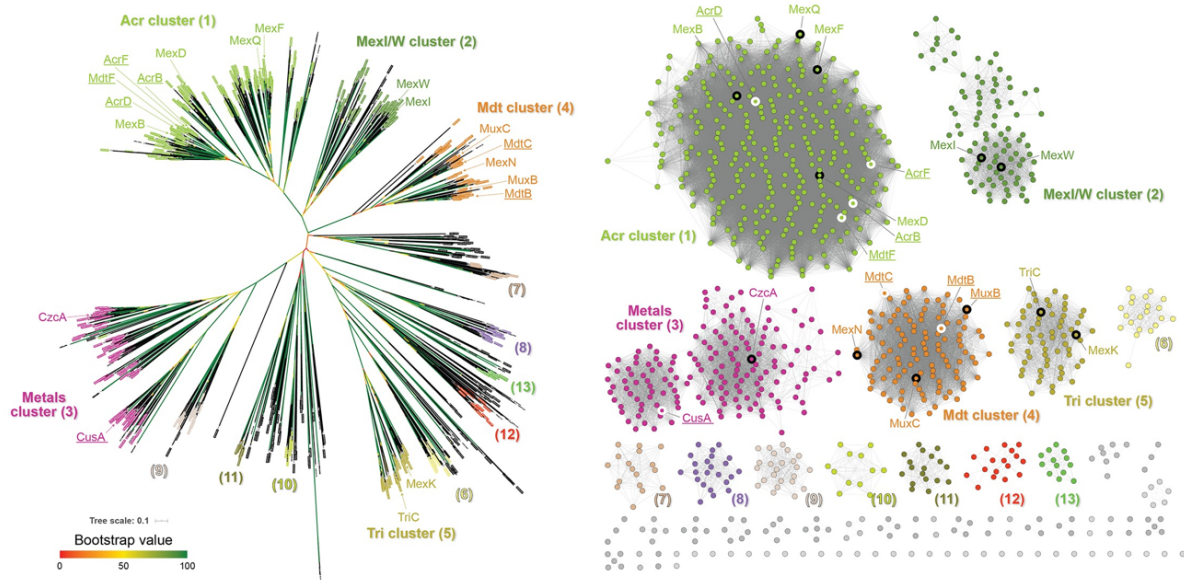
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368 **Supporting information**

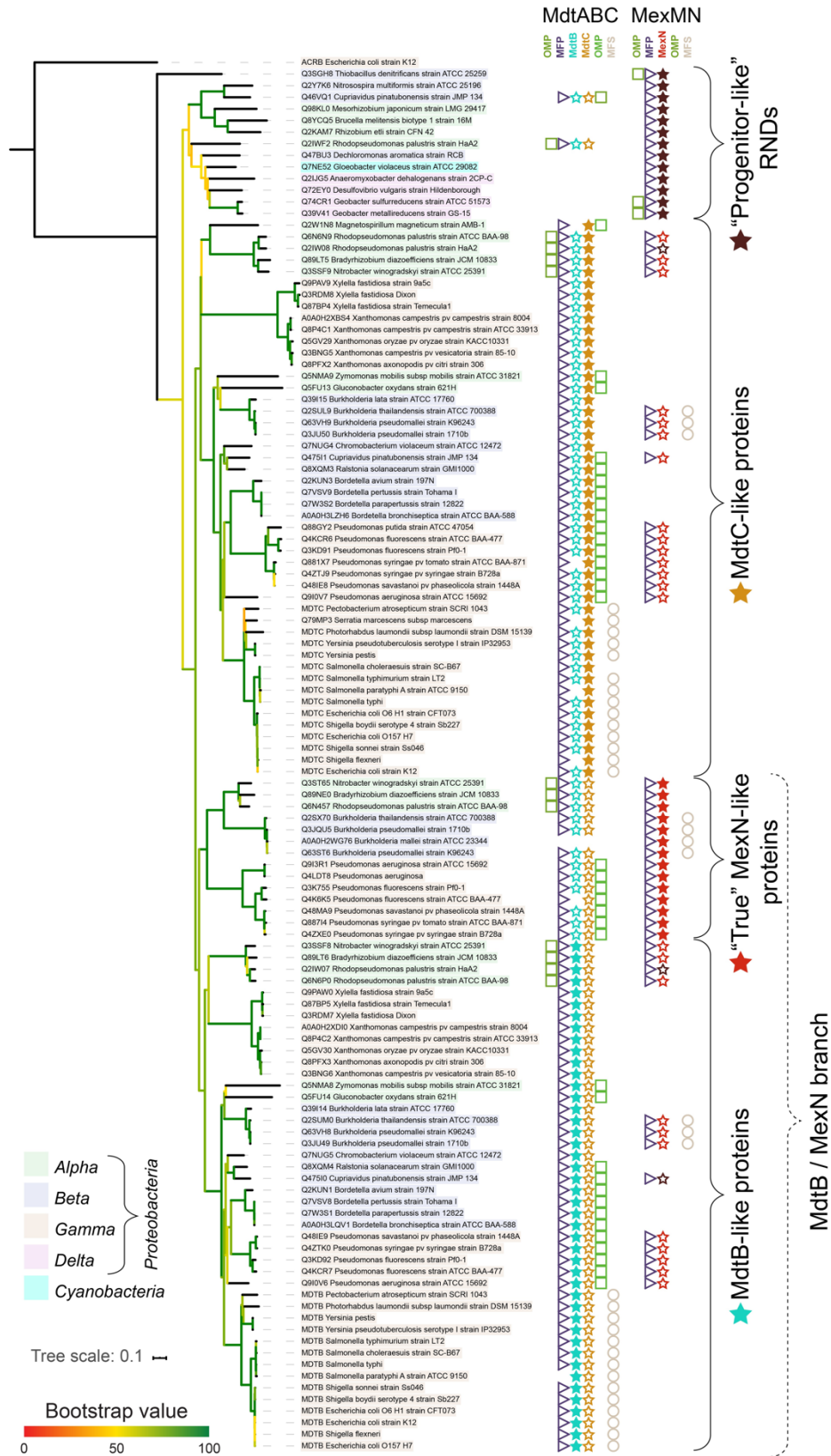
369 S1 _File. Supporting information containing the list of used sequences, as well as detailed
370 discussion, is available.
371

372 Figure 1

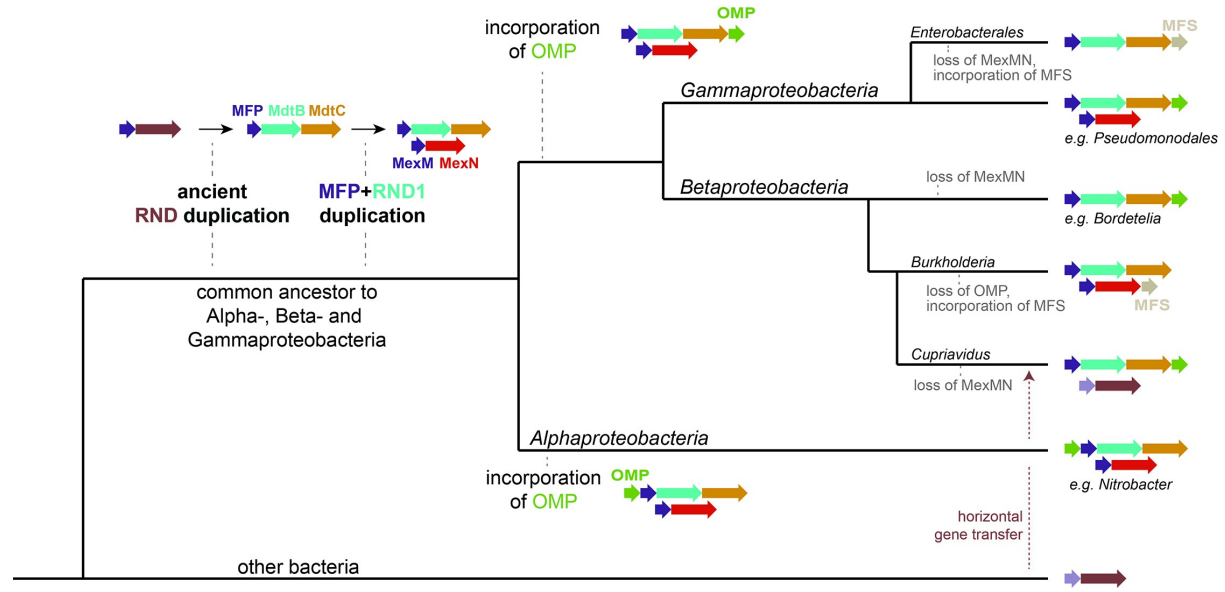


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377 Figure 3



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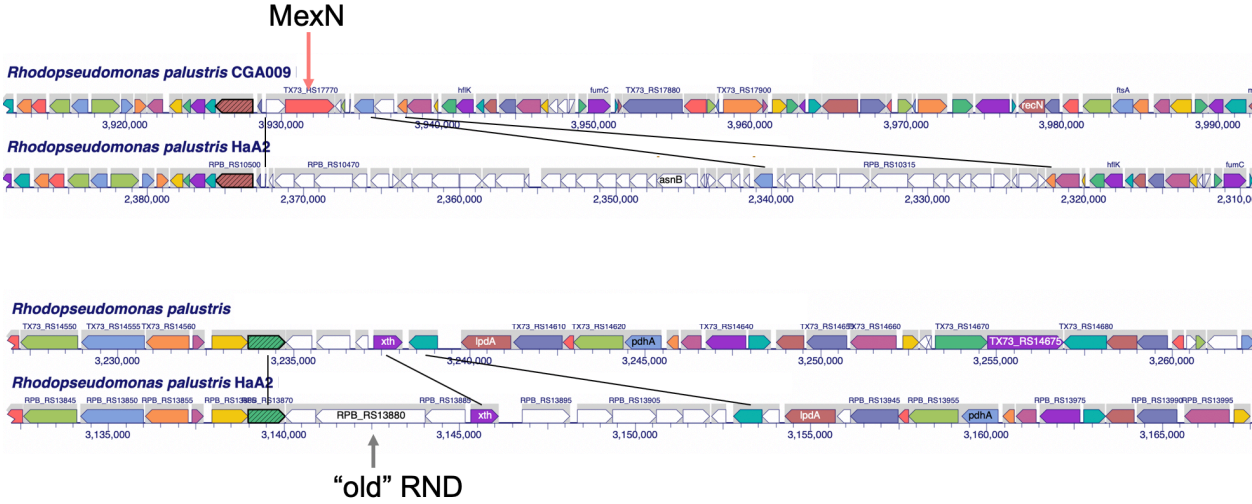
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Supplementary material

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.

