

| ARO_acce<br>ssion | ARO_na<br>me | ARO_description   | AMR Gene<br>Family  | Drug<br>Class                          | Antibioti<br>c class | Resistance<br>Mechanis<br>m  | HB_3_2 | HB_3_1 | XZ_2_2 | BG_1_3 | XZ_2_1 | HB_3_3 | BG_1_1 | BG_1_2 | XZ_2_3 | SC_2_3 | SC_2_1 | SC_2_2 | Total |
|-------------------|--------------|---|---|--|----------------------|------------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------|
| ARO:3000005       | vanD         | VanD is a D-Ala-D-Ala ligase homolog similar to VanA, and can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is associated with both vancomycin and teicoplanin resistance.  | glycopeptide resistance gene cluster;van ligase           | glycopeptide antibiotic                | Glycopeptide         | Antibiotic target alteration | 186    | 182    | 378    | 142    | 100    | 182    | 168    | 136    | 178    | 294    | 254    | 270    | 2470  |
| ARO:3000010       | vanA         | VanA is a D-Ala-D-Ala ligase homolog that synthesizes D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It has been isolated from VREs. It is associated with both vancomycin and teicoplanin resistance.                               | glycopeptide resistance gene cluster;van ligase           | glycopeptide antibiotic                | Glycopeptide         | Antibiotic target alteration | 580    | 340    | 660    | 328    | 906    | 454    | 346    | 570    | 994    | 852    | 1172   | 1020   | 8222  |
| ARO:3000013       | vanB         | VanB is a D-Ala-D-Ala ligase homolog similar to VanA, and can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It has been isolated from VREs. It is associated with vancomycin resistance, but not teicoplanin resistance. | glycopeptide resistance gene cluster;van ligase           | glycopeptide antibiotic                | Glycopeptide         | Antibiotic target alteration | 876    | 84     | 32     | 82     | 12     | 1016   | 60     | 52     | 70     | 158    | 314    | 122    | 2878  |
| ARO:3000024       | patA         | PatA is an ABC transporter of Streptococcus pneumoniae that interacts with PatB to confer fluoroquinolone resistance.   | ATP-binding cassette (ABC) antibiotic efflux pump         | fluoroquinolone antibiotic             | Fluoroquinolone      | Antibiotic efflux            | 6780   | 5618   | 6626   | 5262   | 10274  | 6004   | 6540   | 6898   | 10718  | 5460   | 5064   | 5244   | 80488 |
| ARO:3000025       | patB         | PatB is an ABC transporter of Streptococcus pneumoniae that interacts with PatA to confer fluoroquinolone resistance..  | ATP-binding cassette (ABC) antibiotic efflux pump         | fluoroquinolone antibiotic             | Fluoroquinolone      | Antibiotic efflux            | 5802   | 7748   | 5240   | 3008   | 2502   | 7904   | 2818   | 3382   | 3198   | 3928   | 3860   | 4336   | 53726 |
| ARO:3000026       | mepA         | MepA is an efflux protein regulated by MepR and part of the MepRAB cluster. Its presence in Staphylococcus aureus led to multidrug resistance, while it has also  | multidrug and toxic compound extrusion (MATE) transporter | glycylcysteine;tetracycline antibiotic | Multidrug            | Antibiotic efflux            | 908    | 624    | 1312   | 264    | 464    | 954    | 258    | 332    | 570    | 304    | 172    | 178    | 6340  |

|             |      |   |  |   |   |      |      |      |      |     |      |      |      |     |     |      |     |       |
|-------------|------|---|--|---|---|------|------|------|------|-----|------|------|------|-----|-----|------|-----|-------|
| ARO:3000027 | emrA | been shown to decrease tigecycline susceptibility. EmrA is a membrane fusion protein, providing an efflux pathway with EmrB and TolC between the inner and outer membranes of E. coli, a Gram-negative bacterium.   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic  | Fluoroquinolone Antibiotic efflux       | 1060 | 652  | 1022 | 1034 | 728 | 488  | 1512 | 1116 | 588 | 288 | 302  | 186 | 8976  |
| ARO:3000074 | emrB | emrB is a translocase in the emrB-TolC efflux protein in E. coli. It recognizes substrates including carbonyl cyanide m-chlorophenylhydrazone (CCCP), nalidixic acid, and thioloactomycin.  | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic  | Fluoroquinolone Antibiotic efflux       | 1018 | 280  | 470  | 1330 | 712 | 514  | 2030 | 1480 | 750 | 508 | 1030 | 434 | 10556 |
| ARO:3000118 | vgaB | Vga(B) is an ABC-F protein expressed in staphylococci that confers resistance to streptogramin A antibiotics and related compounds. It is associated with plasmid DNA.  | ABC-F ATP-binding cassette ribosomal protection protein    | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic carbapenem;cephalosporin;cephamycin;monobactam;penam | Multidrug Antibiotic target protection  | 1642 | 2490 | 1988 | 910  | 516 | 1884 | 830  | 1048 | 638 | 994 | 802  | 868 | 14610 |
| ARO:3000124 | mecI | mecI acts as a repressor of transcription of the mecA/mecR1/mecI operon.  | methicillin resistant PBP2                                 | carbapenem;cephalosporin;cephamycin;monobactam;penam  | Multidrug Antibiotic target replacement | 88   | 134  | 98   | 74   | 112 | 120  | 82   | 80   | 128 | 116 | 148  | 124 | 1304  |
| ARO:3000149 | FosA | An enzyme that confers resistance to fosfomycin in Serratia marcescens by breaking the epoxide ring of the molecule. It depends on the cofactors Manganese (II) and Potassium and uses Glutathione (GSH) as the nucleophilic molecule. In Pseudomonas aeruginosa, FosA catalyzes the conjugation of glutathione to carbon-1 of fosfomycin, rendering it ineffective as an antibacterial drug. | fosfomycin thiol transferase                               | fosfomycin  | Fosfomycin Antibiotic inactivation      | 0    | 2    | 20   | 14   | 14  | 0    | 8    | 10   | 4   | 18  | 18   | 12  | 120   |

|                 |        |   |  |                         |              |                         |      |     |     |      |      |     |      |      |      |      |      |      |       |
|-----------------|--------|---|--|-------------------------|--------------|-------------------------|------|-----|-----|------|------|-----|------|------|------|------|------|------|-------|
| ARO:3000<br>165 | tet(A) | TetA is a tetracycline efflux pump found in many species of Gram-negative bacteria.   | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 1402 | 524 | 336 | 2510 | 2680 | 390 | 3604 | 2834 | 2288 | 682  | 750  | 568  | 18568 |
| ARO:3000<br>166 | tet(B) | Tet(B) is a tetracycline efflux protein expressed in many Gram-negative bacteria. It confers resistance to tetracycline, doxycycline, and minocycline, but not tigecycline.   | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 36   | 6   | 16  | 58   | 16   | 2   | 124  | 150  | 10   | 48   | 66   | 54   | 586   |
| ARO:3000<br>167 | tet(C) | Tet(C) is a tetracycline efflux pump found in many species of Gram-negative bacteria. It is typically found in plasmid DNA.   | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 0    | 2   | 2   | 24   | 16   | 0   | 128  | 60   | 18   | 92   | 98   | 26   | 466   |
| ARO:3000<br>168 | tet(D) | TetD is a tetracycline efflux pump found exclusively in Gram-negative bacteria.   | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 4    | 0   | 0   | 0    | 0    | 0   | 0    | 0    | 0    | 0    | 4    | 0    | 8     |
| ARO:3000<br>172 | FosB   | A thiol transferase that leads to the resistance of fosfomycin. Contrasting FosA, FosB is dependent on the cofactor Magnesium (II) and uses either bacillithiol or L-cysteine to open up the epoxide ring of fosfomycin.  | fosfomycin thiol transferase                               | fosfomycin              | Fosfomycin   | Antibiotic inactivation | 28   | 2   | 0   | 0    | 0    | 20  | 2    | 6    | 0    | 0    | 0    | 0    | 58    |
| ARO:3000<br>173 | tet(E) | TetE is a tetracycline efflux pump found in many Gram-negative bacteria, especially those in water environments. The gene is found on large plasmids.   | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 0    | 0   | 0   | 32   | 0    | 0   | 10   | 40   | 2    | 0    | 0    | 0    | 84    |
| ARO:3000<br>174 | tet(G) | TetG is a tetracycline efflux protein found in Gram-negative bacteria. The encoding gene is found in both chromosomal and plasmid DNA where it is frequently linked to the floR, sul1, and cmlA9 genes which encode proteins that can confer florfenicol/chloramphenicol, | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux       | 10   | 64  | 200 | 200  | 648  | 26  | 580  | 318  | 808  | 2810 | 2820 | 4214 | 12698 |

|             |         |  |  |                         |                                |     |     |     |    |     |     |     |    |     |      |      |      |      |
|-------------|---------|--|--|-------------------------|--------------------------------|-----|-----|-----|----|-----|-----|-----|----|-----|------|------|------|------|
|             |         | sulfamethoxazole, and chloramphenicol resistance, respectively.<br>TetH is a tetracycline efflux protein expressed in Gram-negative bacteria (Actinobacillus, Acinetobacter, Gallibacterium, Histophilus, Mannheimia, Moraxella, Pasteurella, and Psychrobacter). Its gene is linked to the resistance genes sul2, and strAB, which confer resistance to sulfamethoxazole and streptomycin, respectively.<br>TetK is a tetracycline efflux protein found in both Gram-negative (Haemophilus and Gallibacterium) and Gram-positive (many species, including mycobacteria) bacteria. | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline Antibiotic efflux | 4   | 0   | 26  | 12 | 24  | 0   | 4   | 34 | 180 | 1446 | 1200 | 2076 | 5006 |
| ARO:3000175 | tet(H)  |  |  |                         |                                |     |     |     |    |     |     |     |    |     |      |      |      |      |
| ARO:3000178 | tet(K)  |  |  |                         |                                | 0   | 0   | 0   | 0  | 0   | 0   | 0   | 0  | 0   | 24   | 16   | 48   | 88   |
| ARO:3000179 | tet(L)  |  |  |                         |                                | 58  | 78  | 10  | 28 | 58  | 124 | 40  | 42 | 62  | 172  | 208  | 138  | 1018 |
| ARO:3000180 | tetA(P) |  |  |                         |                                | 78  | 34  | 8   | 34 | 28  | 118 | 40  | 58 | 44  | 170  | 152  | 62   | 826  |
| ARO:3000181 | tet(V)  |  |  |                         |                                | 2   | 26  | 24  | 52 | 22  | 28  | 106 | 36 | 38  | 98   | 142  | 44   | 618  |
| ARO:3000182 | tet(Y)  |  |  |                         |                                | 106 | 196 | 310 | 38 | 408 | 222 | 70  | 16 | 280 | 582  | 672  | 744  | 3644 |