Translation	MNMSRLFILRFVATTLMSLAIIVLAGLIAAYTLPLVVSALPQVDYPTIRVMTLYPGASPVMT	60
PSEU2 MdtB	MNMSRLFILRFVATTLMSLAIIVLAGLIAAYTLPLVVSALPQVDYPTIRVMTLYPGASPVMT	60
Translation	SSVTPAPLERQFGQMPGLTQMASTSSGGASVITLRFSLINMDVAEQVQAAINAATNLLP	120
PSEU2 MdtB	SSVTPAPLERQFGQMPGLTQMASTSSGGASVITLRFSLINMDVAEQVQAAINAATNLLP	120
Translation	TDLPPAPPVYNKVNPA DTFVLT LAITSKTMLLPRLNDLV DTRMAQKISQISGVGMVSIAGG	180
PSEU2 MdtB	TDLPPAPPVYNKVNPA DTFVLT LAITSKTMLLPRLNDLV DTRMAQKISQISGVGMVSIAGG	180
Translation	QRQAVRIKVNPEALAA NSLN LADVRTLISASN VNQPKGNFDGPTRV SMLDANDQLRSFEE	240
PSEU2 MdtB	QRQAVRIKVNPEALAA NSLN LADVRTLISASN VNQPKGNFDGPTRV SMLDANDQLRSFEE	240
Translation	YANLILAYKDGAPLR LKDVAEIVDGAENERLA AWANRNQAVLLNIQRQPGANVIDVVDRI	300
PSEU2 MdtB	YANLILAYKDGAPLR LKDVAEIVDGAENERLA AWANRNQAVLLNIQRQPGANVIDVVDRI	300
Translation	KALLPGITDNLPA GLDVGAD-PHADHSGVCHRC SAR TADRHRAGGTGH-VPVSA-EVQR	357
PSEU2 MdtB	KALLPSTENLPA GLDVVLTDR TQTIRASVTD----VQH ELLIAIVLVVLTFFLRR	355
Translation	HNHS---LDCGTAVTGGHVRCHV PGRFLDQPPDL DGDIDHRHRFCRRRHRDAGKHLPAY	413
PSEU2 MdtB	FSATIIPIPSIAVPLSLVGTFFGVMYLAG-FSVN NLTLMAMT IATGFVVDDAIVMLENISRHI	414
Translation	RRGRNPHAGRAQGRKTRDFHAD-LPDPVADCGADPA---AVHGRGGG---SVPRVR	463
PSEU2 MdtB	EEGETPIQAALKA LKAKQIGFTLISLTL SLIA-VLIPLLFMADVGR LFRFAITLAVAILI	473
Translation	--DHPGGRHPDLAGGIADPD PDDVRAPAQTRAE RGRPEPFLPGQ---WCVDRLADRYLC-	517
PSEU2 MdtB	SLVVSLTLTPM M CARLLKREPREEBE---QSRF-----YRASGAWIDW LIDIYAGR LRWV	524
Translation	---GPVA---LGTQ-----ASAFDPAGRAGDAGV DCAAVYRGAQGLLSGAGHGS	560
PSEU2 MdtB	LKHQPLLLVALATLALT VLLYIVVPKGF FVQD-----TGV IQGIS EAP	569
Translation	DSRYFRST---AVGVR RHEPASTGT-----RRHYSQGP GGGQP VVL	599
PSEU2 MdtB	QSVSFAAMSQRQALAD IILKDPAVVSLSSYIGVDGDNATLNSGRLLINL KPHGARDLTA	629
Translation	YWCR-WRQRNAQ-----QWSPADQSQTA--PGTRPDR SHPAPATGGRQAFGHPPVHA	650
PSEU2 MdtB	SEVIQRLQPEVDKLSDI RLFMQPVQDLTIEDRVSR TQYQFSMSSPDAELLTLWSEKLVDA	689
Translation	AGAGPDHRRRPGQP-----YPVPVQHV IARR-----RAVDALERK TGRRARQAG-TDR	696
PSEU2 MdtB	LGKRPELRDVA SDLQDKGLQVYLNIDRDAASRVGVT VANITDALYDAFGQRQIST IYTQA	749
Translation	CGQRPAQGGAAGVPEHRSRCG--QSGRRHGGQYHRC SV-RLRAAADFHHLHPGQPVPGGV	753
PSEU2 MdtB	SQYRVVLQAA SGE L G PAAL EQIHVKT TDGAQVKLSSLARVE-----	791
Translation	AGCVRQRP GPGGAGADPRQDHRWRAGE TVE SGAHRAASGTVGHYSPGAV-----SG	804
PSEU2 MdtB	-----QRQAQLAIAHLGQFPVMM S FNLAPDIALG	821
Translation	GH-DVVQP-GARCCFGQGRAGDRAGPAGDWHADWRAD AISGRC----RSVSGVVVQHAA	857
PSEU2 MdtB	KAVKVI EEVEQEIGMPIGVQTQFQGA AEAFQASLSST LLLILA AVVTMYIVLGVLYESYI	881
Translation	ADSGGSG-DHVHRAGRAL-ELHSPDHHPLD TAVGGCRCLAGVADQRQ RSGHDRDRHHHSA	915
PSEU2 MdtB	HPITILSTLPSAAVGALLALLISGNDLGM-IAIIGIILLIGIVKKNAIMMIDFA--LDA	937
Translation	DRHRQ---EKRHHD---DRLRPGRRTKPRR-----RAGNGHL-SGAAA	951
PSEU2 MdtB	ERNRSVAPEQAIYDAALLRFRPILMTTLAALFGAIPMLASGSGAELRQPLGLVMVGGLL	997
Translation	LPANPDDHTGRVVRCSADAGERLRCRIASAVGPGNGRRSVAEPSADAVYHAGHLPVLR S	1011
PSEU2 MdtB	LSQVLTFTT PVIYLYFDRLGRRWSRKP---ADPDRQER-----ADA-----	1036
Translation	SGQALEPQAGCPGSHRTG-RM	1031
PSEU2 MdtB	-----	1036

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 diazoefficiens* 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.

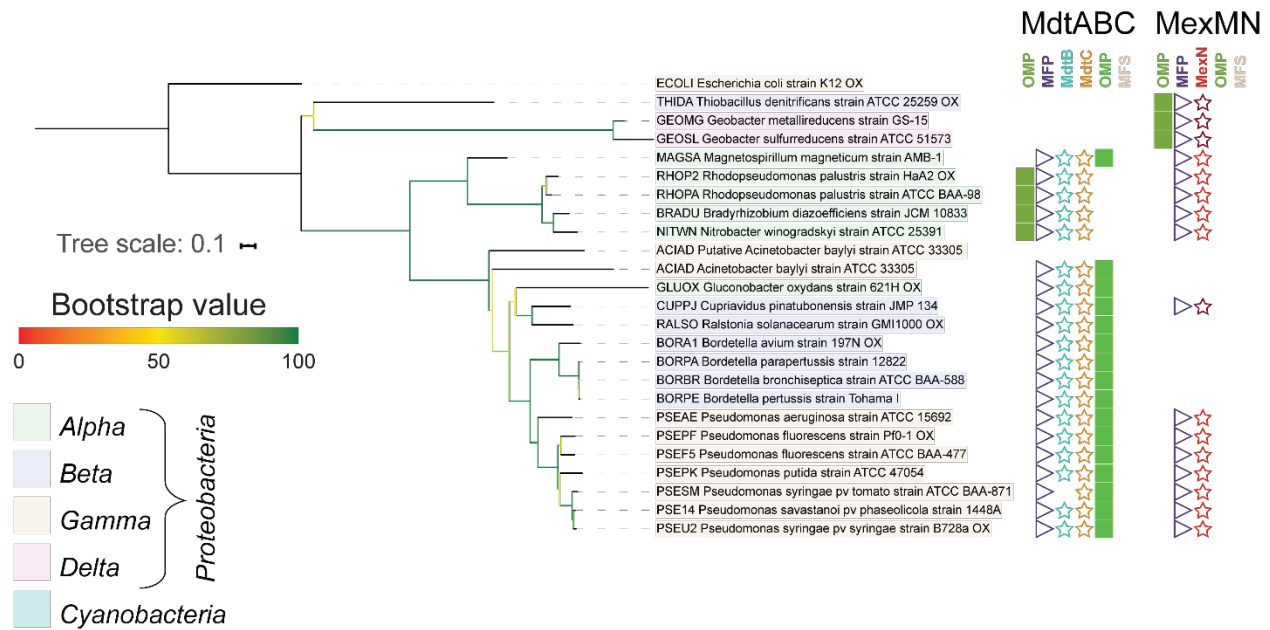
Acinetobacter baylyi contains two sets of RND protein pairs, Q6FD21 & Q6FD22, and Q6F786 & Q6F787. Judging just by their genomic neighborhood they are both two RND subunit containing systems of similar architecture: MFP-RND1-RND2-OMP. The sequence identity and similarity values between the two systems 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

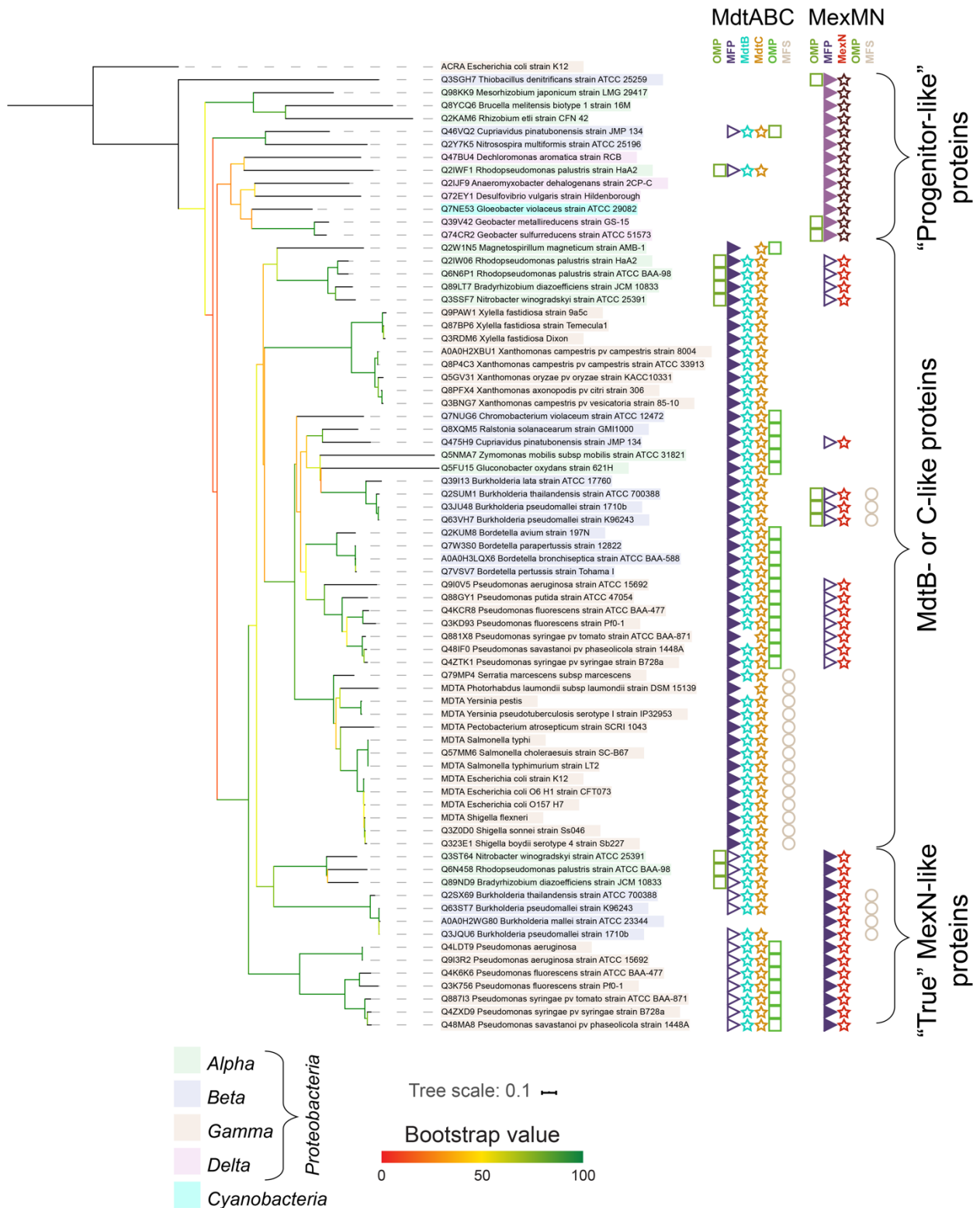
It is particularly difficult to do phylogenetic analyses of outer membrane proteins due to their unique architecture: the outwards facing transmembrane residues are never strongly conserved, seriously decreasing the number of residues available for alignment. Moreover, most outer membrane proteins have 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 flexneri.	Efflux pump membrane transporter
A0A0H2V123	Shigella flexneri.	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)	Acridflavin 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
A0A0H2WWS3	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)	Acridflavin 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

A0A0H2XBS4	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain 8004)	Acridflavin resistance protein
A0A0H2XE02	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain 8004)	Cation efflux system protein
A0A0H3G1R6	<i>Brucella suis</i> biovar 1 (strain 1330)	AcrB/AcrD/AcrF multidrug efflux protein
A0A0H3G714	<i>Brucella suis</i> biovar 1 (strain 1330)	AcrB/AcrD/AcrF multidrug efflux protein
A0A0H3GFZ4	<i>Brucella suis</i> biovar 1 (strain 1330)	AcrB/AcrD/AcrF multidrug efflux protein
A0A0H3JMN8	<i>Escherichia coli</i> O157:H7.	Efflux pump membrane transporter
A0A0H3JN48	<i>Staphylococcus aureus</i> (strain N315)	SA2056 protein
A0A0H3K0N2	<i>Staphylococcus aureus</i> (strain Mu50 / ATCC 700699)	Similar to acridflavin resistance protein
A0A0H3K3Z1	<i>Synechococcus</i> sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1)	RND multidrug efflux transporter
A0A0H3K464	<i>Staphylococcus aureus</i> (strain MW2)	MW2179 protein
A0A0H3K4S1	<i>Synechococcus</i> sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1)	Probable cation efflux system protein
A0A0H3LLX7	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	Efflux pump membrane transporter
A0A0H3LQU0	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	Efflux pump membrane transporter
A0A0H3LQV1	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	AcrB/AcrD/AcrF family protein
A0A0H3LT18	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	Efflux pump membrane transporter
A0A0H3LT79	<i>Bartonella quintana</i> (strain Toulouse)	Acridflavin resistance protein d
A0A0H3LUJ4	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	Integral membrane component of multidrug efflux system
A0A0H3LWT2	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	Probable membrane protein
A0A0H3LZH6	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50)	AcrB/AcrD/AcrF family protein
A0A0H3M8G5	<i>Ehrlichia ruminantium</i> (strain Welgevonden)	Probable aminoglycoside efflux pump (Acridflavine resistance protein D)
A0A0R4J7B3	<i>Bartonella henselae</i> (strain ATCC 49882 / DSM 28221 / Houston 1)	Acridflavin resistance protein d
O06471	<i>Burkholderia cepacia</i>	Efflux pump membrane transporter
O25328	<i>Helicobacter pylori</i> (strain ATCC 700392 / 26695)	Acridflavine resistance protein (AcrB)
O25622	<i>Helicobacter pylori</i> (strain ATCC 700392 / 26695)	Cation efflux system protein (CzcA)
O25887	<i>Helicobacter pylori</i> (strain ATCC 700392 / 26695)	Cation efflux system protein (CzcA)
O31100	<i>Pseudomonas putida</i>	Solvent-resistant pump membrane transporter SrpB
O31501	<i>Bacillus subtilis</i> (strain 168)	Swarming motility protein SwrC
O52248	<i>Pseudomonas putida</i> (strain DOT-T1E)	Toluene efflux pump membrane transporter TtgB
O66770	<i>Aquifex aeolicus</i> (strain VF5)	Cation efflux system (AcrB/AcrD/AcrF family)

O66916	<i>Aquifex aeolicus</i> (strain VF5)	Cation efflux system (AcrB/AcrD/AcrF family)
O66977	<i>Aquifex aeolicus</i> (strain VF5)	Cation efflux (AcrB/AcrD/AcrF family)
O68962	<i>Helicobacter pylori</i>	RND pump protein
O87936	<i>Burkholderia pseudomallei</i>	Efflux pump membrane transporter
POC070	<i>Pseudomonas putida</i>	Multidrug/solvent efflux pump membrane transporter MepB
P13511	<i>Cupriavidus metallidurans</i> (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34)	Cobalt-zinc-cadmium resistance protein CzcA
P24177	<i>Escherichia coli</i> (strain K12)	Probable aminoglycoside efflux pump
P24181	<i>Escherichia coli</i> (strain K12)	Multidrug export protein AcrF
P25197	<i>Rhizobium meliloti</i> (strain 1021)	Nodulation protein NolG
P31224	<i>Escherichia coli</i> (strain K12)	Multidrug efflux pump subunit AcrB
P37637	<i>Escherichia coli</i> (strain K12)	Multidrug resistance protein MdtF
P37972	<i>Cupriavidus metallidurans</i> (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34)	Nickel and cobalt resistance protein CnrA
P38054	<i>Escherichia coli</i> (strain K12)	Cation efflux system protein CusA
P52002	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 /JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Multidrug resistance protein MexB
P69340	<i>Shigella flexneri</i> .	Multidrug resistance protein MdtB
P73998	<i>Synechocystis</i> sp. (strain PCC 6803 / Kazusa)	Cation or drug efflux system protein
P74461	<i>Synechocystis</i> sp. (strain PCC 6803 / Kazusa)	Cation or drug efflux system protein
P76398	<i>Escherichia coli</i> (strain K12)	Multidrug resistance protein MdtB
P76399	<i>Escherichia coli</i> (strain K12)	Multidrug resistance protein MdtC
P94177	<i>Alcaligenes</i> sp. (strain CT14)	Cation efflux system protein CzcA
P95422	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter
Q2IGB6	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Heavy metal efflux pump CzcA
Q2IGC8	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2IGK2	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2IHW6	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2IJG5	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2IK25	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2IMH0	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Acriflavin resistance protein
Q2INB4	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Efflux pump membrane transporter
Q2IPR5	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C)	Heavy metal efflux pump CzcA

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
Q2IUK5	Rhodopseudomonas palustris (strain HaA2)	Acriflavin resistance protein
Q2IUW1	Rhodopseudomonas palustris (strain HaA2)	Efflux pump membrane transporter
Q2IW07	Rhodopseudomonas palustris (strain HaA2)	Acriflavin resistance protein
Q2IW08	Rhodopseudomonas palustris (strain HaA2)	Acriflavin resistance protein
Q2IWF2	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)	Putative 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
Q2KXM0	Bordetella avium (strain 197N)	Efflux pump membrane transporter
Q2KZR5	Bordetella avium (strain 197N)	Efflux pump membrane transporter
Q2L1H0	Bordetella avium (strain 197N)	Efflux pump membrane transporter
Q2LRD7	Syntrophus aciditrophicus (strain SB)	Efflux pump membrane transporter
Q2LY61	Syntrophus aciditrophicus (strain SB)	Efflux pump membrane transporter

Q2NBE8	<i>Erythrobacter litoralis</i> (strain HTCC2594)	Heavy metal RND efflux transporter Czca family protein
Q2NBG2	<i>Erythrobacter litoralis</i> (strain HTCC2594)	Metal ion efflux RND protein family protein
Q2NV66	<i>Sodalis glossinidius</i> (strain morsitans)	Efflux pump membrane transporter
Q2RFY8	<i>Moorella thermoacetica</i> (strain ATCC 39073 / JCM 9320)	Acriflavin resistance protein
Q2RN02	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Acriflavin resistance protein
Q2RQ71	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Acriflavin resistance protein
Q2RSK1	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Acriflavin resistance protein
Q2RSP4	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Efflux pump membrane transporter
Q2RVC6	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Efflux pump membrane transporter
Q2RW08	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG4362 / NCIB 8255 / S1)	Efflux pump membrane transporter
Q2RYR4	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Cation efflux system protein czca
Q2S141	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Transporter AcrB/D/F family
Q2S3C4	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Acriflavine resistance protein (Cation efflux system)
Q2S4L8	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Multidrug resistance protein putative
Q2S5B3	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Multidrug efflux transporter AcrB/AcrD/AcrF family
Q2S5Q5	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Cation/multidrug efflux pump
Q2S6E3	<i>Salinibacter ruber</i> (strain DSM 13855 / M31)	Transporter AcrB/D/F family
Q2S716	<i>Hahella chejuensis</i> (strain KCTC 2396)	Efflux pump membrane transporter
Q2S728	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SB32	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SET3	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SF27	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SFQ4	<i>Hahella chejuensis</i> (strain KCTC 2396)	Efflux pump membrane transporter
Q2SFT2	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SHT7	<i>Hahella chejuensis</i> (strain KCTC 2396)	Putative silver efflux pump
Q2SJY0	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SM00	<i>Hahella chejuensis</i> (strain KCTC 2396)	Cation/multidrug efflux pump
Q2SUM0	<i>Burkholderia thailandensis</i> (strain ATCC 700388 / DSM 13276 / CIP106301 / E264)	AcrB/AcrD/AcrF family protein

Q2SVT4	Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264)	Efflux pump membrane transporter
Q2SW90	Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264)	AcrB/AcrD/AcrF family protein
Q2SX70	Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP106301 / E264)	AcrB/AcrD/AcrF family protein
Q2TOR2	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	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Cobalt-zinc-cadmium resistance protein CzcA
Q2Y7K6	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Acriflavin resistance protein
Q2Y896	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Efflux pump membrane transporter
Q2Y8I2	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Cobalt-zinc-cadmium resistance protein CzcA
Q2Y962	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Cu(I)/Ag(I) efflux system membrane protein CusA/SiA
Q2YA05	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Cobalt-zinc-cadmium resistance protein CzcA
Q2YAR7	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Efflux pump membrane transporter
Q2YB73	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Efflux pump membrane transporter
Q2YB76	Nitrosospora multiformis (strain ATCC 25196 / NCIMB 11849 / C 71)	Efflux pump membrane transporter
Q2YD19	Nitrosospora 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

Q2YPE6	<i>Brucella abortus</i> (strain 2308)	Efflux pump membrane transporter
Q2YPZ1	<i>Brucella abortus</i> (strain 2308)	Acriflavin resistance protein
Q2Z053	uncultured bacterium.	Heavy metal efflux pump
Q30B59	<i>Acinetobacter</i> sp. 4365.	Efflux pump membrane transporter
Q30NZ6	<i>Sulfurimonas denitrificans</i> (strain ATCC 33889 / DSM 1251)	Resistance-Nodulation-Cell Division Superfamily transporter
Q30QL4	<i>Sulfurimonas denitrificans</i> (strain ATCC 33889 / DSM 1251)	Resistance-Nodulation-Cell Division Superfamily transporter
Q30S70	<i>Sulfurimonas denitrificans</i> (strain ATCC 33889 / DSM 1251)	Resistance-Nodulation-Cell Division Superfamily transporter
Q30T66	<i>Sulfurimonas denitrificans</i> (strain ATCC 33889 / DSM 1251)	Efflux pump membrane transporter
Q311N6	<i>Desulfovibrio alaskensis</i> (strain G20)	Acriflavin resistance protein
Q313Y0	<i>Desulfovibrio alaskensis</i> (strain G20)	Acriflavin resistance protein
Q315C5	<i>Desulfovibrio alaskensis</i> (strain G20)	Acriflavin resistance protein
Q315P7	<i>Desulfovibrio alaskensis</i> (strain G20)	Acriflavin resistance protein
Q316E4	<i>Desulfovibrio alaskensis</i> (strain G20)	Efflux pump membrane transporter
Q31DT9	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31E33	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31EH5	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31EQ3	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31EX8	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31FE9	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Efflux pump membrane transporter
Q31FQ2	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31J34	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31JL9	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily transporter
Q31JR8	<i>Hydrogenovibrio crunogenus</i> (strain XCL-2)	Resistance-Nodulation-Cell Division (RND) superfamily cation efflux transporter
Q31KM0	<i>Synechococcus elongatus</i> (strain PCC 7942)	Hydrophobe/amphiphile efflux-1 HAE1
Q31M20	<i>Synechococcus elongatus</i> (strain PCC 7942)	Probable cation efflux system protein
Q31VB1	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Efflux pump membrane transporter
Q31W02	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Efflux pump membrane transporter
Q323D9	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Multidrug resistance protein MdtC
Q323E0	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Multidrug resistance protein MdtB
Q324W8	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Putative inner membrane component for iron transport
Q325D4	<i>Shigella boydii</i> serotype 4 (strain Sb227)	Efflux pump membrane transporter