|                 |         |  |  |                         |              |                              |      |      |       |      |      |      |      |      |      |       |      |       |       |
|-----------------|---------|--|--|-------------------------|--------------|------------------------------|------|------|-------|------|------|------|------|------|------|-------|------|-------|-------|
| ARO:3000<br>183 | tet(Z)  | TetZ is a tetracycline efflux protein found in Gram-positive bacteria (Corynebacterium and Lactobacillus). It is associated with plasmid DNA.  | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | Tetracycline | Antibiotic efflux            | 54   | 22   | 22    | 28   | 108  | 46   | 130  | 68   | 168  | 556   | 1200 | 612   | 3014  |
| ARO:3000<br>186 | tetM    | TetM is a ribosomal protection protein that confers tetracycline resistance. It is found on transposable DNA elements and its horizontal transfer between bacterial species has been documented. | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 2378 | 4030 | 1954  | 1550 | 2596 | 2592 | 2044 | 1986 | 2728 | 5750  | 5590 | 7276  | 40474 |
| ARO:3000<br>190 | tetO    | TetO is a ribosomal protection protein. It is associated with conjugative plasmids.  | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 1778 | 1734 | 1640  | 690  | 648  | 1618 | 758  | 798  | 966  | 352   | 394  | 304   | 11680 |
| ARO:3000<br>191 | tetQ    | TetQ is a ribosomal protection protein. Its gene is associated with a conjugative transposon and has been found in both Gram-positive and Gram-negative bacteria.                                | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 5600 | 9880 | 10588 | 5326 | 2612 | 7342 | 3828 | 5830 | 4058 | 2174  | 1254 | 1056  | 59548 |
| ARO:3000<br>192 | tetS    | Tet(S) is a ribosomal protection protein found in Gram-positive and Gram-negative strains. It is similar to tet(M) and tet(O).   | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 3492 | 5166 | 2770  | 2444 | 2636 | 3358 | 2766 | 2746 | 2616 | 2406  | 1990 | 2806  | 35196 |
| ARO:3000<br>193 | tetT    | Tet(T) is a ribosomal protection protein of streptococci. It is similar to Tet(Q).   | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 6612 | 7960 | 5842  | 2862 | 3666 | 7690 | 3090 | 3622 | 4256 | 10416 | 8722 | 13714 | 78452 |
| ARO:3000<br>194 | tetW    | TetW is a ribosomal protection protein. It is associated with both conjugative and non conjugative DNA and has been found strains of Clostridioides difficile.                                   | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 4930 | 5306 | 4892  | 4798 | 2808 | 6120 | 5646 | 5340 | 3016 | 2554  | 2720 | 2052  | 50182 |
| ARO:3000<br>195 | tetB(P) | TetB(P) is a tetracycline ribosomal protection protein found on the same operon as tetA(P), a tetracycline efflux protein.   | tetracycline-resistant ribosomal protection protein        | tetracycline antibiotic | Tetracycline | Antibiotic target protection | 7536 | 8016 | 7818  | 5570 | 3746 | 8374 | 6512 | 6110 | 3954 | 5516  | 5518 | 6042  | 74712 |
| ARO:3000<br>196 | tet32   | Tet32 is a tetracycline resistance gene similar to Tet(O), and binds   | tetracycline-resistant                                     | tetracycline antibiotic | Tetracycline | Antibiotic target            | 950  | 1010 | 1314  | 334  | 288  | 730  | 388  | 440  | 420  | 312   | 494  | 276   | 6956  |

|                 |       |   |   |   |              |   |     |      |      |      |     |      |      |      |     |      |      |      |       |
|-----------------|-------|---|---|---|--------------|---|-----|------|------|------|-----|------|------|------|-----|------|------|------|-------|
| ARO:3000<br>197 | tet36 | to the ribosome to confer tetracycline resistance as a ribosomal protection protein. Tet36 is a tetracycline resistance gene found in Bacteroides similar to Tet(Q), and binds to the ribosome to confer antibiotic resistance as a ribosomal protection protein. FosX is an enzyme used to confer resistance to fosfomycin. It's dependent on the cofactor, manganese (II), and uses water to generate a vicinal diol. TetX is a flavin-dependent monooxygenase conferring resistance to tetracycline antibiotics. TetX hydroxylates position 11a of the tetraketide group thus inactivating the antibiotic. | ribosomal protection protein<br>tetracycline-resistant ribosomal protection protein | tetracycline antibiotic   | Tetracycline | protecti<br>on<br><br>Antibioti<br>c target<br>protecti<br>on | 976 | 1316 | 1480 | 740  | 706 | 1488 | 902  | 822  | 824 | 2670 | 1934 | 2512 | 16370 |
| ARO:3000<br>198 | FosX  | confer resistance to fosfomycin. It's dependent on the cofactor, manganese (II), and uses water to generate a vicinal diol. TetX is a flavin-dependent monooxygenase conferring resistance to tetracycline antibiotics. TetX hydroxylates position 11a of the tetraketide group thus inactivating the antibiotic.   | fosfomycin thiol transferase  | fosfomycin  | Fosfomycin   | Antibioti<br>c inactivat<br>ion                               | 0   | 0    | 0    | 0    | 0   | 0    | 2    | 4    | 0   | 2    | 16   | 16   | 40    |
| ARO:3000<br>205 | tetX  | emrK is a membrane fusion protein that is a homolog of EmrA. Together with the inner membrane transporter EmrY and the outer membrane channel TolC, it mediates multidrug efflux. mecR1 is a transmembrane spanning and signal transducing protein which in response to interaction with beta-lactam antibiotics results in upregulation of the mecA/mecR1/mecI operon.   | tetracycline inactivation enzyme  | glycylcycline;tetracycline antibiotic   | Tetracycline | Antibioti<br>c inactivat<br>ion                               | 526 | 642  | 568  | 356  | 398 | 610  | 486  | 536  | 432 | 1936 | 1938 | 2492 | 10920 |
| ARO:3000<br>206 | emrK  | Protein subunit of AcrA-AcrB-TolC multidrug efflux complex. AcrB functions as a herterotrimer which forms the inner membrane component and is primarily responsible for substrate recognition and energy transduction by acting as a drug/proton antiporter.  | major facilitator superfamily (MFS) antibiotic efflux pump                          | tetracycline antibiotic   | Multidrug    | Antibioti<br>c efflux   | 502 | 348  | 378  | 838  | 428 | 174  | 1120 | 990  | 364 | 156  | 112  | 56   | 5466  |
| ARO:3000<br>215 | mecR1 |   | methicillin resistant PBP2  | carbapenem;cephalosporin;cephamycin;monobactam;penam  | Beta-lactam  | Antibioti<br>c target<br>replace<br>ment                      | 8   | 14   | 24   | 12   | 4   | 20   | 2    | 4    | 20  | 18   | 6    | 8    | 140   |
| ARO:3000<br>216 | acrB  |   | resistance-nodulation-cell division (RND) antibiotic efflux pump                    | cephalosporin;fluoroquinolone antibiotic;glycylcycline;penam;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic;triclosan | Multidrug    | Antibioti<br>c efflux   | 578 | 352  | 264  | 1334 | 568 | 120  | 2394 | 1804 | 502 | 3106 | 2562 | 4508 | 18092 |

|                 |                |  |   |   |                |                              |     |     |     |     |     |     |      |      |     |     |     |     |      |
|-----------------|----------------|--|---|---|----------------|------------------------------|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|------|
| ARO:3000<br>217 | blaR1          | blaR1 is a transmembrane spanning and signal transducing protein which in response to interaction with beta-lactam antibiotics results in upregulation of the blaZ/blaR1/blal operon. Plasmid or integron-encoded nucleotidylation of 2-deoxystreptamine                 | blaZ beta-lactamase   | penam   | Beta-lactam    | Antibiotic inactivation      | 14  | 80  | 210 | 174 | 142 | 4   | 150  | 296  | 182 | 24  | 6   | 4   | 1286 |
| ARO:3000<br>230 | ANT(2")<br>-la | aminoglycosides at the hydroxyl group at position 2" in <i>P. aeruginosa</i> , <i>K. pneumoniae</i> , <i>Morganella morganii</i> , <i>E. coli</i> , <i>S. typhimurium</i> , <i>C. freundii</i> and <i>A. baumannii</i>   | ANT(2")   | aminoglycoside antibiotic   | Aminoglycoside | Antibiotic inactivation      | 2   | 6   | 40  | 12  | 182 | 6   | 68   | 24   | 162 | 170 | 210 | 222 | 1104 |
| ARO:3000<br>237 | ToIC           | ToIC is a protein subunit of many multidrug efflux complexes in Gram negative bacteria. It is an outer membrane efflux protein and is constitutively open. Regulation of efflux activity is often at its periplasmic entrance by other components of the efflux complex. | ATP-binding cassette (ABC) antibiotic efflux pump; major facilitator superfamily (MFS) antibiotic efflux pump; resistance-nodulation-cell division (RND) antibiotic efflux pump | aminocoumarin antibiotic; aminoglycoside antibiotic; carbapenem; cephalosporin; fluoroquinolone antibiotic; glycolyl cycline; macrolide antibiotic; penam; penem; peptide antibiotic; phenicol antibiotic; rifamycin antibiotic; tetracycline antibiotic; triclosan | Multidrug      | Antibiotic efflux            | 492 | 264 | 122 | 902 | 488 | 52  | 1466 | 1142 | 360 | 292 | 406 | 334 | 6320 |
| ARO:3000<br>245 | RbpA           | RNA-polymerase binding protein which confers resistance to rifampin.   | RbpA bacterial RNA polymerase-binding protein   | rifamycin antibiotic  | Rifamycin      | Antibiotic target protection | 8   | 2   | 2   | 4   | 18  | 18  | 26   | 10   | 24  | 74  | 304 | 98  | 588  |
| ARO:3000<br>250 | ErmC           | ErmC is a methyltransferase that catalyzes the methylation of A2058 of the 23S ribosomal RNA in two steps. Expression of ErmC is inducible by erythromycin. The leader peptide causes  | Erm 23S ribosomal RNA methyltransferase   | lincosamide antibiotic; macrolide antibiotic; streptogramin antibiotic  | MLS            | Antibiotic target alteration | 190 | 56  | 460 | 18  | 124 | 290 | 106  | 58   | 124 | 184 | 172 | 216 | 1998 |