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)	Acridin 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)	Acridin 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)	Acridin 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	<i>Geobacter metallireducens</i> (strain GS-15 / ATCC 53774 / DSM 7210)	Efflux pump membrane transporter
Q39V41	<i>Geobacter metallireducens</i> (strain GS-15 / ATCC 53774 / DSM 7210)	Efflux pump RND family inner membrane protein AcrB/AcrD/AcrF family
Q39VE3	<i>Geobacter metallireducens</i> (strain GS-15 / ATCC 53774 / DSM 7210)	Metal ion efflux pump RND family inner membrane protein
Q39XH2	<i>Geobacter metallireducens</i> (strain GS-15 / ATCC 53774 / DSM 7210)	Efflux pump membrane transporter
Q39ZX7	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / NBRC 103641 / GraBd1)	Efflux pump membrane transporter
Q3A2C4	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / NBRC 103641 / GraBd1)	Efflux pump RND family inner membrane protein AcrB/AcrD/AcrF family
Q3A5K8	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / NBRC 103641 / GraBd1)	Efflux pump membrane transporter
Q3A6S9	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / NBRC 103641 / GraBd1)	Efflux pump RND family inner membrane protein
Q3A7U6	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / NBRC 103641 / GraBd1)	Efflux pump membrane transporter
Q3ARB0	<i>Chlorobium chlorochromatii</i> (strain CaD3)	Hydrophobe/amphiphile efflux-1 HAE1
Q3ARZ1	<i>Chlorobium chlorochromatii</i> (strain CaD3)	NolG efflux transporter
Q3AUC4	<i>Chlorobium chlorochromatii</i> (strain CaD3)	AcrB/AcrD/AcrF family protein
Q3B1E0	<i>Chlorobium luteolum</i> (strain DSM 273 / 2530)	AcrB/AcrD/AcrF family protein
Q3B4Q3	<i>Chlorobium luteolum</i> (strain DSM 273 / 2530)	Hydrophobe/amphiphile efflux-1 HAE1
Q3B4Z4	<i>Chlorobium luteolum</i> (strain DSM 273 / 2530)	RND family efflux transporter
Q3BMM3	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BNG5	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BPY9	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BR79	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	Efflux pump membrane transporter
Q3BRC2	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BS55	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	Efflux pump membrane transporter
Q3BSU9	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	Efflux pump membrane transporter
Q3BTF0	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BTF1	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BTS5	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BVE1	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	Efflux pump membrane transporter

Q3BYG6	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	RND superfamily protein
Q3BYU5	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)	Efflux pump membrane transporter
Q3ER77	<i>Bacillus thuringiensis</i> serovar <i>israelensis</i> ATCC 35646.	Acriflavin resistance plasma membrane protein
Q3IBZ0	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Efflux pump membrane transporter
Q3IC20	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Efflux pump membrane transporter
Q3ICA5	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative metabolite exporter AcrB/D/F family
Q3ICE4	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative metabolite exporter AcrB/D/F family
Q3IHS9	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative <i>acrB/acrD/acrF</i> acriflavin resistance family protein
Q3IK01	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative multidrug resistance protein AcrB/AcrD/AcrF family
Q3IKS0	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative transport protein
Q3ILD1	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Cation efflux system protein <i>cusA</i>
Q3ILG7	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Cobalt-zinc-cadmium resistance protein <i>czcA</i> (Cation efflux system protein <i>czcA</i>)
Q3ILI6	<i>Pseudoalteromonas haloplanktis</i> (strain TAC 125)	Putative multidrug resistance protein(AcrB/AcrD/AcrF family)
Q3IX11	<i>Rhodobacter sphaeroides</i> (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158)	Efflux pump membrane transporter
Q3J0Q2	<i>Rhodobacter sphaeroides</i> (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158)	AcrB/AcrD/AcrF family cation/multidrug efflux pump
Q3J2H3	<i>Rhodobacter sphaeroides</i> (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158)	Multidrug/cation efflux pump RND superfamily
Q3J2M9	<i>Rhodobacter sphaeroides</i> (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158)	Cation/multidrug efflux pump RND superfamily
Q3J4A5	<i>Rhodobacter sphaeroides</i> (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM158)	AcrB/AcrD/AcrF multidrug efflux pump
Q3J715	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Acriflavin resistance protein
Q3J9P1	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Acriflavin resistance protein
Q3JA51	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Efflux pump membrane transporter
Q3JAX7	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Heavy metal efflux pump
Q3JBG1	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Heavy metal efflux pump
Q3JC12	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Efflux pump membrane transporter
Q3JEC3	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Heavy metal efflux pump

Q3JEL4	Nitrosococcus oceani (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Acridflavin resistance protein
Q3JERO	Nitrosococcus oceani (strain ATCC 19707 / BCRC 17464 / NCIMB 11848 /C-107)	Heavy metal efflux pump
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
Q3KCK7	Pseudomonas fluorescens (strain Pf0-1)	Efflux pump membrane transporter
Q3KCV6	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
Q3KHD3	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 / PCC 7937)	Acridflavin resistance protein
Q3M6E3	Anabaena variabilis (strain ATCC 29413 / PCC 7937)	Hydrophobe/amphiphile efflux-1 HAE1
Q3MA27	Anabaena variabilis (strain ATCC 29413 / PCC 7937)	Acridflavin resistance protein
Q3RC69	Xylella fastidiosa Dixon.	Efflux pump membrane transporter
Q3RC79	Xylella fastidiosa Dixon.	Acridflavin resistance protein
Q3RDM8	Xylella fastidiosa Dixon.	Acridflavin resistance protein
Q3SFX2	Thiobacillus denitrificans (strain ATCC 25259)	Probable transmembrane drug efflux protein

Q3SGA0	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Acriflavin resistance protein
Q3SGH8	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Probable RND efflux transporter
Q3SI34	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Heavy metal efflux pump CzcA
Q3SI00	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Efflux pump membrane transporter
Q3SI81	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Heavy metal efflux pump CzcA
Q3SI87	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Heavy metal efflux pump CzcA
Q3SKD0	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Heavy metal efflux pump CzcA
Q3SME9	<i>Thiobacillus denitrificans</i> (strain ATCC 25259)	Heavy metal efflux pump CzcA
Q3SMW3	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Heavy metal efflux pump CzcA
Q3SN60	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Acriflavin resistance protein
Q3SNIO	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Heavy metal efflux pump CzcA
Q3SNZ7	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Efflux pump membrane transporter
Q3SQA4	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Acriflavin resistance protein
Q3SSF8	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Acriflavin resistance protein
Q3SSF9	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Acriflavin resistance protein
Q3SSM3	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Heavy metal efflux pump CzcA
Q3ST65	<i>Nitrobacter winogradskyi</i> (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)	Acriflavin resistance protein
Q3YRZ9	<i>Ehrlichia canis</i> (strain Jake)	Acriflavin resistance protein
Q3YWI8	<i>Shigella sonnei</i> (strain Ss046)	Efflux pump membrane transporter
Q3YZ83	<i>Shigella sonnei</i> (strain Ss046)	Efflux pump membrane transporter
Q3Z0C8	<i>Shigella sonnei</i> (strain Ss046)	Multidrug resistance protein MdtC
Q3Z0C9	<i>Shigella sonnei</i> (strain Ss046)	Multidrug resistance protein MdtB
Q3Z4L7	<i>Shigella sonnei</i> (strain Ss046)	Putative inner membrane component for iron transport
Q3Z4T7	<i>Shigella sonnei</i> (strain Ss046)	Efflux pump membrane transporter
Q44586	<i>Alcaligenes xylosoxydans xylosoxydans</i>	Nickel-cobalt-cadmium resistance protein NccA
Q46MN5	<i>Cupriavidus necator</i> (strain JMP 134 / LMG 1197)	Efflux pump membrane transporter

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
Q47EW0	Dechloromonas aromatica (strain RCB)	Heavy metal efflux pump CzcA
Q47GU7	Dechloromonas aromatica (strain RCB)	Heavy metal efflux pump CzcA
Q47IW5	Dechloromonas aromatica (strain RCB)	Acriflavin resistance protein
Q47JC6	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

Q47UM5	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	Cation efflux system protein CusA
Q47V77	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q47VA5	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q47VP1	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q47X86	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q480E7	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	Heavy metal efflux pump CzcA family
Q480Y8	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q483S5	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q483S7	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	Putative RND efflux system protein
Q484D7	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q485I6	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	Efflux pump membrane transporter
Q486B7	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	Efflux pump membrane transporter
Q48815	<i>Legionella pneumophila</i> .	Protein HeIA
Q488L9	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q48A59	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	AcrB/AcrD/AcrF family protein
Q48CG6	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Cation efflux family protein
Q48EP3	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Efflux pump membrane transporter
Q48HB1	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Transporter AcrB/AcrD/AcrF family
Q48HP4	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Efflux pump membrane transporter
Q48IE8	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Multidrug RND efflux transporter permease protein MdtC
Q48IE9	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Multidrug RND efflux transporter permease protein MdtB
Q48J50	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Efflux pump membrane transporter
Q48JE7	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	Efflux pump membrane transporter
Q48MA9	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	RND efflux transporter AcrB/AcrD/AcrF family
Q48NJ4	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	RND efflux transporter hydrophobe/amphiphile efflux-1 (HAE1) family

Q48PN7	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6)	RND efflux transporter hydrophobe/amphiphile efflux-1 (HAE1) family
Q49ZH9	<i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41)	Putative cation multidrug efflux pump
Q4BYX0	<i>Crocospaera watsonii</i> WH 8501.	Hydrophobe/amphiphile efflux-1 HAE1
Q4C067	<i>Crocospaera watsonii</i> WH 8501.	Hydrophobe/amphiphile efflux-1 HAE1
Q4ECJ9	<i>Wolbachia</i> endosymbiont of <i>Drosophila ananassae</i> .	MMPL family protein
Q4FP77	<i>Pelagibacter ubique</i> (strain HTCC1062)	AcrB/AcrD/AcrF family protein (Acriflavin resistance)
Q4FPX8	<i>Psychrobacter arcticus</i> (strain DSM 17307 / 273-4)	RND superfamily multidrug efflux pump
Q4FRD4	<i>Psychrobacter arcticus</i> (strain DSM 17307 / 273-4)	Efflux pump membrane transporter
Q4K638	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Cobalt/zinc/cadmium resistance protein CzcA
Q4K6K5	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter heavy metal efflux (HME) family permease protein
Q4KAL4	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter HAE1 family
Q4KBK7	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Efflux pump membrane transporter
Q4KBN7	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Efflux pump membrane transporter
Q4KCR6	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Multidrug RND efflux transporter permease protein MdtC
Q4KCR7	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Multidrug RND efflux transporter permease protein MdtB
Q4KDL8	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter heavy metal efflux (HME) family permease protein
Q4KH23	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	Efflux pump membrane transporter
Q4KHJ4	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter hydrophobe/amphiphile efflux-1 (HAE1) family permease protein
Q4KHX4	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter HAE1 family
Q4KK49	<i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23932 / Pf-5)	RND transporter hydrophobe/amphiphile efflux-1 (HAE1) family permease protein
Q4L8C5	<i>Staphylococcus haemolyticus</i> (strain JCSC1435)	Uncharacterized protein
Q4LDT6	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter
Q4LDT8	<i>Pseudomonas aeruginosa</i> .	RND multidrug efflux transporter MexN
Q4QM13	<i>Haemophilus influenzae</i> (strain 86-028NP)	Predicted cation/multidrug efflux pump
Q4UKH1	<i>Rickettsia felis</i> (strain ATCC VR-1525 / URRWXCa2)	Hydrophobe/amphiphile efflux-1 HAE1 family protein
Q4VSJ4	<i>Burkholderia glumae</i>	Probable RND efflux transporter

Q4ZLZ2	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Heavy metal efflux pump CzcA
Q4ZP84	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Efflux pump membrane transporter
Q4ZRQ8	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZS70	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Efflux pump membrane transporter
Q4ZSH1	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Efflux pump membrane transporter
Q4ZT61	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZTJ9	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZTK0	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZU47	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Efflux pump membrane transporter
Q4ZUD5	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZXE0	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q4ZZK4	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a)	Acridflavin resistance protein
Q51073	<i>Neisseria gonorrhoeae</i> .	Efflux pump membrane transporter
Q51396	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter
Q55584	<i>Synechocystis</i> sp. (strain PCC 6803 / Kazusa)	Cation or drug efflux system protein
Q55935	<i>Synechocystis</i> sp. (strain PCC 6803 / Kazusa)	Cation or drug efflux system protein
Q57124	<i>Haemophilus influenzae</i> (strain ATCC 51907 / DSM 11121 / KW20 / Rd)	Uncharacterized transporter HI_0895
Q579D3	<i>Brucella abortus</i> biovar 1 (strain 9-941)	AcrB/AcrD/AcrF multidrug efflux protein
Q57D49	<i>Brucella abortus</i> biovar 1 (strain 9-941)	AcrB/AcrD/AcrF multidrug efflux protein
Q57F66	<i>Brucella abortus</i> biovar 1 (strain 9-941)	Efflux pump membrane transporter
Q57F78	<i>Brucella abortus</i> biovar 1 (strain 9-941)	AcrB/AcrD/AcrF multidrug efflux protein
Q57J78	<i>Salmonella choleraesuis</i> (strain SC-B67)	Efflux pump membrane transporter
Q57LN0	<i>Salmonella choleraesuis</i> (strain SC-B67)	Efflux pump membrane transporter
Q57MM4	<i>Salmonella choleraesuis</i> (strain SC-B67)	Multidrug resistance protein MdtC
Q57MM5	<i>Salmonella choleraesuis</i> (strain SC-B67)	Multidrug resistance protein MdtB
Q57S88	<i>Salmonella choleraesuis</i> (strain SC-B67)	Efflux pump membrane transporter
Q58AF4	<i>Cupriavidus metallidurans</i> (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	<i>Cupriavidus metallidurans</i> (strain ATCC 43123 / DSM 2839 / NBRC 102507/ CH34)	NccA three components proton antiporter cation efflux system cation efflux pump
Q5DYC7	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Efflux pump membrane transporter

Q5DZ19	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Efflux pump membrane transporter
Q5E0D1	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Copper/silver efflux system membrane component
Q5E0L9	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5E1S7	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5E2W9	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5E4H0	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5E5L7	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5E853	<i>Aliivibrio fischeri</i> (strain ATCC 700601 / ES114)	Acriflavin resistance plasma membrane protein
Q5F725	<i>Neisseria gonorrhoeae</i> (strain ATCC 700825 / FA 1090)	Efflux pump membrane transporter
Q5FGX1	<i>Ehrlichia ruminantium</i> (strain Gardel)	Probable aminoglycoside efflux pump (Acriflavine resistance protein D)
Q5FSA3	<i>Gluconobacter oxydans</i> (strain 621H)	Cation efflux system protein CzcA
Q5FT29	<i>Gluconobacter oxydans</i> (strain 621H)	Efflux pump membrane transporter
Q5FTG4	<i>Gluconobacter oxydans</i> (strain 621H)	Heavy-metal ion transporter Hela
Q5FTX0	<i>Gluconobacter oxydans</i> (strain 621H)	Putative transport transmembrane protein
Q5FU14	<i>Gluconobacter oxydans</i> (strain 621H)	Acriflavin resistance protein D
Q5G7J3	<i>Rhizobium etli</i> .	Efflux pump membrane transporter
Q5GV29	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain KACC10331 / KXO85)	Acriflavin resistance protein
Q5GXC3	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain KACC10331 / KXO85)	Acriflavin resistance protein
Q5GZ12	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain KACC10331 / KXO85)	Efflux pump membrane transporter
Q5H2K4	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain KACC10331 / KXO85)	Acriflavin resistance protein
Q5HLY7	<i>Staphylococcus epidermidis</i> (strain ATCC 35984 / RP62A)	AcrB/AcrD/AcrF family protein
Q5IS02	<i>Morganella morganii</i>	Efflux pump membrane transporter
Q5KWT2	<i>Geobacillus kaustophilus</i> (strain HTA426)	Hypothetical conserved protein
Q5L7H0	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative transmembrane AcrB/D/F-family transporter
Q5L8F0	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative transmembrane Acr-type transport protein
Q5L8Q3	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative transport related membrane protein
Q5L990	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative transport-related membrane protein
Q5L9M7	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative metal resistance related transport membrane protein

Q5LA33	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative multidrug resistance/siderophore transport related membrane protein
Q5LAI6	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative transport-related membrane protein
Q5LB81	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative aminoglycoside efflux pump
Q5LCI8	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative drug resistance transport-related membrane protein
Q5LD76	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative cation efflux-related membrane protein
Q5LDG2	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative cation transport related membrane protein
Q5LHM2	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative AcrB/AcrD/AcrF family efflux transporter
Q5LIU3	<i>Bacteroides fragilis</i> (strain ATCC 25285 / DSM 2151 / JCM 11019 /NCTC 9343)	Putative AcrB/AcrD family RND transport protein
Q5LT89	<i>Ruegeria pomeroyi</i> (strain ATCC 700808 / DSM 15171 / DSS-3)	Transporter AcrB/AcrD/AcrF family
Q5LTL7	<i>Ruegeria pomeroyi</i> (strain ATCC 700808 / DSM 15171 / DSS-3)	Efflux pump membrane transporter
Q5LUY1	<i>Ruegeria pomeroyi</i> (strain ATCC 700808 / DSM 15171 / DSS-3)	Transporter AcrB/AcrD/AcrF family
Q5LX87	<i>Ruegeria pomeroyi</i> (strain ATCC 700808 / DSM 15171 / DSS-3)	Transporter AcrB/AcrD/AcrF family
Q5NIG7	<i>Francisella tularensis</i> subsp. <i>tularensis</i> (strain SCHU S4 / Schu 4)	Transporter AcrB/AcrD/AcrF family
Q5NMA8	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> (strain ATCC 31821 / ZM4 / CP4)	Acriflavin resistance protein
Q5NQU7	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> (strain ATCC 31821 / ZM4 / CP4)	Efflux pump membrane transporter
Q5NXR2	<i>Aromatoleum aromaticum</i> (strain EbN1)	Cation/multidrug efflux pump protein
Q5P2W3	<i>Aromatoleum aromaticum</i> (strain EbN1)	Probable cation efflux system protein CZCA
Q5P2Z3	<i>Aromatoleum aromaticum</i> (strain EbN1)	Predicted acriflavin resistance protein
Q5P5T6	<i>Aromatoleum aromaticum</i> (strain EbN1)	Cation efflux system protein
Q5P649	<i>Aromatoleum aromaticum</i> (strain EbN1)	Efflux pump membrane transporter
Q5P6P0	<i>Aromatoleum aromaticum</i> (strain EbN1)	Probable RND efflux transporter
Q5PDW7	<i>Salmonella paratyphi</i> A (strain ATCC 9150 / SARB42)	Multidrug resistance protein MdtB
Q5PDW8	<i>Salmonella paratyphi</i> A (strain ATCC 9150 / SARB42)	Multidrug resistance protein MdtC
Q5QUF0	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Co/Zn/Cd efflux system membrane component
Q5QVV8	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	RND family efflux transporter
Q5QWZ8	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	RND family efflux transporter
Q5QYY6	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	RND family efflux transporter

Q5R021	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Probable Co/Zn/Cd efflux system membrane component
Q5R024	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	RND family efflux transporter
Q5R0E7	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Efflux pump membrane transporter
Q5R0R1	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	RND family efflux transporter
Q5R0W3	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Metal efflux system membrane component (Silver efflux pump related)
Q5R0W8	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Metal efflux system membrane component (Silver efflux pump related)
Q5R138	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR)	Co/Zn/Cd efflux system membrane component
Q5WCH2	<i>Bacillus clausii</i> (strain KSM-K16)	AcrB/AcrD/AcrF family cation/multidrug efflux pump
Q5WTT9	<i>Legionella pneumophila</i> (strain Lens)	Efflux pump membrane transporter
Q5WUR4	<i>Legionella pneumophila</i> (strain Lens)	Efflux pump membrane transporter
Q5WUV4	<i>Legionella pneumophila</i> (strain Lens)	Chemiosmotic efflux system protein A-like protein
Q5WXP7	<i>Legionella pneumophila</i> (strain Lens)	HelA protein
Q5WYH9	<i>Legionella pneumophila</i> (strain Lens)	Uncharacterized protein
Q5ZSK5	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Efflux pump membrane transporter
Q5ZTI4	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Efflux pump membrane transporter
Q5ZTM7	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Chemiosmotic efflux system protein A (CzcA)
Q5ZWI9	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Chemiosmotic efflux system B protein A
Q5ZWQ6	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Chemiosmotic efflux system protein A-like protein
Q5ZWR5	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Chemiosmotic efflux system B protein A
Q5ZWS7	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Cobalt/zinc/cadmium efflux RND transporter permease protein HelA
Q5ZXL1	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> (strain Philadelphia 1 /ATCC 33152 / DSM 7513)	Multidrug resistance protein
Q603J0	<i>Methylococcus capsulatus</i> (strain ATCC 33009 / NCIMB 11132 / Bath)	AcrB/AcrD/AcrF family protein
Q603S9	<i>Methylococcus capsulatus</i> (strain ATCC 33009 / NCIMB 11132 / Bath)	Heavy metal efflux pump CzcA family