|             |      |  |  |  |           |  |     |     |     |      |     |      |      |      |     |     |     |     |       |
|-------------|------|--|--|--|-----------|--|-----|-----|-----|------|-----|------|------|------|-----|-----|-----|-----|-------|
| ARO:3000251 | msrA | attenuation of the mRNA and stabilizes the structure preventing further translation. When erythromycin is present, it binds the leader peptide causing a change in conformation allowing for the expression of ErmC. | ABC-F ATP-binding cassette ribosomal protection protein  | lincomamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic             | Multidrug | Antibiotic target protection                         | 50  | 80  | 60  | 22   | 30  | 38   | 14   | 26   | 52  | 26  | 18  | 38  | 454   |
| ARO:3000254 | emrY | emrY is a multidrug transport that moves substrates across the inner membrane of the Gram-negative E. coli. It is a homolog of emrB.   | major facilitator superfamily (MFS) antibiotic efflux pump   | tetracycline antibiotic  | Multidrug | Antibiotic efflux                                    | 892 | 372 | 268 | 1924 | 850 | 192  | 2650 | 2052 | 776 | 860 | 724 | 706 | 12266 |
| ARO:3000263 | marA | In the presence of antibiotic stress, E. coli overexpresses the global activator protein MarA, which besides inducing MDR efflux pump AcrAB, also down-regulates synthesis of the porin OmpF.                        | General Bacterial Porin with reduced permeability to beta-lactams;resistance-nodulation-cell division (RND) antibiotic efflux pump | carbapenem;cephalosporin;cephamycin;fluoroquinolone antibiotic;glycylcycline;monobactam;penam;penem;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic;triclosan | Multidrug | Antibiotic efflux;reduced permeability to antibiotic | 840 | 466 | 478 | 1464 | 778 | 262  | 1980 | 1628 | 634 | 272 | 318 | 144 | 9264  |
| ARO:3000300 | lsaA | LsaA is an ABC-F subfamily protein expressed in Enterococcus faecalis. It confers resistance to clindamycin, quinupristin-dalfopristin, and dalfopristin.  | ABC-F ATP-binding cassette ribosomal protection protein  | lincomamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenic  | Multidrug | Antibiotic target protection                         | 630 | 726 | 212 | 176  | 166 | 1302 | 210  | 214  | 162 | 244 | 186 | 152 | 4380  |



|                 |      |  |  |   |           |                              |     |      |      |      |     |      |      |      |     |     |     |      |      |
|-----------------|------|--|--|---|-----------|------------------------------|-----|------|------|------|-----|------|------|------|-----|-----|-----|------|------|
|                 |      |  | ol<br>antibiotic;pleuro<br>mutilin<br>antibiotic;strepto<br>gramin<br>antibiotic;tetracy<br>cline antibiotic |   |           |                              |     |      |      |      |     |      |      |      |     |     |     |      |      |
| ARO:3000<br>316 | mphA | The mphA gene encodes for resistance enzyme MPH(2')-I which preferentially inactivate 14-membered macrolides (e.g.erythromycin, telithromycin, roxithromycin) over 16-membered macrolides (e.g.tylosin, spiramycin). It phosphorylates macrolides at 2'-OH hydroxyl of desosamine sugar of macrolides in a GTP-dependent manner.<br>The mphB gene encodes for MPH(2')-II. This enzymes phosphorylates 14-membered and 16-membered macrolides. It phosphorylates macrolides in GTP- dependent manner at 2'-OH hydroxyl of desosamine sugar of macrolides. | macrolide phosphotransferase (MPH)   | macrolide antibiotic  | MLS       | Antibiotic inactivation      | 56  | 42   | 8    | 212  | 82  | 18   | 344  | 196  | 34  | 92  | 98  | 48   | 1230 |
| ARO:3000<br>318 | mphB | The mphB gene encodes for MPH(2')-II. This enzymes phosphorylates 14-membered and 16-membered macrolides. It phosphorylates macrolides in GTP- dependent manner at 2'-OH hydroxyl of desosamine sugar of macrolides.<br>ErmE is a methyltransferase found in the erythromycin producer Saccharopolyspora erythraea. Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. The gene is found within the erythromycin biosynthetic cluster and is responsible for self-resistance.                                       | macrolide phosphotransferase (MPH)   | macrolide antibiotic  | MLS       | Antibiotic inactivation      | 466 | 182  | 132  | 1076 | 396 | 32   | 1418 | 1132 | 326 | 128 | 140 | 44   | 5472 |
| ARO:3000<br>326 | ErmE | ErmE is a methyltransferase found in the erythromycin producer Saccharopolyspora erythraea. Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. The gene is found within the erythromycin biosynthetic cluster and is responsible for self-resistance.   | Erm 23S ribosomal RNA methyltransferase  | lincosamide antibiotic;macrolide<br>antibiotic;streptogramin antibiotic | MLS       | Antibiotic target alteration | 748 | 1772 | 1390 | 400  | 412 | 1246 | 398  | 488  | 452 | 652 | 400 | 738  | 9096 |
| ARO:3000<br>343 | tap  | Efflux pump proteins contained within Mycobacterial genomes which confer resistance to a number of different antibiotics including aminoglycosides, and tetracyclines.   | major facilitator superfamily (MFS) antibiotic efflux pump   | tetracycline antibiotic   | Multidrug | Antibiotic efflux            | 0   | 0    | 4    | 2    | 0   | 0    | 46   | 14   | 0   | 34  | 42  | 28   | 170  |
| ARO:3000<br>347 | ErmA | ErmA confers the MLSb phenotype. Similar to ErmC, Expression of ErmA is inducible by erythromycin. The leader  | Erm 23S ribosomal RNA  | lincosamide antibiotic;macrolide  | MLS       | Antibiotic target alteration | 102 | 66   | 60   | 26   | 56  | 104  | 28   | 24   | 56  | 798 | 994 | 1014 | 3328 |

|             |      |   |   |   |              |                              |      |      |      |     |      |      |     |      |      |      |      |      |       |
|-------------|------|---|---|---|--------------|------------------------------|------|------|------|-----|------|------|-----|------|------|------|------|------|-------|
|             |      | peptide causes attenuation of the mRNA and stabilizes the structure preventing further translation. When erythromycin is present, it binds the leader peptide causing a change in conformation allowing for the expression of ErmA.   | methyltransferase   | antibiotic; streptomycin antibiotic                                   |              |                              |      |      |      |     |      |      |     |      |      |      |      |      |       |
| ARO:3000361 | EreA | EreA is an erythromycin esterase that hydrolyses the drug's lactone ring.   | macrolide esterase  | macrolide antibiotic  | MLS          | Antibiotic inactivation      | 2    | 0    | 2    | 10  | 4    | 2    | 30  | 6    | 2    | 8    | 8    | 4    | 78    |
| ARO:3000363 | EreB | EreB is an erythromycin esterase-like protein that hydrolyses the drug's lactone ring.  | macrolide esterase  | macrolide antibiotic  | MLS          | Antibiotic inactivation      | 40   | 2    | 0    | 0   | 0    | 0    | 0   | 0    | 0    | 0    | 0    | 0    | 42    |
| ARO:3000368 | vanC | VanC is a D-Ala-D-Ala ligase homolog that synthesizes D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is specific to <i>Enterococcus gallinarum</i> and <i>E. casseliflavus</i> , providing intrinsic resistance.  | glycopeptide resistance gene cluster; van ligase  | glycopeptide antibiotic   | Glycopeptide | Antibiotic target alteration | 8    | 160  | 100  | 26  | 22   | 52   | 38  | 84   | 48   | 80   | 138  | 164  | 920   |
| ARO:3000375 | ErmB | ErmB confers the MLSb phenotype. Similar to ErmC, expression of ErmB is inducible by erythromycin. The leader peptide causes attenuation of the mRNA and stabilizes the structure preventing further translation. When erythromycin is present, it binds the leader peptide causing a change in conformation allowing for the expression of ErmB. | Erm 23S ribosomal RNA methyltransferase   | lincosamide antibiotic; macrolide antibiotic; streptomycin antibiotic | MLS          | Antibiotic target alteration | 1544 | 1196 | 534  | 424 | 170  | 1818 | 424 | 558  | 248  | 1666 | 1270 | 2316 | 12168 |
| ARO:3000377 | MexA | MexA is the membrane fusion protein of the MexAB-OprM multidrug efflux complex.   | aminocoumarin antibiotic; carbapenem; cephalosporin; cephamycin; cell division (RND) antibiotic efflux pump | antibiotic; fluoroquinolone antibiotic; macrolide                     | Multidrug    | Antibiotic efflux            | 306  | 260  | 1010 | 604 | 4954 | 280  | 862 | 1116 | 5076 | 3518 | 3682 | 4232 | 25900 |

|                 |      |   |  |   |           |                   |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|------|---|--|---|-----------|-------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3000<br>378 | MexB | MexB is the inner membrane multidrug exporter of the efflux complex MexAB-OprM.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol antibiotic;sulfonamide antibiotic;tetracycline antibiotic aminocoumarin antibiotic;carbapenem;cephalosporin;cephamycin;diaminopyrimidine  | Multidrug | Antibiotic efflux | 1774 | 2104 | 1582 | 1212 | 5378 | 1756 | 1638 | 1816 | 5702 | 4262 | 3914 | 4780 | 35918 |
|                 |      |   |  | antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol antibiotic;sulfonamide antibiotic;tetracycline antibiotic acridine dye;aminocoumarin antibiotic;aminoglycoside antibiotic;carbapenem;cephalosporin;cephamycin;diaminopyrimidine antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol |           |                   |      |      |      |      |      |      |      |      |      |      |      |      |       |
| ARO:3000<br>379 | OprM | OprM is an outer membrane factor protein found in Pseudomonas aeruginosa and Burkholderia vietnamiensis. It is part of the MexAB-OprM, MexVW-OprM, MexXY-OprM and the AmrAB-OprM complex. | resistance-nodulation-cell division (RND) antibiotic efflux pump | antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol   | Multidrug | Antibiotic efflux | 690  | 978  | 1978 | 1202 | 4872 | 784  | 1672 | 1554 | 5142 | 4250 | 4064 | 5306 | 32492 |
|                 |      |   |  | antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol   |           |                   |      |      |      |      |      |      |      |      |      |      |      |      |       |

|             |         |  |  |   |             |                               |      |      |      |      |      |      |      |      |      |       |       |       |       |  |
|-------------|---------|--|--|---|-------------|-------------------------------|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|--|
|             |         |  |  | antibiotic;sulfonamide<br>antibiotic;tetracycline antibiotic            |             |                               |      |      |      |      |      |      |      |      |      |       |       |       |       |  |
| ARO:3000391 | norA    | NorA is a multidrug efflux pump in Staphylococcus aureus that confers resistance to fluoroquinolones and other structurally unrelated antibiotics like acriflavine. It shares 30% similarity with NorA, and is a structural homolog of Bmr of Bacillus subtilis. It is regulated by arlRS and mgrA, the latter also known as NorR. Erm(37) is found in | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic                                 | Multidrug   | Antibiotic efflux             | 2    | 34   | 4    | 30   | 10   | 14   | 10   | 60   | 0    | 0     | 0     | 0     | 164   |  |
| ARO:3000392 | Erm(37) | Mycobacterium species and confers the MLSb phenotype. In addition to methylation of A2058 this Erm methylates adjacent adenosines (A2057 and A2059) as well.   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide<br>antibiotic;streptogramin antibiotic | MLS         | Antibiotic target alteration  | 0    | 0    | 6    | 0    | 0    | 0    | 0    | 0    | 0    | 92    | 180   | 156   | 434   |  |
| ARO:3000410 | sul1    | Sul1 is a sulfonamide resistant dihydropteroate synthase of Gram-negative bacteria. It is linked to other resistance genes of class 1 integrons.   | sulfonamide resistant sul                                  | sulfonamide antibiotic;sulfonamide antibiotic                           | Sulfonamide | Antibiotic target replacement | 290  | 1006 | 1370 | 1320 | 5190 | 322  | 2432 | 2192 | 4818 | 10550 | 11592 | 15170 | 56252 |  |
| ARO:3000412 | sul2    | Sul2 is a sulfonamide resistant dihydropteroate synthase of Gram-negative bacteria, usually found on small plasmids.   | sulfonamide resistant sul                                  | sulfonamide antibiotic;sulfonamide antibiotic                           | Sulfonamide | Antibiotic target replacement | 2290 | 4526 | 1866 | 3326 | 9054 | 1860 | 3264 | 4332 | 8092 | 13988 | 13790 | 18046 | 84434 |  |
| ARO:3000413 | sul3    | Sul3 is a sulfonamide resistant dihydropteroate synthase similar to Sul1 and Sul2. Its resistance gene was found encoded in E. coli plasmid DNA of sulfonamide resistant isolates.   | sulfonamide resistant sul                                  | sulfonamide antibiotic;sulfonamide antibiotic                           | Sulfonamide | Antibiotic target replacement | 206  | 638  | 524  | 728  | 392  | 278  | 1144 | 790  | 436  | 224   | 222   | 170   | 5752  |  |
| ARO:3000421 | norB    | NorB is a multidrug efflux pump in Staphylococcus aureus that confers resistance to fluoroquinolones and other structurally unrelated antibiotics like tetracycline. It shares 30% similarity with NorB, and is a structural homolog of Blt of   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic  | Multidrug   | Antibiotic efflux             | 22   | 180  | 62   | 4    | 84   | 174  | 30   | 6    | 52   | 234   | 250   | 376   | 1474  |  |

|                 |         |  |  |                            |                 |                         |     |     |     |     |     |     |     |     |     |     |     |      |      |
|-----------------|---------|--|--|----------------------------|-----------------|-------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|
| ARO:3000<br>444 | rphA    | Bacillus subtilis. It is regulated by mgrA, also known as NorR.<br><br>The enzymatic inactivation of rifampin by phosphorylation at the 21-OH position.  | rifampin phosphotransferase                                | rifamycin antibiotic       | Rifamycin       | Antibiotic inactivation | 86  | 72  | 158 | 262 | 384 | 200 | 402 | 342 | 416 | 926 | 900 | 1148 | 5296 |
| ARO:3000<br>448 | QepA1   | QepA1 is a plasmid-mediated efflux pump in E. coli, shown to contribute to fluoroquinolone resistance. It is regulated by sox genes, also known as global stress regulators.   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic efflux       | 2   | 0   | 4   | 10  | 2   | 0   | 46  | 22  | 0   | 450 | 418 | 598  | 1552 |
| ARO:3000<br>462 | mgtA    | A macrolide glycosyltransferase encoded by the mgtA gene in Streptomyces lividans. This enzyme inactivates macrolides using UDP-glucose as a cofactor. Its optimal substrates are lankamycin, calcomycin, rosaramycin, methymycin, and pikromycin, while interactions with erythromycin, oldeandomycin, azithromycin, and tylosin were weaker. It is inactive against spiramycin and carbomycin. Mechanism first described by Cundliffe, 1992.                               | mgt macrolide glycotransferase                             | macrolide antibiotic       | MLS             | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 4   | 2   | 0    | 6    |
| ARO:3000<br>463 | gimA    | A macrolide glycosyltransferase encoded by the gimA gene in Streptomyces ambofaciens, a natural producer of the macrolide antibiotic spiramycin. Chalconomycin, methymycin, tylosin, pikromycin, rosaramycin, oleandomycin, josamycin, and carbomycin are preferred substrates of gimA glycosyltransferase, while erythromycin and spiramycin have notably low binding affinities. GimA may be able to inactivate spiramycin precursors. Described by Gourmelen et al. 1998. | gimA family macrolide glycosyltransferase                  | macrolide antibiotic       | MLS             | Antibiotic inactivation | 194 | 266 | 176 | 152 | 122 | 238 | 194 | 186 | 176 | 22  | 42  | 16   | 1784 |
| ARO:3000<br>476 | tet(31) | Tet31 is a tetracycline efflux pump found in Aeromonas salmonicida, a Gram-negative  | major facilitator superfamily                              | tetracycline antibiotic    | Tetracycline    | Antibiotic efflux       | 0   | 2   | 10  | 34  | 84  | 0   | 90  | 116 | 124 | 92  | 140 | 94   | 786  |

|                 |         |  |   |   |                |  |      |       |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|---------|--|---|---|----------------|--|------|-------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3000<br>478 | tet(33) | bacteria. It has also been shown to be expressed in <i>Gallibacterium anatis</i> .<br><br>Tet33 is a tetracycline efflux pump found in Gram-positive bacteria, including <i>Arthrobacter</i> and <i>Corynebacterium</i> .  | (MFS) antibiotic efflux pump major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic                                   | Tetracycline   | Antibiotic efflux  | 36   | 20    | 26   | 62   | 30   | 82   | 104  | 42   | 96   | 234  | 414  | 198  | 1344  |
| ARO:3000<br>481 | tet(35) | Tet35 is a tetracycline efflux pump found in the Gram-negative <i>Vibrio</i> and <i>Stenotrophomonas</i> . It is unrelated to other tet resistance genes.  | ATP-binding cassette (ABC) antibiotic efflux pump                                       | tetracycline antibiotic                                   | Tetracycline   | Antibiotic efflux  | 2630 | 4790  | 3182 | 1460 | 1230 | 3932 | 1646 | 1798 | 1398 | 4672 | 3758 | 6594 | 37090 |
| ARO:3000<br>491 | acrD    | AcrD is an aminoglycoside efflux pump expressed in <i>E. coli</i> . Its expression can be induced by indole, and is regulated by <i>baeRS</i> and <i>cpxAR</i> .   | resistance-nodulation-cell division (RND) antibiotic efflux pump                        | aminoglycoside antibiotic                                 | Aminoglycoside | Antibiotic efflux  | 620  | 354   | 266  | 1132 | 590  | 174  | 2074 | 1354 | 472  | 422  | 576  | 398  | 8432  |
| ARO:3000<br>495 | ErmD    | ErmD confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase   | lincosamide antibiotic;macrolide                          | MLS            | Antibiotic target alteration                               | 212  | 180   | 258  | 144  | 72   | 184  | 110  | 166  | 72   | 114  | 80   | 88   | 1680  |
| ARO:3000<br>498 | ErmF    | ErmF confers the MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase   | lincosamide antibiotic;macrolide                          | MLS            | Antibiotic target alteration                               | 1694 | 2040  | 2908 | 1122 | 800  | 2006 | 964  | 1542 | 1142 | 2130 | 1830 | 2128 | 20306 |
| ARO:3000<br>499 | AcrE    | AcrE is a membrane fusion protein, similar to AcrA.  | resistance-nodulation-cell division (RND) antibiotic efflux pump                        | cephalosporin;cephamycin;fluoroquinolone antibiotic;penam | Multidrug      | Antibiotic efflux  | 862  | 200   | 288  | 1194 | 652  | 246  | 1606 | 1140 | 512  | 188  | 190  | 36   | 7114  |
| ARO:3000<br>501 | rpoB2   | Due to gene duplication, the genomes of <i>Nocardia</i> species include both rifampin-sensitive beta-subunit of RNA polymerase ( <i>rpoB</i> ) and rifampin-resistant beta-subunit of RNA polymerase ( <i>rpoB2</i> ) genes, with ~88% similarity between the two gene products. Expression of the <i>rpoB2</i> variant results in | rifamycin-resistant beta-subunit of RNA polymerase ( <i>rpoB</i> )                      | peptide antibiotic;rifamycin antibiotic                   | Multidrug      | Antibiotic target alteration;antibiotic target replacement | 7536 | 10658 | 8100 | 5790 | 3284 | 9102 | 6540 | 6986 | 4430 | 7704 | 8110 | 8140 | 86380 |

|             |  |  |  |  |           |                              |       |       |      |      |      |       |      |      |      |       |      |       |        |  |
|-------------|--|--|--|--|-----------|------------------------------|-------|-------|------|------|------|-------|------|------|------|-------|------|-------|--------|--|
|             |  | replacement of rifampin sensitivity with rifampin resistance.  |  |  |           |                              |       |       |      |      |      |       |      |      |      |       |      |       |        |  |
| ARO:3000502 | AcrF   | AcrF is a inner membrane transporter, similar to AcrB.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | cephalosporin;cephamycin;fluoroquinolone antibiotic;penam                          | Multidrug | Antibiotic efflux            | 640   | 264   | 240  | 1144 | 524  | 138   | 1784 | 1408 | 476  | 278   | 310  | 116   | 7322   |  |
| ARO:3000504 | golS   | GolS is a regulator activated by the presence of gold, and promotes the expression of the MdsABC efflux pump.                  | resistance-nodulation-cell division (RND) antibiotic efflux pump | carbapenem;cephalosporin;cephamycin;monobactam;penam;pencillin;phenicol antibiotic | Multidrug | Antibiotic efflux            | 1574  | 1354  | 1160 | 1882 | 4050 | 1460  | 2712 | 2792 | 3750 | 3064  | 3288 | 3782  | 30868  |  |
| ARO:3000508 | gadX   | GadX is an AraC-family regulator that promotes mdtEF expression to confer multidrug resistance.                                | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;penam                              | Multidrug | Antibiotic efflux            | 1210  | 452   | 408  | 2216 | 1156 | 200   | 3330 | 2650 | 872  | 362   | 414  | 306   | 13576  |  |
| ARO:3000510 | Staphylococcus mupB conferring resistance to mupirocin | An alternative isoleucyl-tRNA synthetase conferring resistance to mupirocin.   | antibiotic-resistant isoleucyl-tRNA synthetase (ileS)            | mupirocin  | Mupirocin | Antibiotic target alteration | 4940  | 8568  | 7036 | 3006 | 4442 | 6800  | 3480 | 3856 | 4848 | 4944  | 4406 | 4434  | 60760  |  |
| ARO:3000516 | emrR   | EmrR is a negative regulator for the EmrAB-TolC multidrug efflux pump in E. coli. Mutations lead to EmrAB-TolC overexpression. | major facilitator superfamily (MFS) antibiotic efflux pump       | fluoroquinolone antibiotic   | Multidrug | Antibiotic efflux            | 326   | 152   | 106  | 608  | 320  | 62    | 964  | 752  | 224  | 120   | 108  | 112   | 3854   |  |
| ARO:3000518 | CRP  | CRP is a global regulator that represses MdtEF multidrug efflux pump expression.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;penam                              | Multidrug | Antibiotic efflux            | 694   | 738   | 538  | 914  | 1476 | 520   | 1276 | 1060 | 1218 | 1700  | 1562 | 1946  | 13642  |  |
| ARO:3000521 | Staphylococcus mupA conferring                         | An alternative isoleucyl-tRNA synthetase conferring resistance to mupirocin.   | antibiotic-resistant isoleucyl-tRNA                              | mupirocin  | Mupirocin | Antibiotic target alteration | 10090 | 11988 | 8818 | 6642 | 3906 | 10866 | 8402 | 7442 | 4916 | 10114 | 8276 | 11532 | 102992 |  |