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

Q64PF1	<i>Bacteroides fragilis</i> (strain YCH46)	AcrB/AcrD/AcrF family cation efflux system protein
Q64PW6	<i>Bacteroides fragilis</i> (strain YCH46)	AcrB/AcrD/AcrF family cation efflux system protein
Q64QE5	<i>Bacteroides fragilis</i> (strain YCH46)	AcrB/AcrD family multidrug resistance protein
Q64RM7	<i>Bacteroides fragilis</i> (strain YCH46)	Putative aminoglycoside efflux pump
Q64TN7	<i>Bacteroides fragilis</i> (strain YCH46)	Putative cation efflux pump
Q64U98	<i>Bacteroides fragilis</i> (strain YCH46)	Cation efflux system protein CzcA
Q64UJ0	<i>Bacteroides fragilis</i> (strain YCH46)	CzcA family cation efflux system protein
Q64YJ6	<i>Bacteroides fragilis</i> (strain YCH46)	Multidrug efflux membrane fusion protein
Q64ZY7	<i>Bacteroides fragilis</i> (strain YCH46)	AcrB/AcrD family multidrug resistance protein
Q65MP2	<i>Bacillus licheniformis</i> (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	Swarming and motility protein SwrC
Q65QR6	<i>Mannheimia succiniciproducens</i> (strain MBEL55E)	AcrB protein
Q65VE8	<i>Mannheimia succiniciproducens</i> (strain MBEL55E)	AcrB protein
Q662M2	<i>Borrelia burgdorferi sensu stricto</i> (strain ATCC BAA-2496 / DSM 23469 / PBi)	Acriflavine resistance protein
Q666F2	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Efflux pump membrane transporter
Q668C5	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Multidrug resistance protein MdtC
Q668C6	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Multidrug resistance protein MdtB
Q668H5	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Efflux pump membrane transporter
Q66DR0	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Efflux pump membrane transporter
Q66EX5	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Putative heavy metal/multi-drug efflux protein RND family
Q66F48	<i>Yersinia pseudotuberculosis</i> serotype I (strain IP32953)	Efflux pump membrane transporter
Q67J93	<i>Symbiobacterium thermophilum</i> (strain T / IAM 14863)	AcrB family membrane transport protein
Q68XJ7	<i>Rickettsia typhi</i> (strain ATCC VR-144 / Wilmington)	Acriflavin resistance protein D
Q69HW2	<i>Escherichia coli</i> .	Efflux pump membrane transporter
Q6AJB4	<i>Desulfotalea psychrophila</i> (strain Lsv54 / DSM 12343)	Related to cobalt-zinc-cadmium resistance protein (CzcA)
Q6ALC4	<i>Desulfotalea psychrophila</i> (strain Lsv54 / DSM 12343)	Related to multidrug-efflux transport protein
Q6AMJ9	<i>Desulfotalea psychrophila</i> (strain Lsv54 / DSM 12343)	Efflux pump membrane transporter
Q6ARC4	<i>Desulfotalea psychrophila</i> (strain Lsv54 / DSM 12343)	Probable cation efflux system protein (CzcA)

Q6CZM0	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Efflux pump membrane transporter
Q6D1J9	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Efflux pump membrane transporter
Q6D2B0	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Multidrug resistance protein MdtC
Q6D2B1	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Multidrug resistance protein MdtB
Q6D315	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Putative efflux protein
Q6D7E2	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Cation efflux system protein
Q6D806	<i>Pectobacterium atrosepticum</i> (strain SCRI 1043 / ATCC BAA-672)	Efflux pump membrane transporter
Q6EMD9	<i>Escherichia coli</i> .	Cu(+)/Ag(+) efflux RND transporter permease subunit SilA
Q6F6Q9	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Putative efflux transporter causing drug resistance (Acr family)
Q6F786	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Multidrug transport protein (RND family)
Q6F787	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Multidrug transport protein outer membrane (RND family)
Q6F7C5	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	RND divalent metal cation efflux transporter
Q6F8F6	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Efflux pump membrane transporter
Q6F8P8	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Efflux pump membrane transporter
Q6FD21	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Putative multidrug transporter
Q6FD22	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Putative RND efflux transporter
Q6FE22	<i>Acinetobacter baylyi</i> (strain ATCC 33305 / BD413 / ADP1)	Nodulation protein
Q6HAK2	<i>Bacillus thuringiensis</i> subsp. <i>konkukian</i> (strain 97-27)	Conserved transporter possible acriflavin resistance protein
Q6HN96	<i>Bacillus thuringiensis</i> subsp. <i>konkukian</i> (strain 97-27)	Acriflavin resistance protein
Q6IVS4	uncultured gamma proteobacterium eBACHOT4E07.	Predicted cation efflux system
Q6KAY1	<i>Stenotrophomonas maltophilia</i>	Efflux pump membrane transporter
Q6KAZ0	<i>Stenotrophomonas maltophilia</i>	Efflux pump membrane transporter
Q6KAZ6	<i>Stenotrophomonas maltophilia</i>	Efflux pump membrane transporter
Q6LGP3	<i>Photobacterium profundum</i> (strain SS9)	Putative transporter AcrB/D/F family
Q6LGT2	<i>Photobacterium profundum</i> (strain SS9)	Efflux pump membrane transporter
Q6LIY4	<i>Photobacterium profundum</i> (strain SS9)	Efflux pump membrane transporter
Q6LNM7	<i>Photobacterium profundum</i> (strain SS9)	Putative multidrug resistance protein
Q6LPI6	<i>Photobacterium profundum</i> (strain SS9)	Putative AcrB Cation/multidrug efflux pump

Q6LPS3	<i>Photobacterium profundum</i> (strain SS9)	Hypothetical transporter AcrB/D/F family
Q6LTG2	<i>Photobacterium profundum</i> (strain SS9)	Putative cation efflux system transmembrane protein
Q6LV21	<i>Photobacterium profundum</i> (strain SS9)	Putative Cation/multidrug efflux pump
Q6LVZ3	<i>Photobacterium profundum</i> (strain SS9)	Putative multidrug resistance protein
Q6MDJ2	<i>Protochlamydia amoebophila</i> (strain UWE25)	Uncharacterized protein
Q6MDS4	<i>Protochlamydia amoebophila</i> (strain UWE25)	Uncharacterized protein
Q6MEI7	<i>Protochlamydia amoebophila</i> (strain UWE25)	Uncharacterized protein
Q6MIU0	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	Efflux transporter
Q6ML00	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	Cation efflux system protein AcrB/AcrD/AcrF family protein
Q6MM46	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	NoIG efflux transporter
Q6MM88	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	NoIG efflux transporter
Q6MNU1	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	Acriflavin resistance protein
Q6MP63	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	Acriflavin resistance protein
Q6MPG6	<i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIB 9529/ HD100)	Acriflavin resistance protein
Q6MXQ0	<i>Serratia marcescens</i> .	Putative cation efflux system protein (Silver resistance)
Q6N0T1	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Putative efflux transporter
Q6N1C7	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Putative heavy metal cation efflux system protein
Q6N1J1	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Putative RND efflux transporter
Q6N2F5	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Efflux pump membrane transporter
Q6N2Z4	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Efflux pump membrane transporter
Q6N3B9	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Putative RND efflux transporter
Q6N457	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	RND efflux transporter
Q6N5L8	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Efflux pump membrane transporter
Q6N682	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Efflux pump membrane transporter
Q6N6N9	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Possible RND efflux transporter
Q6N6P0	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Possible RND efflux transporter
Q6N787	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009)	Efflux pump membrane transporter

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
Q6NDK9	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.	SiIA
Q6V6X8	Pseudomonas fluorescens.	Efflux pump membrane transporter
Q6VV68	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
Q725M1	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 serovar copenhageni (strain Fiocruz L1-130)	Acriflavin resistance
Q72MU9	Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)	Acriflavin resistance
Q72MW5	Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)	Acriflavin resistance

Q72Q88	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)	Heavy metal efflux pump
Q72V12	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)	Acriflavin resistance
Q72X10	<i>Bacillus cereus</i> (strain ATCC 10987 / NRS 248)	Transporter AcrB/AcrD/AcrF family
Q73DC5	<i>Bacillus cereus</i> (strain ATCC 10987 / NRS 248)	Transporter AcrB/AcrD/AcrF family
Q73FK8	<i>Wolbachia pipientis</i> wMel.	Multidrug resistance protein D
Q746W8	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Heavy metal efflux pump RND family inner membrane protein CzcA family
Q749G1	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner membrane protein AcrB/AcrD/AcrF family
Q749P6	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump membrane transporter
Q749S8	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner and outer membrane proteins
Q74BA6	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner membrane protein
Q74CR1	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner membrane protein AcrB/AcrD/AcrF family
Q74DI4	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Metal ion efflux pump RND family inner membrane protein
Q74EX9	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner membrane protein
Q74G55	<i>Geobacter sulfurreducens</i> (strain ATCC 51573 / DSM 12127 / PCA)	Efflux pump RND family inner membrane protein
Q79MP3	<i>Serratia marcescens</i> subsp. marcescens.	Multidrug resistance protein MdtC
Q7ACM1	<i>Escherichia coli</i> O157:H7.	Multidrug resistance protein MdtC
Q7B054	<i>Cupriavidus metallidurans</i> .	CnrA protein
Q7M912	<i>Wolinella succinogenes</i> (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W)	RND PUMP PROTEIN
Q7M9I0	<i>Wolinella succinogenes</i> (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W)	Efflux pump membrane transporter
Q7M9P9	<i>Wolinella succinogenes</i> (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W)	Efflux pump membrane transporter
Q7MCH1	<i>Vibrio vulnificus</i> (strain YJ016)	Putative multidrug resistance protein
Q7MCR8	<i>Vibrio vulnificus</i> (strain YJ016)	Putative silver efflux pump
Q7MDF8	<i>Vibrio vulnificus</i> (strain YJ016)	Efflux pump membrane transporter
Q7MDY8	<i>Vibrio vulnificus</i> (strain YJ016)	Transporter AcrB/D/F family
Q7MEG9	<i>Vibrio vulnificus</i> (strain YJ016)	Transporter AcrB/D/F family
Q7MEY5	<i>Vibrio vulnificus</i> (strain YJ016)	Transporter AcrB/D/F family
Q7MG13	<i>Vibrio vulnificus</i> (strain YJ016)	Uncharacterized protein

Q7MHZ2	<i>Vibrio vulnificus</i> (strain YJ016)	Putative multidrug resistance protein
Q7MLN0	<i>Vibrio vulnificus</i> (strain YJ016)	Transporter AcrB/D/F family
Q7MME3	<i>Vibrio vulnificus</i> (strain YJ016)	Putative multidrug resistance protein
Q7MQH1	<i>Vibrio vulnificus</i> (strain YJ016)	Putative multidrug resistance protein
Q7MWQ6	<i>Porphyromonas gingivalis</i> (strain ATCC BAA-308 / W83)	AcrB/AcrD/AcrF family protein
Q7MXU3	<i>Porphyromonas gingivalis</i> (strain ATCC BAA-308 / W83)	Heavy metal efflux pump CzcA family
Q7N0N0	<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> (strain DSM 15139 / CIP105565 / TT01)	Efflux pump membrane transporter
Q7N3E1	<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> (strain DSM 15139 / CIP105565 / TT01)	Multidrug resistance protein MdtC
Q7N3E2	<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> (strain DSM 15139 / CIP105565 / TT01)	Multidrug resistance protein MdtB
Q7N8G7	<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> (strain DSM 15139 / CIP105565 / TT01)	Uncharacterized protein
Q7NCY7	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	RND multidrug efflux transporter
Q7NDR2	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	GII4170 protein
Q7NE52	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	Glr4028 protein
Q7NE92	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	RND multidrug efflux transporter
Q7NFA7	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	GII3619 protein
Q7NHP1	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	AcrB/AcrD/AcrF family protein
Q7NJ01	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	Cation efflux system protein
Q7NL29	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	AcrB/AcrD/AcrF family protein
Q7NM91	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	GII0876 protein
Q7NMG0	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	AcrB/AcrD/AcrF family protein
Q7NNM9	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	Glr0382 protein
Q7NNZ4	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	AcrB/AcrD/AcrF family protein
Q7NP24	<i>Gloeobacter violaceus</i> (strain ATCC 29082 / PCC 7421)	AcrB/AcrD/AcrF family protein
Q7NR60	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Probable transmembrane drug efflux protein
Q7NRE6	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Probable multidrug efflux membrane protein

Q7NUG4	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Probable drug efflux pump transmembrane protein
Q7NUG5	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Probable drug efflux pump transmembrane protein
Q7NVV1	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Efflux pump membrane transporter
Q7NWL0	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	NoIG efflux transporter
Q7NXK0	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Probable multidrug efflux protein
Q7POY1	<i>Chromobacterium violaceum</i> (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	Efflux pump membrane transporter
Q7UDI0	<i>Shigella flexneri</i> .	Efflux pump membrane transporter
Q7UEM8	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Cation efflux system protein CZCA
Q7UH35	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Predicted cation efflux system (AcrB/AcrD/AcrF family)
Q7UJP2	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Probable multidrug resistance protein
Q7UJT6	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Acridine resistance protein B
Q7ULF2	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	RND multidrug efflux transporter MexF
Q7USF5	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Cation efflux system protein czcA-1
Q7UZ48	<i>Rhodopirellula baltica</i> (strain DSM 10527 / NCIMB 13988 / SH1)	Cation efflux system AcrB/AcrD/AcrF family
Q7VII0	<i>Helicobacter hepaticus</i> (strain ATCC 51449 / 3B1)	Uncharacterized protein
Q7VJM1	<i>Helicobacter hepaticus</i> (strain ATCC 51449 / 3B1)	SSD domain-containing protein
Q7VJR9	<i>Helicobacter hepaticus</i> (strain ATCC 51449 / 3B1)	Efflux pump membrane transporter
Q7VLE5	<i>Haemophilus ducreyi</i> (strain 35000HP / ATCC 700724)	Acridine resistance protein
Q7VSV8	<i>Bordetella pertussis</i> (strain Tohama I / ATCC BAA-589 / NCTC 13251)	AcrB/AcrD/AcrF family protein
Q7VSV9	<i>Bordetella pertussis</i> (strain Tohama I / ATCC BAA-589 / NCTC 13251)	AcrB/AcrD/AcrF family protein
Q7VWW1	<i>Bordetella pertussis</i> (strain Tohama I / ATCC BAA-589 / NCTC 13251)	Efflux pump membrane transporter
Q7VZD3	<i>Bordetella pertussis</i> (strain Tohama I / ATCC BAA-589 / NCTC 13251)	Efflux pump membrane transporter
Q7VZR4	<i>Bordetella pertussis</i> (strain Tohama I / ATCC BAA-589 / NCTC 13251)	Integral membrane component of multidrug efflux system

Q7W3S1	<i>Bordetella parapertussis</i> (strain 12822 / ATCC BAA-587 / NCTC 13253)	AcrB/AcrD/AcrF family protein
Q7W3S2	<i>Bordetella parapertussis</i> (strain 12822 / ATCC BAA-587 / NCTC 13253)	AcrB/AcrD/AcrF family protein
Q7W438	<i>Bordetella parapertussis</i> (strain 12822 / ATCC BAA-587 / NCTC 13253)	Probable membrane protein
Q7WAC5	<i>Bordetella parapertussis</i> (strain 12822 / ATCC BAA-587 / NCTC 13253)	Efflux pump membrane transporter
Q7WC93	<i>Bordetella parapertussis</i> (strain 12822 / ATCC BAA-587 / NCTC 13253)	Efflux pump membrane transporter
Q7WSD5	<i>Serratia marcescens</i> .	Efflux pump membrane transporter
Q7WTQ9	<i>Erwinia amylovora</i>	Efflux pump membrane transporter
Q7X364	uncultured <i>Acidobacteria</i> bacterium.	Putative multidrug resistance pump
Q814J5	<i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	Acriflavin resistance plasma membrane protein
Q81HR8	<i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	Acriflavin resistance plasma membrane protein
Q81JL8	<i>Bacillus anthracis</i> .	Transporter AcrB/AcrD/AcrF family
Q820K8	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Acriflavin resistance protein:Heavy metal efflux pump CzcA
Q820R2	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Acriflavin resistance protein:Heavy metal efflux pump CzcA
Q820R6	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Acriflavin resistance protein:Heavy metal efflux pump CzcA
Q82AL7	<i>Streptomyces avermitilis</i> (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	Putative cation/multidrug efflux protein
Q82T82	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Acriflavin resistance protein
Q82VH6	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Efflux pump membrane transporter
Q82WK5	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Acriflavin resistance protein
Q82XT4	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Efflux pump membrane transporter
Q82XU2	<i>Nitrosomonas europaea</i> (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298)	Efflux pump membrane transporter
Q83CM1	<i>Coxiella burnetii</i> (strain RSA 493 / Nine Mile phase I)	Acriflavin resistance plasma membrane protein
Q83DD4	<i>Coxiella burnetii</i> (strain RSA 493 / Nine Mile phase I)	Acriflavin resistance plasma membrane protein
Q83DH8	<i>Coxiella burnetii</i> (strain RSA 493 / Nine Mile phase I)	Acriflavin resistance plasma membrane protein
Q83KI4	<i>Shigella flexneri</i> .	Multidrug resistance protein MdtC
Q83SC3	<i>Shigella flexneri</i> .	Putative inner membrane component for iron transport
Q840D3	<i>Acinetobacter baumannii</i> .	Efflux pump membrane transporter

Q849R0	<i>Pseudomonas putida</i> (strain ATCC 700007 / DSM 6899 / BCRC 17059 / F1)	Probable efflux pump membrane transporter SepB
Q84GI9	<i>Serratia marcescens</i> subsp. <i>marcescens</i> .	Efflux pump membrane transporter
Q87BP4	<i>Xylella fastidiosa</i> (strain Temecula1 / ATCC 700964)	Acriflavin resistance protein
Q87DA3	<i>Xylella fastidiosa</i> (strain Temecula1 / ATCC 700964)	Efflux pump membrane transporter
Q87EU7	<i>Xylella fastidiosa</i> (strain Temecula1 / ATCC 700964)	Acriflavin resistance protein
Q87GX5	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Efflux pump membrane transporter
Q87HZ7	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Transporter AcrB/D/F family
Q87IX6	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative cation efflux system transmembrane protein
Q87IY5	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Efflux pump membrane transporter
Q87J90	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative efflux protein
Q87JA9	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative multidrug resistance protein
Q87LY6	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative multidrug resistance protein
Q87QH1	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Transporter AcrB/D/F family
Q87QQ7	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Efflux pump membrane transporter
Q87R57	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative multidrug resistance protein
Q87TN1	<i>Vibrio parahaemolyticus</i> serotype O3:K6 (strain RIMD 2210633)	Putative multidrug resistance protein
Q87UV1	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	AcrB/AcrD/AcrF family protein
Q87X84	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	Efflux pump membrane transporter
Q87ZX0	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	AcrB/AcrD/AcrF family protein
Q880Q4	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	Efflux pump membrane transporter
Q881X7	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	AcrB/AcrD/AcrF family protein
Q882N4	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	Efflux pump membrane transporter
Q887I4	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	AcrB/AcrD/AcrF family protein
Q889D0	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	AcrB/AcrD/AcrF family protein
Q88AL5	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000)	Cation efflux family protein
Q88BZ6	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Probable copper efflux transporter Czca family

Q88CK7	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	RND efflux transporter
Q88GY2	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Multidrug efflux transport system-membrane subunit
Q88HA4	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Efflux pump membrane transporter
Q88HD4	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Efflux pump membrane transporter
Q88HQ1	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	RND efflux transporter
Q88J31	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Efflux pump membrane transporter
Q88K81	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Cation efflux system protein
Q88L70	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Multidrug efflux RND transporter
Q88MQ3	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	RND efflux transporter
Q88N31	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Probable efflux pump membrane transporter TtgB
Q88PE4	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Putative Multidrug efflux RND transporter
Q88RT6	<i>Pseudomonas putida</i> (strain ATCC 47054 / DSM 6125 / NCIMB 11950 /KT2440)	Cation efflux system protein
Q89DV7	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89DX5	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	AcrB/AcrD/AcrF family protein
Q89EQ3	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	AcrB/AcrD/AcrF family protein
Q89FH4	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89I68	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	AcrB/AcrD/AcrF family cation efflux protein
Q89K38	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89KG8	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Blr4937 protein
Q89KH2	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Blr4933 protein
Q89LT5	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Blr4458 protein
Q89LT6	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	AcrB/AcrD/AcrF family protein
Q89M74	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Bll4319 protein
Q89MT0	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Probable cation efflux system protein
Q89NE0	<i>Bradyrhizobium diazoefficiens</i> (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	AcrB/AcrD/AcrF family protein

Q89NG9	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89QU2	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Cation efflux system protein
Q89R38	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	RagC protein
Q89RB1	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Blr2861 protein
Q89SH7	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Cation efflux system protein
Q89TZ3	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Multidrug resistance protein
Q89UA1	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89VP8	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Efflux pump membrane transporter
Q89XF8	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Acr family transport protein
Q89XK8	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC14792 / USDA 110)	Cation efflux protein
Q89XN1	Bradyrhizobium diazoefficiens (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
Q8A0Q2	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

Q8A9C9	<i>Bacteroides thetaiotaomicron</i> (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	Putative cation efflux pump
Q8A9Y5	<i>Bacteroides thetaiotaomicron</i> (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	Cation efflux system protein <i>czcA</i>
Q8AB07	<i>Bacteroides thetaiotaomicron</i> (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	Putative aminoglycoside efflux pump (Acriflavine resistance protein)
Q8AB13	<i>Bacteroides thetaiotaomicron</i> (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	Cation efflux system (AcrB/AcrD/AcrF family)
Q8CK05	<i>Streptomyces coelicolor</i> (strain ATCC BAA-471 / A3(2))	Putative integral membrane efflux protein
Q8CX78	<i>Oceanobacillus iheyensis</i> (strain DSM 14371 / CIP 107618 / JCM 11309 / KCTC 3954 / HTE831)	Acriflavine resistance protein (Cation efflux system)
Q8DIH0	<i>Thermosynechococcus elongatus</i> (strain BP-1)	Multidrug efflux transporter
Q8DJR3	<i>Thermosynechococcus elongatus</i> (strain BP-1)	AcrB/AcrD/AcrF family protein
Q8E808	<i>Shewanella oneidensis</i> (strain MR-1)	Copper/silver efflux pump permease component <i>CusA</i>
Q8E8H2	<i>Shewanella oneidensis</i> (strain MR-1)	Efflux pump membrane transporter
Q8E8R3	<i>Shewanella oneidensis</i> (strain MR-1)	Copper/silver efflux pump permease component <i>CusA</i>
Q8EA94	<i>Shewanella oneidensis</i> (strain MR-1)	HAE1 family efflux pump permease component
Q8EBL9	<i>Shewanella oneidensis</i> (strain MR-1)	Efflux pump membrane transporter
Q8EBM6	<i>Shewanella oneidensis</i> (strain MR-1)	HAE1 family efflux pump permease component
Q8EC65	<i>Shewanella oneidensis</i> (strain MR-1)	RND superfamily efflux pump permease component
Q8ECN3	<i>Shewanella oneidensis</i> (strain MR-1)	Thiophosphate efflux pump permease component
Q8EFP6	<i>Shewanella oneidensis</i> (strain MR-1)	RND superfamily efflux pump permease component 2
Q8EFP7	<i>Shewanella oneidensis</i> (strain MR-1)	RND superfamily efflux pump permease component 1
Q8EFT4	<i>Shewanella oneidensis</i> (strain MR-1)	HAE1 family efflux pump permease component
Q8EI98	<i>Shewanella oneidensis</i> (strain MR-1)	RND superfamily efflux pump permease component
Q8EJE7	<i>Shewanella oneidensis</i> (strain MR-1)	Heavy metal efflux pump permease component <i>CzcA</i> family
Q8EZC8	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	Cation/multidrug efflux pump
Q8EZI2	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	Acriflavine resistance protein