|             | resistance to mupirocin |  | synthetase (ileS)  |  |              |                              |       |       |       |       |       |       |       |       |       |       |       |       |        |  |
|-------------|-------------------------|--|--|--|--------------|------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--|
| ARO:3000522 | ErmG                    | ErmG is a rRNA adenine N-6-methyltransferase that protects the ribosome from inactivation due to antibiotic binding.   | Erm 23S ribosomal RNA methyltransferase                          | lincosamide antibiotic;macrolide   | MLS          | Antibiotic target alteration | 308   | 730   | 492   | 94    | 52    | 590   | 132   | 114   | 118   | 98    | 84    | 40    | 2852   |  |
| ARO:3000526 | cmeR                    | CmeR is a repressor for the CmeABC multidrug efflux pump, binding to the cmeABC promoter region.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | cephalosporin;fluoroquinolone antibiotic;fusidic acid;macrolide antibiotic | Multidrug    | Antibiotic efflux            | 16    | 18    | 10    | 10    | 8     | 14    | 18    | 12    | 6     | 34    | 126   | 146   | 418    |  |
| ARO:3000533 | macA                    | MacA is a membrane fusion protein that forms an antibiotic efflux complex with MacB and TolC. macA corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.   | ATP-binding cassette (ABC) antibiotic efflux pump                | macrolide antibiotic   | MLS          | Antibiotic efflux            | 2162  | 2388  | 1396  | 2010  | 1546  | 2036  | 2274  | 2014  | 1812  | 3826  | 3772  | 5452  | 30688  |  |
| ARO:3000535 | macB                    | MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15-membered lactones. It forms an antibiotic efflux complex with MacA and TolC. macB corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58. | ATP-binding cassette (ABC) antibiotic efflux pump                | macrolide antibiotic   | MLS          | Antibiotic efflux            | 48978 | 48486 | 42436 | 36076 | 32332 | 48462 | 46500 | 41274 | 35282 | 38412 | 37434 | 42408 | 498080 |  |
| ARO:3000549 | adeS                    | AdeS is a sensor kinase in the AdeRS regulatory system of AdeABC. It is essential for AdeABC expression.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | glycylcycline;tetracycline antibiotic                                      | Multidrug    | Antibiotic efflux            | 1042  | 1696  | 1210  | 1382  | 892   | 972   | 1346  | 1618  | 760   | 1718  | 1612  | 2074  | 16322  |  |
| ARO:3000553 | adeR                    | AdeR is a positive regulator of AdeABC efflux system. AdeR inactivation leads to susceptibility to aminoglycoside antibiotics.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | glycylcycline;tetracycline antibiotic                                      | Multidrug    | Antibiotic efflux            | 1232  | 1220  | 1022  | 838   | 552   | 1148  | 908   | 966   | 916   | 2860  | 1942  | 3392  | 16996  |  |
| ARO:3000556 | tet(44)                 | Tet44 is a tetracycline resistance gene found in Campylobacter   | tetracycline-resistant   | tetracycline antibiotic  | Tetracycline | Antibiotic target            | 2028  | 2718  | 1130  | 966   | 446   | 2302  | 742   | 994   | 614   | 1608  | 1394  | 1934  | 16876  |  |



|             |         |  |  |   |                   |      |      |      |      |      |      |      |      |      |     |     |     |       |  |  |
|-------------|---------|--|--|---|-------------------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-------|--|--|
|             |         | fetus, and binds to the ribosome to confer antibiotic resistance as a ribosomal protection protein.  | ribosomal protection protein                                     |   | protection        |      |      |      |      |      |      |      |      |      |     |     |     |       |  |  |
|             |         |  |  | carbapenem;cephalosporin;diaminopyrimidine antibiotic;fluoroquinolone antibiotic;lincosamide antibiotic;macrolide antibiotic;penem;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic |                   |      |      |      |      |      |      |      |      |      |     |     |     |       |  |  |
| ARO:3000559 | adeN    | AdeN is a repressor of AdeIJK, a RND-type efflux pump in <i>Acinetobacter baumannii</i> . Its inactivation increases expression of AdeJ.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | Multidrug   | Antibiotic efflux | 608  | 1038 | 50   | 148  | 114  | 572  | 182  | 188  | 124  | 428 | 310 | 486 | 4248  |  |  |
| ARO:3000561 | tet(30) | Tet30 is a tetracycline efflux pump found in <i>agrobacterium</i> , a Gram-negative bacterium.   | major facilitator superfamily (MFS) antibiotic efflux pump       | tetracycline antibiotic   | Tetracycline      | 0    | 0    | 36   | 0    | 12   | 0    | 0    | 2    | 10   | 16  | 2   | 0   | 78    |  |  |
| ARO:3000565 | tet(38) | Tet38 is a tetracycline efflux pump found in the Gram-positive <i>Staphylococcus aureus</i> . It is regulated by <i>mgrA</i> , which also regulates <i>NorB</i> .  | major facilitator superfamily (MFS) antibiotic efflux pump       | tetracycline antibiotic   | Tetracycline      | 6    | 4    | 6    | 4    | 16   | 8    | 52   | 10   | 22   | 164 | 330 | 120 | 742   |  |  |
| ARO:3000566 | tet(39) | Tet39 is a tetracycline efflux pump found in Gram-negative bacteria, including <i>Brevundimonas</i> , <i>Stenotrophomonas</i> , <i>Enterobacter</i> , <i>Alcaligenes</i> , <i>Acinetobacter</i> , and <i>Providencia</i> . | major facilitator superfamily (MFS) antibiotic efflux pump       | tetracycline antibiotic   | Tetracycline      | 90   | 340  | 22   | 38   | 70   | 160  | 40   | 102  | 86   | 126 | 84  | 118 | 1276  |  |  |
| ARO:3000567 | tet(40) | Tet40 is a tetracycline efflux pump found in the Gram-positive <i>Clostridium</i> . It is similar to <i>tetA(P)</i> .  | major facilitator superfamily (MFS) antibiotic efflux pump       | tetracycline antibiotic   | Tetracycline      | 2732 | 2662 | 2908 | 1172 | 1184 | 2796 | 1220 | 1244 | 1662 | 482 | 266 | 206 | 18534 |  |  |
| ARO:3000569 | tet(41) | Tet41 is a tetracycline efflux pump found in <i>Serratia</i> , a Gram-negative bacterium. It is related to <i>Acinetobacter Tet(39)</i> .  | major facilitator superfamily (MFS)                              | tetracycline antibiotic   | Tetracycline      | 0    | 96   | 36   | 6    | 66   | 40   | 10   | 6    | 18   | 234 | 258 | 266 | 1036  |  |  |

|                 |                   |   |  |  |              |                              |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----------------|-------------------|---|--|--|--------------|------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ARO:3000<br>572 | tet(42)           | Tet42 is a tetracycline efflux pump found in both Gram-negative ( <i>Pseudomonas</i> ) and Gram-positive ( <i>Microbacterium</i> , <i>Bacillus</i> , <i>Staphylococcus</i> , <i>Paenibacillus</i> ) bacteria.   | antibiotic efflux pump major facilitator superfamily (MFS) antibiotic efflux pump major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic                      | Tetracycline | Antibiotic efflux            | 10  | 8   | 8   | 14  | 40  | 16  | 38  | 22  | 80  | 328 | 618 | 422 | 1604 |
| ARO:3000<br>573 | tet(43)           | Tet(43) is a tetracycline resistance gene with unknown origins, isolated from metagenomic DNA.  | antibiotic efflux pump major facilitator superfamily (MFS) antibiotic efflux pump  | tetracycline antibiotic                      | Tetracycline | Antibiotic efflux            | 0   | 0   | 0   | 4   | 20  | 4   | 30  | 2   | 10  | 40  | 74  | 16  | 200  |
| ARO:3000<br>582 | L1 beta-lactamase | L1 is an Ambler class B MBL; subclass B3 originally isolated from <i>Stenotrophomonas maltophilia</i> . It has activity against a broad range of beta-lactams and is only active with two Zn(II) ions in the active site.   | L1 family beta-lactamase   | cephalosporin                                | Beta-lactam  | Antibiotic inactivation      | 24  | 6   | 4   | 0   | 0   | 8   | 0   | 0   | 0   | 2   | 10  | 6   | 60   |
| ARO:3000<br>589 | NDM-1             | NDM-1 is a metallo-beta-lactamase isolated from <i>Klebsiella pneumoniae</i> with nearly complete resistance to all beta-lactam antibiotics.  | NDM beta-lactamase   | carbapenem; cephalosporin; cephamycin; penam | Beta-lactam  | Antibiotic inactivation      | 0   | 0   | 2   | 2   | 184 | 0   | 0   | 0   | 180 | 14  | 32  | 8   | 422  |
| ARO:3000<br>592 | ErmN              | ErmN is a methyltransferase found in the tylosin producer <i>Streptomyces fradiae</i> . Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. Specifically, this enzyme transfers only one methyl group. The gene is found in the tylosin biosynthetic cluster and is responsible for self-resistance to tylosin. | Erm 23S ribosomal RNA methyltransferase  | lincosamide antibiotic; macrolide            | MLS          | Antibiotic target alteration | 314 | 12  | 46  | 8   | 0   | 134 | 4   | 12  | 0   | 202 | 314 | 248 | 1294 |
| ARO:3000<br>593 | ErmQ              | ErmQ confers MLSb phenotype.  | Erm 23S ribosomal RNA methyltransferase  | lincosamide antibiotic; macrolide            | MLS          | Antibiotic target alteration | 42  | 180 | 230 | 248 | 64  | 110 | 180 | 210 | 60  | 86  | 90  | 38  | 1538 |
| ARO:3000<br>594 | ErmR              | ErmR is a methyltransferase found in the erythromycin producer <i>Aeromicrobium erythreum</i> . Like other Erm enzymes, it catalyzes the  | Erm 23S ribosomal RNA methyltransferase  | lincosamide antibiotic; macrolide            | MLS          | Antibiotic target alteration | 42  | 588 | 172 | 68  | 42  | 312 | 44  | 66  | 76  | 14  | 8   | 10  | 1442 |

|             |         |  |   |                                  |             |                              |     |     |     |      |      |     |      |      |      |      |      |      |       |  |
|-------------|---------|--|---|----------------------------------|-------------|------------------------------|-----|-----|-----|------|------|-----|------|------|------|------|------|------|-------|--|
|             |         | methylation of A2058 of the 23S ribosomal RNA. The gene is found within the erythromycin biosynthetic cluster and is responsible for self-resistance.  |   |                                  |             |                              |     |     |     |      |      |     |      |      |      |      |      |      |       |  |
| ARO:3000595 | ErmT    | ErmT confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 100 | 116 | 72  | 22   | 32   | 74  | 12   | 2    | 50   | 392  | 382  | 346  | 1600  |  |
| ARO:3000596 | ErmX    | ErmX is a rRNA methyltransferase that protects the ribosome from inactivation due to antibiotic binding.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 24  | 28  | 30  | 38   | 104  | 96  | 120  | 46   | 228  | 394  | 744  | 514  | 2366  |  |
| ARO:3000598 | Erm(31) | Erm(31) confers a MLSb resistant phenotype. Along with erm(30), these genes are responsible for self-resistance in the pikromycin/narbomycin/methylmycin/neomethylmycin producer, Streptomyces venezuelae. | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 14  | 0   | 16  | 22   | 48   | 26  | 94   | 22   | 52   | 242  | 394  | 218  | 1148  |  |
| ARO:3000600 | Erm(34) | ErmD confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 776 | 490 | 684 | 1702 | 2134 | 316 | 1976 | 1862 | 1870 | 1474 | 1382 | 1760 | 16426 |  |
| ARO:3000601 | Erm(38) | ErmD confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 0   | 12  | 8   | 40   | 10   | 0   | 56   | 68   | 10   | 22   | 26   | 6    | 258   |  |
| ARO:3000604 | Erm(35) | ErmD confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 36  | 82  | 176 | 80   | 14   | 54  | 32   | 74   | 18   | 546  | 440  | 834  | 2386  |  |
| ARO:3000605 | Erm(36) | ErmD confers MLSb phenotype.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS         | Antibiotic target alteration | 6   | 4   | 24  | 22   | 4    | 12  | 58   | 22   | 14   | 142  | 276  | 168  | 752   |  |
| ARO:3000606 | FEZ-1   | FEZ-1 is an Ambler class B MBL; subclass B3 first isolated from Legionella gormanii. It has  | FEZ beta-lactamase                      | carbapenem;cephalosporin;penam   | Beta-lactam | Antibiotic                   | 4   | 22  | 6   | 4    | 10   | 4   | 0    | 2    | 8    | 0    | 0    | 0    | 60    |  |

|             |      |  |  |  |             |                               |      |      |      |      |      |      |      |      |      |      |      |       |       |
|-------------|------|--|--|--|-------------|-------------------------------|------|------|------|------|------|------|------|------|------|------|------|-------|-------|
| ARO:3000614 | mefE | activity against a broad range of beta-lactams and is only active with two Zn(II) ions in the active site.<br><br>mefE is a proton motive efflux pump in Streptococcus pneumoniae that confers resistance to macrolides. It is found on the same operon as mefA and the ABC-efflux pump mel. | major facilitator superfamily (MFS) antibiotic efflux pump       | macrolide antibiotic   | MLS         | Antibiotic efflux             | 286  | 32   | 200  | 34   | 162  | 394  | 42   | 54   | 172  | 52   | 66   | 92    | 1586  |
| ARO:3000616 | mel  | Mel, a homolog of MsrA, is an ABC-F subfamily protein associated with macrolide resistance. It is expressed on the same operon as mefA and mefE, both MFS-type efflux proteins that confer macrolide resistance.   | ABC-F ATP-binding cassette ribosomal protection protein          | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic | Multidrug   | Antibiotic target protection  | 4028 | 5566 | 6072 | 3408 | 2070 | 4882 | 2706 | 3624 | 2598 | 1902 | 1402 | 1196  | 39454 |
| ARO:3000617 | mecA | A foreign PBP2a acquired by lateral gene transfer that able to perform peptidoglycan synthesis in the presence of beta-lactams.  | methicillin resistant PBP2                                       | carbapenem;cephalosporin;cephamycin;monobactam;penam   | Beta-lactam | Antibiotic target replacement | 190  | 640  | 830  | 516  | 480  | 428  | 568  | 632  | 620  | 340  | 324  | 358   | 5926  |
| ARO:3000620 | adeL | AdeL is a regulator of AdeFGH in Acinetobacter baumannii. AdeL mutations are associated with AdeFGH overexpression and multidrug resistance.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;tetracycline antibiotic   | Multidrug   | Antibiotic efflux             | 4072 | 3702 | 2978 | 6934 | 6278 | 2018 | 9760 | 7944 | 5272 | 8650 | 8456 | 11584 | 77648 |
| ARO:3000656 | AcrS | AcrS is a repressor of the AcrAB efflux complex and is associated with the expression of AcrEF. AcrS is believed to regulate a switch between AcrAB and AcrEF efflux.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | cephalosporin;cephamycin;fluoroquinolone antibiotic;glycylcycline;penam;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic;triclosan                 | Multidrug   | Antibiotic efflux             | 958  | 496  | 1306 | 1930 | 4778 | 436  | 3148 | 2872 | 4330 | 2602 | 2674 | 2570  | 28100 |

|                 |      |   |   |  |                   |                   |      |      |      |      |     |      |      |      |      |      |      |       |      |
|-----------------|------|---|---|--|-------------------|-------------------|------|------|------|------|-----|------|------|------|------|------|------|-------|------|
| ARO:3000<br>676 | H-NS | H-NS is a histone-like protein involved in global gene regulation in Gram-negative bacteria. It is a repressor of the membrane fusion protein genes <i>acrE</i> , <i>mdtE</i> , and <i>emrK</i> as well as nearby genes of many RND-type multidrug exporters. | major facilitator superfamily (MFS) antibiotic efflux pump;resistance-nodulation-cell division (RND) antibiotic efflux pump multidrug and toxic compound extrusion (MATE) transporter multidrug and toxic compound extrusion (MATE) transporter small | cephalosporin;cephamycin;fluoroquinolone antibiotic;macrolide antibiotic;penam;tetracycline antibiotic | Multidrug         | Antibiotic efflux | 468  | 196  | 100  | 818  | 506 | 40   | 1312 | 896  | 396  | 118  | 164  | 76    | 5090 |
| ARO:3000<br>746 | mepR | MepR is an upstream repressor of MepA in <i>Staphylococcus aureus</i> . It is part of the <i>mepRAB</i> operon.   | glycylcycline;tetracycline antibiotic   | Multidrug  | Antibiotic efflux | 56                | 36   | 224  | 14   | 24   | 94  | 42   | 34   | 36   | 48   | 24   | 14   | 646   |      |
| ARO:3000<br>753 | abeM | AbeM is an multidrug efflux pump found in <i>Acinetobacter baumannii</i> .  | acridine dye;fluoroquinolone antibiotic;triclosan   | Multidrug  | Antibiotic efflux | 714               | 1916 | 420  | 248  | 412  | 986 | 320  | 294  | 326  | 666  | 546  | 1000 | 7848  |      |
| ARO:3000<br>768 | abeS | AbeS in an efflux pump of the SMR family of transporters found in <i>Acinetobacter baumannii</i> .  | aminocoumarin antibiotic;macrolide antibiotic   | Multidrug  | Antibiotic efflux | 8                 | 46   | 148  | 34   | 72   | 78  | 120  | 44   | 50   | 192  | 236  | 284  | 1312  |      |
| ARO:3000<br>774 | adeA | AdeA is the membrane fusion protein of the multidrug efflux complex AdeABC.   | glycylcycline;tetracycline antibiotic   | Multidrug  | Antibiotic efflux | 424               | 678  | 1014 | 128  | 222  | 326 | 118  | 236  | 294  | 410  | 454  | 472  | 4776  |      |
| ARO:3000<br>775 | adeB | AdeB is the multidrug transporter of the <i>adeABC</i> efflux system.   | glycylcycline;tetracycline antibiotic   | Multidrug  | Antibiotic efflux | 184               | 148  | 132  | 270  | 82   | 154 | 256  | 320  | 90   | 2166 | 2116 | 3288 | 9206  |      |
| ARO:3000<br>777 | adeF | AdeF is the membrane fusion protein of the multidrug efflux complex AdeFGH.   | fluoroquinolone antibiotic;tetracycline antibiotic  | Multidrug  | Antibiotic efflux | 542               | 1520 | 2162 | 1426 | 1036 | 780 | 1200 | 1532 | 1322 | 1068 | 668  | 660  | 13916 |      |

|                 |      |   |   |  |           |                      |      |      |      |      |     |      |      |      |     |      |      |      |       |
|-----------------|------|---|---|--|-----------|----------------------|------|------|------|------|-----|------|------|------|-----|------|------|------|-------|
| ARO:3000<br>778 | adeG | AdeG is the inner membrane transporter of the AdeFGH multidrug efflux complex.  | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | fluoroquinolone<br>antibiotic;tetracycline antibiotic  | Multidrug | Antibiotic<br>efflux | 1458 | 616  | 586  | 1082 | 534 | 652  | 1546 | 1290 | 536 | 2568 | 2938 | 3918 | 17724 |
| ARO:3000<br>779 | adeH | AdeH is the outer membrane channel protein of the AdeFGH multidrug efflux complex.  | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | fluoroquinolone<br>antibiotic;tetracycline antibiotic  | Multidrug | Antibiotic<br>efflux | 776  | 2156 | 1974 | 1336 | 856 | 1082 | 796  | 1170 | 964 | 1118 | 598  | 858  | 13684 |
| ARO:3000<br>780 | adel | Adel is the membrane fusion protein of the AdelJK multidrug efflux complex.   | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | carbapenem;cephalosporin;diaminopyrimidine<br>antibiotic;fluoroquinolone<br>antibiotic;lincosamide<br>antibiotic;macrolide<br>antibiotic;penam;<br>phenicol<br>antibiotic;rifamycin<br>antibiotic;tetracycline antibiotic<br>carbapenem;cephalosporin;diaminopyrimidine<br>antibiotic;fluoroquinolone<br>antibiotic;lincosamide<br>antibiotic;macrolide<br>antibiotic;penam;<br>phenicol<br>antibiotic;rifamycin<br>antibiotic;tetracycline antibiotic | Multidrug | Antibiotic<br>efflux | 906  | 1768 | 324  | 334  | 258 | 1126 | 314  | 388  | 238 | 306  | 204  | 478  | 6644  |
| ARO:3000<br>781 | adeJ | AdeJ is a RND efflux protein that acts as the inner membrane transporter of the AdelJK efflux complex. It has 57% identity with E. coli AcrB. | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | carbapenem;cephalosporin;diaminopyrimidine<br>antibiotic;fluoroquinolone<br>antibiotic;lincosamide<br>antibiotic;macrolide<br>antibiotic;penam;<br>phenicol<br>antibiotic;rifamycin<br>antibiotic;tetracycline antibiotic  | Multidrug | Antibiotic<br>efflux | 988  | 2594 | 344  | 448  | 316 | 1498 | 386  | 450  | 332 | 412  | 372  | 754  | 8894  |
| ARO:3000<br>782 | adeK | AdeK is the outer membrane factor protein in the adelJK multidrug efflux complex.   | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | carbapenem;cephalosporin;diaminopyrimidine   | Multidrug | Antibiotic<br>efflux | 1082 | 2728 | 1178 | 1026 | 670 | 1720 | 870  | 1156 | 666 | 1394 | 1210 | 1796 | 15496 |