Q8EZK7	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	Cation/multidrug efflux pump
Q8EZW3	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	Acridine resistance protein
Q8F5X3	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	Heavy metal efflux pump
Q8FCI8	<i>Escherichia coli</i> O6:H1 (strain CFT073 / ATCC 700928 / UPEC)	Multidrug resistance protein MdtF
Q8FG03	<i>Escherichia coli</i> O6:H1 (strain CFT073 / ATCC 700928 / UPEC)	Multidrug resistance protein MdtC
Q8FG04	<i>Escherichia coli</i> O6:H1 (strain CFT073 / ATCC 700928 / UPEC)	Multidrug resistance protein MdtB
Q8FK36	<i>Escherichia coli</i> O6:H1 (strain CFT073 / ATCC 700928 / UPEC)	Cation efflux system protein CusA
Q8FWV9	<i>Brucella suis</i> biovar 1 (strain 1330)	Efflux pump membrane transporter BepG
Q8G2M6	<i>Brucella suis</i> biovar 1 (strain 1330)	Efflux pump membrane transporter BepE
Q8GC83	<i>Klebsiella aerogenes</i>	Efflux pump membrane transporter
Q8GKU1	<i>Acinetobacter</i> sp. 4365.	Efflux pump membrane transporter
Q8KAV4	<i>Chlorobaculum tepidum</i> (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS)	AcrB/AcrD/AcrF family protein
Q8KCX0	<i>Chlorobaculum tepidum</i> (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS)	Multidrug resistance protein AcrB/AcrD family
Q8P3N5	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Cation efflux system protein
Q8P4C1	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Acridine resistance protein
Q8P613	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Acridine resistance protein
Q8P7C9	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Efflux pump membrane transporter
Q8P875	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Efflux pump membrane transporter
Q8P8U2	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Transport protein
Q8P8U3	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Transport protein
Q8PAN9	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Efflux pump membrane transporter

Q8PDB8	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	Cation efflux system protein
Q8PF28	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Cation efflux system protein
Q8PFX2	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Acriflavin resistance protein
Q8PHD3	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Acriflavin resistance protein
Q8PIQ2	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Efflux pump membrane transporter
Q8PIU6	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Acriflavin resistance protein
Q8PJN1	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Efflux pump membrane transporter
Q8PKM4	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Cation efflux system protein
Q8PKU6	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Transport protein
Q8PKU7	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Transport protein
Q8PME6	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Efflux pump membrane transporter
Q8PQ89	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Cation efflux system protein
Q8PQJ5	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (strain 306)	Efflux pump membrane transporter
Q8RE51	<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131)	Acriflavin resistance protein B
Q8RG07	<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131)	Acriflavin resistance protein D
Q8RG44	<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> (strain ATCC 25586 / CIP101130 / JCM 8532 / LMG 13131)	Acriflavin resistance protein B
Q8RNP2	<i>Legionella pneumophila</i> .	Chemiosmotic efflux system B protein A
Q8RNQ8	<i>Legionella pneumophila</i> .	AcrB/AcrD/AcrF family protein
Q8RSM1	uncultured bacterium.	MexD protein
Q8RTE4	<i>Campylobacter jejuni</i> .	Efflux pump membrane transporter
Q8VPA8	<i>Proteus mirabilis</i> .	Efflux pump membrane transporter
Q8X3J5	<i>Escherichia coli</i> O157:H7.	Multidrug resistance protein MdtF
Q8X7E2	<i>Escherichia coli</i> O157:H7.	Efflux pump membrane transporter
Q8X7J4	<i>Escherichia coli</i> O157:H7.	Multidrug resistance protein MdtB
Q8XBY1	<i>Escherichia coli</i> O157:H7.	Cation efflux system protein CusA
Q8XD55	<i>Escherichia coli</i> O157:H7.	Efflux pump membrane transporter
Q8XEH2	<i>Escherichia coli</i> O157:H7.	Efflux pump membrane transporter

Q8XPP1	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable transport transmembrane protein
Q8XQ28	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable transporter transmembrane protein
Q8XQM3	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable drug efflux transmembrane protein
Q8XQM4	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable drug efflux pump transmembrane protein
Q8XQV5	<i>Ralstonia solanacearum</i> (strain GMI1000)	Efflux pump membrane transporter
Q8XR28	<i>Ralstonia solanacearum</i> (strain GMI1000)	Putative cation efflux system transmembrane protein
Q8XRD0	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable cation efflux system transmembrane protein
Q8XRL3	<i>Ralstonia solanacearum</i> (strain GMI1000)	Efflux pump membrane transporter
Q8XSE6	<i>Ralstonia solanacearum</i> (strain GMI1000)	Putative cation efflux system transmembrane protein
Q8XS11	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable cation efflux system transmembrane protein
Q8XT05	<i>Ralstonia solanacearum</i> (strain GMI1000)	Efflux pump membrane transporter
Q8XUI3	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable transmembrane drug efflux protein
Q8XYV2	<i>Ralstonia solanacearum</i> (strain GMI1000)	Probable transmembrane drug efflux protein
Q8Y3H0	<i>Ralstonia solanacearum</i> (strain GMI1000)	Efflux pump membrane transporter
Q8YCQ5	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)	Acridflavin resistance protein f
Q8YCZ5	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)	Acridflavin resistance protein d
Q8YF77	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)	Acridflavin resistance protein b
Q8YF93	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)	Efflux pump membrane transporter
Q8YHA9	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)	Acridflavin resistance protein b
Q8YLK4	<i>Nostoc</i> sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576)	Alr5294 protein
Q8YSE5	<i>Nostoc</i> sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576)	RND multidrug efflux transporter
Q8YWF7	<i>Nostoc</i> sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576)	Alr1656 protein
Q8Z4S4	<i>Salmonella typhi</i> .	Efflux pump membrane transporter
Q8Z5F6	<i>Salmonella typhi</i> .	Multidrug resistance protein MdtC
Q8Z5F7	<i>Salmonella typhi</i> .	Multidrug resistance protein MdtB
Q8Z8T8	<i>Salmonella typhi</i> .	Efflux pump membrane transporter
Q8ZCV9	<i>Yersinia pestis</i> .	Multidrug resistance protein MdtC
Q8ZCW0	<i>Yersinia pestis</i> .	Multidrug resistance protein MdtB
Q8ZLN4	<i>Salmonella typhimurium</i> (strain LT2 / SGSC1412 / ATCC 700720)	Efflux pump membrane transporter
Q8ZN77	<i>Salmonella typhimurium</i> (strain LT2 / SGSC1412 / ATCC 700720)	Efflux pump membrane transporter

Q8ZNO1	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	Multidrug resistance protein MdtC
Q8ZNO2	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

Q9A3K6	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	AcrB/AcrD/AcrF family protein
Q9A4V1	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	Metal ion efflux RND protein family
Q9A5Q7	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	AcrB/AcrD/AcrF family protein
Q9A7D5	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	AcrB/AcrD/AcrF family protein
Q9A8Z1	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	AcrB/AcrD/AcrF family protein
Q9AA04	<i>Caulobacter vibrioides</i> (strain ATCC 19089 / CB15)	Efflux pump membrane transporter
Q9AEG1	<i>Klebsiella aerogenes</i>	Efflux pump membrane transporter
Q9AG05	<i>Wolbachia</i> sp. subsp. <i>Drosophila simulans</i> (strain wRi)	Multidrug resistance protein D
Q9ALR2	<i>Pseudomonas fluorescens</i> .	CztA
Q9CLS7	<i>Pasteurella multocida</i> (strain Pm70)	AcrB
Q9F240	<i>Stenotrophomonas maltophilia</i>	Efflux pump membrane transporter
Q9F7M0	<i>Gamma-proteobacterium</i> EBAC31A08.	Predicted cation efflux system (AcrB/AcrD/AcrF family)
Q9F8V7	<i>Rhizobium radiobacter</i>	Efflux pump membrane transporter
Q9HVI9	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Efflux pump membrane transporter
Q9HW27	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9HWH4	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9HXW4	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9HY87	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Efflux pump membrane transporter
Q9IOV6	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9IOV7	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9IOW2	<i>Pseudomonas aeruginosa</i> (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
Q9IOY8	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Efflux pump membrane transporter

Q9I3R1	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 /JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9I6X4	<i>Pseudomonas aeruginosa</i> (strain ATCC 15692 / DSM 22644 / CIP 104116 /JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)	Probable Resistance-Nodulation-Cell Division (RND) efflux transporter
Q9JY67	<i>Neisseria meningitidis</i> serogroup B (strain MC58)	Efflux pump membrane transporter
Q9K6B3	<i>Bacillus halodurans</i> (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM9153 / C-125)	Cation efflux system
Q9KJC2	<i>Pseudomonas putida</i>	Antibiotic efflux pump membrane transporter ArpB
Q9KLV3	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Transporter AcrB/D/F family
Q9KR85	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Transporter AcrB/D/F family
Q9KRG9	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Transporter AcrB/D/F family
Q9KT18	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Multidrug resistance protein putative
Q9KU94	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Multidrug resistance protein putative
Q9KVI2	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	Multidrug resistance protein putative
Q9KW65	<i>Pseudomonas syringae</i> .	ORFF protein
Q9KWV4	<i>Pseudomonas putida</i> (strain DOT-T1E)	Toluene efflux pump membrane transporter TtgE
Q9PAV9	<i>Xylella fastidiosa</i> (strain 9a5c)	Acriflavin resistance protein
Q9PBP6	<i>Xylella fastidiosa</i> (strain 9a5c)	Efflux pump membrane transporter
Q9PBQ7	<i>Xylella fastidiosa</i> (strain 9a5c)	Cation efflux system protein
Q9PGQ5	<i>Xylella fastidiosa</i> (strain 9a5c)	Acriflavin resistance protein
Q9RBY8	<i>Stenotrophomonas maltophilia</i>	Efflux pump membrane transporter
Q9RG59	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter
Q9RLI8	<i>Pseudomonas aeruginosa</i> .	CzrA protein
Q9RQG6	<i>Staphylococcus aureus</i> .	AcrB/AcrD/AcrF family protein
Q9WYK5	<i>Thermotoga maritima</i> (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	Cation efflux system protein putative
Q9ZDZ3	<i>Rickettsia prowazekii</i> (strain Madrid E)	ACRIFLAVIN RESISTANCE PROTEIN D (AcrD)
Q9ZH24	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter
Q9ZHC9	<i>Salmonella typhimurium</i> .	Putative cation efflux system protein SilA
Q9ZJQ5	<i>Helicobacter pylori</i> (strain J99 / ATCC 700824)	CATION EFFLUX SYSTEM PROTEIN
Q9ZKN2	<i>Helicobacter pylori</i> (strain J99 / ATCC 700824)	Putative cation efflux system protein
Q9ZLM5	<i>Helicobacter pylori</i> (strain J99 / ATCC 700824)	Putative efflux transporter
Q9ZNG8	<i>Pseudomonas aeruginosa</i> .	Efflux pump membrane transporter