|                 |      |   | (RND)<br>antibiotic<br>efflux pump  | antibiotic;fluoro<br>quinolone<br>antibiotic;lincosa<br>mide<br>antibiotic;macrol<br>ide<br>antibiotic;penem<br>;phenicol<br>antibiotic;rifamy<br>cin<br>antibiotic;tetracy<br>cline antibiotic |           |                       |     |      |      |     |     |      |     |     |     |      |      |      |       |  |  |
|-----------------|------|---|---|---|-----------|-----------------------|-----|------|------|-----|-----|------|-----|-----|-----|------|------|------|-------|--|--|
| ARO:3000<br>783 | cmeA | CmeA is the membrane fusion<br>protein of the CmeABC<br>multidrug efflux complex.   | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | cephalosporin;flu<br>oroquinolone<br>antibiotic;fusidic<br>acid;macrolide<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 242 | 270  | 356  | 174 | 198 | 292  | 128 | 170 | 256 | 428  | 356  | 706  | 3576  |  |  |
| ARO:3000<br>784 | cmeB | CmeB is the inner membrane<br>transporter the CmeABC<br>multidrug efflux complex.   | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | cephalosporin;flu<br>oroquinolone<br>antibiotic;fusidic<br>acid;macrolide<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 918 | 1682 | 1690 | 942 | 368 | 1484 | 790 | 976 | 578 | 2816 | 2906 | 4004 | 19154 |  |  |
| ARO:3000<br>785 | cmeC | CmeC is the outer membrane<br>channel protein of the CmeABC<br>multidrug efflux complex.  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | cephalosporin;flu<br>oroquinolone<br>antibiotic;fusidic<br>acid;macrolide<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 22  | 48   | 32   | 18  | 16  | 24   | 30  | 16  | 20  | 1322 | 1142 | 2230 | 4920  |  |  |
| ARO:3000<br>789 | mdsA | MdsA is the membrane fusion<br>protein of the multidrug and<br>metal efflux complex MdsABC.   | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | carbapenem;cep<br>halosporin;cepha<br>mycin;monobact<br>am;penam;pene<br>m;phenicol<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 12  | 0    | 80   | 78  | 28  | 20   | 28  | 32  | 14  | 28   | 60   | 12   | 392   |  |  |
| ARO:3000<br>790 | mdsB | MdsB is the inner membrane<br>transporter of the multidrug and<br>metal efflux complex MdsABC.<br>mdsB corresponds to 1 locus in<br>Pseudomonas aeruginosa PAO1<br>(gene name: mexQ) and 2 loci in<br>Pseudomonas aeruginosa<br>LESB58. | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | carbapenem;cep<br>halosporin;cepha<br>mycin;monobact<br>am;penam;pene<br>m;phenicol<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 98  | 258  | 386  | 78  | 196 | 196  | 146 | 130 | 158 | 590  | 746  | 836  | 3818  |  |  |
| ARO:3000<br>791 | mdsC | MdsC is the outer membrane<br>channel of the multidrug and<br>metal efflux complex MdsABC.  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | carbapenem;cep<br>halosporin;cepha<br>mycin;monobact  | Multidrug | Antibioti<br>c efflux | 134 | 186  | 168  | 148 | 46  | 112  | 176 | 172 | 92  | 56   | 100  | 62   | 1452  |  |  |

|                 |      |   |  |  |           |                       |      |      |      |      |      |      |      |      |      |      |      |       |       |
|-----------------|------|---|--|--|-----------|-----------------------|------|------|------|------|------|------|------|------|------|------|------|-------|-------|
| ARO:3000<br>792 | mdtA | MdtA is the membrane fusion protein of the multidrug efflux complex mdtABC.   | (RND)<br>antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | am;penam;pene<br>m;phenicol<br>antibiotic<br><br>aminocoumarin<br>antibiotic | Multidrug | Antibioti<br>c efflux | 750  | 1026 | 542  | 1140 | 678  | 732  | 1492 | 1814 | 658  | 900  | 1150 | 1138  | 12020 |
| ARO:3000<br>793 | mdtB | MdtB is a transporter that forms a heteromultimer complex with MdtC to form a multidrug transporter. MdtBC is part of the MdtABC-TolC efflux complex.   | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | aminocoumarin<br>antibiotic  | Multidrug | Antibioti<br>c efflux | 1846 | 1658 | 1548 | 1904 | 1252 | 1630 | 2566 | 2266 | 1420 | 7374 | 6156 | 10672 | 40292 |
| ARO:3000<br>794 | mdtC | MdtC is a transporter that forms a heteromultimer complex with MdtB to form a multidrug transporter. MdtBC is part of the MdtABC-TolC efflux complex. In the absence of MdtB, MdtC can form a homomultimer complex that results in a functioning efflux complex with a narrower drug specificity. mdtC corresponds to 3 loci in Pseudomonas aeruginosa PAO1 (gene name: muxC/muxB) and 3 loci in Pseudomonas aeruginosa LESB58. | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump  | aminocoumarin<br>antibiotic  | Multidrug | Antibioti<br>c efflux | 2874 | 3070 | 4014 | 3380 | 7980 | 2006 | 4538 | 4828 | 7710 | 4564 | 4006 | 4552  | 53522 |
| ARO:3000<br>795 | mdtE | MdtE is the membrane fusion protein of the MdtEF multidrug efflux complex. It shares 70% sequence similarity with AcrA.   | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | fluoroquinolone<br>antibiotic;macrol<br>ide<br>antibiotic;penam              | Multidrug | Antibioti<br>c efflux | 522  | 284  | 332  | 1286 | 606  | 158  | 1782 | 1320 | 586  | 386  | 368  | 324   | 7954  |
| ARO:3000<br>796 | mdtF | MdtF is the multidrug inner membrane transporter for the MdtEF-TolC efflux complex.   | fluoroquinolone<br>antibiotic;macrol<br>ide<br>antibiotic;penam  | aminocoumarin<br>antibiotic;amino<br>glycoside<br>antibiotic;cephal          | Multidrug | Antibioti<br>c efflux | 740  | 466  | 226  | 1260 | 640  | 258  | 1924 | 1550 | 586  | 446  | 282  | 248   | 8626  |
| ARO:3000<br>800 | MexC | MexC is the membrane fusion protein of the MexCD-OprJ multidrug efflux complex.   | resistance-<br>nodulation-<br>cell division<br>(RND)   | aminocoumarin<br>antibiotic;amino<br>glycoside<br>antibiotic;cephal          | Multidrug | Antibioti<br>c efflux | 102  | 186  | 1504 | 518  | 5738 | 176  | 912  | 1438 | 5328 | 1914 | 2244 | 2534  | 22594 |



|             |      |  |   |                                    |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|-------------|------|--|---|------------------------------------|-----------|-------------------|-----|-----|------|------|-------|-----|------|------|-------|------|------|------|-------|
| ARO:3000801 | MexD | MexD is the multidrug inner membrane transporter of the MexCD-OprJ complex.              | antibiotic efflux pump                    | osporin;diamino pyrimidine         | Multidrug | Antibiotic efflux | 312 | 358 | 3528 | 2142 | 17074 | 270 | 3066 | 5504 | 15418 | 5610 | 6216 | 7364 | 66862 |
|             |      |  |   | antibiotic;fluoro quinolone        |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;macrolide               |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;penam;phenicol          |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;tetracycline antibiotic |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | aminocoumarin                      |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;amino glycoside         |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;cephal                  |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | osporin;diamino pyrimidine         |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
| ARO:3000802 | OprJ | OprJ is the outer membrane channel component of the MexCD-OprJ multidrug efflux complex. | resistance-nodulation-cell division (RND) | antibiotic;fluoro quinolone        | Multidrug | Antibiotic efflux | 62  | 122 | 1354 | 826  | 7020  | 46  | 1308 | 1812 | 6268  | 1910 | 2204 | 2256 | 25188 |
|             |      |  | antibiotic efflux pump                    | antibiotic;macrolide               |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;penam;phenicol          |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;tetracycline antibiotic |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | aminocoumarin                      |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;amino glycoside         |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;cephal                  |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | osporin;diamino pyrimidine         |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;fluoro quinolone        |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
| ARO:3000803 | MexE | MexE is the membrane fusion protein of the MexEF-OprN multidrug efflux complex.          | antibiotic efflux pump                    | antibiotic;macrolide               | Multidrug | Antibiotic efflux | 222 | 24  | 44   | 26   | 14    | 154 | 18   | 70   | 40    | 492  | 498  | 458  | 2060  |
|             |      |  |   | antibiotic;penam;phenicol          |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;tetracycline antibiotic |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | diaminopyrimidine                  |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;fluoro quinolone        |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   | antibiotic;phenicol antibiotic     |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
| ARO:3000804 | MexF | MexF is the multidrug inner membrane transporter of the MexEF-OprN complex. mexF         | resistance-nodulation-cell division       | diaminopyrimidine                  | Multidrug | Antibiotic efflux | 368 | 192 | 262  | 216  | 82    | 356 | 208  | 224  | 146   | 314  | 388  | 450  | 3206  |
|             |      |  |   | antibiotic;fluoro                  |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |
|             |      |  |   |                                    |           |                   |     |     |      |      |       |     |      |      |       |      |      |      |       |

|             |      |   |  |   |           |                   |     |     |     |     |      |     |     |      |      |      |      |      |       |
|-------------|------|---|--|---|-----------|-------------------|-----|-----|-----|-----|------|-----|-----|------|------|------|------|------|-------|
|             |      | corresponds to 2 loci in <i>Pseudomonas aeruginosa</i> PAO1 (gene name: mexF/mexB) and 4 loci in <i>Pseudomonas aeruginosa</i> LESB58 (gene name: mexD/mexB). | (RND) antibiotic efflux pump                                     | quinolone antibiotic;phenicol antibiotic                                    |           |                   |     |     |     |     |      |     |     |      |      |      |      |      |       |
| ARO:3000805 | OprN | OprN is the outer membrane channel component of the MexEF-OprN multidrug efflux complex.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | diaminopyrimidine antibiotic;fluoroquinolone antibiotic;phenicol antibiotic | Multidrug | Antibiotic efflux | 688 | 264 | 336 | 166 | 128  | 640 | 140 | 194  | 274  | 352  | 512  | 502  | 4196  |
| ARO:3000806 | MexG | MexG is a membrane protein required for MexGHI-OpmD efflux activity.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic;tetracycline antibiotic             | Multidrug | Antibiotic efflux | 0   | 20  | 0   | 4   | 2    | 2   | 0   | 2    | 0    | 0    | 0    | 2    | 32    |
| ARO:3000807 | MexH | MexH is the membrane fusion protein of the efflux complex MexGHI-OpmD.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic;tetracycline antibiotic             | Multidrug | Antibiotic efflux | 674 | 146 | 680 | 616 | 4520 | 380 | 804 | 1248 | 3864 | 4312 | 4056 | 5826 | 27126 |
| ARO:3000808 | MexI | MexI is the inner membrane transporter of the efflux complex MexGHI-OpmD.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic;tetracycline antibiotic             | Multidrug | Antibiotic efflux | 360 | 292 | 466 | 228 | 1694 | 322 | 320 | 254  | 1694 | 1352 | 1392 | 1842 | 10216 |
| ARO:3000809 | OpmD | OpmD is the outer membrane channel protein of the efflux complex MexGHI-OpmD.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic;tetracycline antibiotic             | Multidrug | Antibiotic efflux | 0   | 6   | 76  | 62  | 12   | 8   | 224 | 90   | 12   | 82   | 138  | 112  | 822   |
| ARO:3000810 | mtrC | MtrC is the membrane fusion protein of the MtrCDE multidrug efflux complex.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | macrolide antibiotic;penam  | Multidrug | Antibiotic efflux | 140 | 142 | 322 | 132 | 38   | 198 | 250 | 170  | 26   | 258  | 296  | 140  | 2112  |
| ARO:3000811 | mtrD | MtrD is the inner membrane multidrug transporter of the MtrCDE efflux complex.  | resistance-nodulation-cell division (RND)                        | macrolide antibiotic;penam  | Multidrug | Antibiotic efflux | 38  | 40  | 314 | 172 | 304  | 82  | 338 | 276  | 208  | 2654 | 2088 | 3668 | 10182 |

|                 |      |  |  |  |                 |  |      |      |      |      |      |      |      |      |      |       |       |       |       |
|-----------------|------|--|--|--|-----------------|--|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|
| ARO:3000<br>812 | mtrE | MtrE is an outer membrane exporter protein that is part of the MtrCDE multidrug efflux complex.  | antibiotic efflux pump resistance-nodulation-cell division (RND) antibiotic efflux pump ATP-binding cassette                       | macrolide antibiotic;penam   | Multidrug       | Antibiotic efflux                                    | 44   | 74   | 84   | 58   | 44   | 54   | 46   | 84   | 40   | 732   | 542   | 962   | 2764  |
| ARO:3000<br>815 | mgrA | MgrA, also known as NorR, is a regulator for norA, norB, and tet38. It is a positive regulator for norA expression, but is a direct repressor for norB and an indirect repressor of tet38.   | acridine dye;cephalosporin;fluoroquinolone antibiotic;penam;peptide antibiotic;tetracycline antibiotic                             | antibiotic efflux pump;major facilitator superfamily (MFS)   | Multidrug       | Antibiotic efflux                                    | 110  | 60   | 58   | 6    | 22   | 84   | 54   | 18   | 22   | 76    | 186   | 80    | 776   |
| ARO:3000<br>816 | mtrA | MtrA is a transcriptional activator of the MtrCDE multidrug efflux pump of Neisseria gonorrhoeae.  | antibiotic efflux pump resistance-nodulation-cell division (RND)   | macrolide antibiotic;penam   | Multidrug       | Antibiotic efflux                                    | 5490 | 5614 | 5570 | 4928 | 6486 | 6142 | 5674 | 5814 | 6836 | 10122 | 11564 | 13126 | 87366 |
| ARO:3000<br>822 | pmrA | PmrA is a MFS-type efflux pump expressed in Streptococcus pneumoniae that confers low-level resistance to norfloxacin, ciprofloxacin, and acriflavine.   | major facilitator superfamily (MFS) antibiotic efflux pump   | fluoroquinolone antibiotic   | Fluoroquinolone | Antibiotic efflux                                    | 56   | 28   | 330  | 2    | 184  | 22   | 6    | 14   | 122  | 366   | 586   | 496   | 2212  |
| ARO:3000<br>823 | ramA | RamA (resistance multiple) is a positive regulator of AcrAB-TolC and leads to high level multidrug resistance in Klebsiella pneumoniae, Salmonella enterica, and Enterobacter aerogenes, increasing the expression of both the mar operon as well as AcrAB. RamA also decreases OmpF expression. | General Bacterial Porin with reduced permeability to beta-lactams;resistance-nodulation-cell division (RND) antibiotic efflux pump | carbapenem;cephalosporin;cephamycin;fluoroquinolone antibiotic;glycylcycline;monobactam;penam;pencillin;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic;triclosan | Multidrug       | Antibiotic efflux;reduced permeability to antibiotic | 1174 | 662  | 534  | 1056 | 608  | 600  | 1546 | 1282 | 658  | 378   | 320   | 234   | 9052  |
| ARO:3000<br>826 | sdiA | SdiA is a cell division regulator that is also a positive regulator  | resistance-nodulation-   | cephalosporin;fluoroquinolone  | Multidrug       | Antibiotic efflux                                    | 400  | 134  | 94   | 506  | 258  | 136  | 742  | 790  | 232  | 108   | 84    | 54    | 3538  |

|             |      |  |   |  |           |                   |       |       |       |       |       |       |       |       |       |       |       |       |        |  |
|-------------|------|--|---|--|-----------|-------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--|
|             |      | of AcrAB only when it's expressed from a plasmid. When the sdiA gene is on the chromosome, it has no effect on expression of acrAB   | cell division (RND) antibiotic efflux pump  | antibiotic;glycylc ycline;penam;phenicol antibiotic;rifamycin antibiotic;tetracycline antibiotic;triclosan |           |                   |       |       |       |       |       |       |       |       |       |       |       |       |        |  |
| ARO:3000828 | baeR | BaeR is a response regulator that promotes the expression of MdtABC and AcrD efflux complexes.   | resistance-nodulation-cell division (RND) antibiotic efflux pump  | aminocoumarin antibiotic;aminoglycoside antibiotic   | Multidrug | Antibiotic efflux | 2426  | 2602  | 2278  | 3054  | 2614  | 1710  | 4296  | 3324  | 2284  | 3282  | 3330  | 3754  | 34954  |  |
| ARO:3000829 | baeS | BaeS is a sensor kinase in the BaeSR regulatory system. While it phosphorylates BaeR to increase its activity, BaeS is not necessary for overexpressed BaeR to confer resistance. CpxA is a membrane-localized sensor kinase that is activated by envelope stress. It starts a kinase cascade that activates CpxR, which promotes efflux complex expression. | resistance-nodulation-cell division (RND) antibiotic efflux pump  | aminocoumarin antibiotic;aminoglycoside antibiotic   | Multidrug | Antibiotic efflux | 6794  | 7178  | 6340  | 5124  | 6582  | 7430  | 5628  | 5966  | 6886  | 12956 | 12494 | 16012 | 99390  |  |
| ARO:3000830 | cpxA | CpxA is a membrane-localized sensor kinase that is activated by envelope stress. It starts a kinase cascade that activates CpxR, which promotes efflux complex expression.   | resistance-nodulation-cell division (RND) antibiotic efflux pump  | aminocoumarin antibiotic;aminoglycoside antibiotic   | Multidrug | Antibiotic efflux | 4246  | 3838  | 4278  | 7252  | 16344 | 3250  | 10160 | 9982  | 14652 | 16662 | 16590 | 22046 | 129300 |  |
| ARO:3000832 | evgA | EvgA, when phosphorylated, is a positive regulator for efflux protein complexes emrKY and mdtEF. While usually phosphorylated in a EvgS dependent manner, it can be phosphorylated in the absence of EvgS when overexpressed.  | major facilitator superfamily (MFS) antibiotic efflux pump;resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;penam;tetracycline antibiotic                              | Multidrug | Antibiotic efflux | 4104  | 2418  | 2522  | 3268  | 2694  | 2608  | 4726  | 4018  | 2842  | 2170  | 2298  | 2456  | 36124  |  |
| ARO:3000833 | evgS | EvgS is a sensor protein that phosphorylates the regulatory protein EvgA. evgS corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.   | major facilitator superfamily (MFS) antibiotic efflux pump;resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;penam;tetracycline antibiotic                              | Multidrug | Antibiotic efflux | 19064 | 15552 | 14500 | 15514 | 28772 | 14200 | 20340 | 21002 | 29780 | 25110 | 22942 | 27384 | 254160 |  |

|                 |                             |   |   |   |             |                                 |      |      |      |      |       |      |      |      |       |       |       |       |        |  |
|-----------------|-----------------------------|---|---|---|-------------|---------------------------------|------|------|------|------|-------|------|------|------|-------|-------|-------|-------|--------|--|
|                 |                             |   | nce-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump<br>major |   |             |                                 |      |      |      |      |       |      |      |      |       |       |       |       |        |  |
| ARO:3000<br>838 | arlR                        | ArlR is a response regulator that binds to the norA promoter to activate expression. ArlR must first be phosphorylated by ArlS.   | facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump<br>major           | acridine<br>dye;fluoroquinol<br>one antibiotic              | Multidrug   | Antibioti<br>c efflux           | 8972 | 7126 | 7420 | 6498 | 13220 | 8122 | 7494 | 8856 | 13628 | 14376 | 13932 | 18122 | 127766 |  |
| ARO:3000<br>839 | arlS                        | ArlS is a protein histidine kinase that phosphorylates ArlR, a promoter for norA expression.  | facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump<br>major           | acridine<br>dye;fluoroquinol<br>one antibiotic              | Multidrug   | Antibioti<br>c efflux           | 8890 | 7120 | 5446 | 3246 | 2612  | 9792 | 3184 | 3912 | 3550  | 5760  | 4950  | 5500  | 63962  |  |
| ARO:3000<br>842 | EBR-1<br>beta-lactama<br>se | EBR-1 is an Ambler class B beta-lactamase found in <i>Empedobacter brevis</i> and is known to mediate the hydrolysis of penicillins, cephalosporins, and carbapenems efficiently but not aztreonam. | EBR beta-lactamase  | carbapenem;cep<br>halosporin;pena<br>m                      | Beta-lactam | Antibioti<br>c inactivat<br>ion | 0    | 0    | 8    | 0    | 0     | 0    | 0    | 0    | 0     | 0     | 0     | 0     | 8      |  |
| ARO:3000<br>843 | MUS-1                       | MUS-1 is a chromosome-encoded beta-lactamase from <i>Myroides odoratus</i> and <i>Myroides odoratimimus</i> .   | MUS beta-lactamase  | carbapenem  | Beta-lactam | Antibioti<br>c inactivat<br>ion | 0    | 2    | 14   | 0    | 20    | 0    | 2    | 0    | 0     | 100   | 114   | 104   | 356    |  |
| ARO:3000<br>847 | KHM-1                       | KHM-1 is a plasmid-mediated metallo-beta-lactamase found in <i>Citrobacter freundii</i> that confers resistance to all broad-spectrum beta-lactams, execept for monobactams.                        | KHM beta-latamase   | carbapenem;cep<br>halosporin;cepha<br>mycin;penam;pe<br>nem | Beta-lactam | Antibioti<br>c inactivat<br>ion | 0    | 0    | 140  | 0    | 2     | 0    | 0    | 0    | 2     | 0     | 0     | 0     | 144    |  |
| ARO:3000<br>850 | GOB-1                       | GOB-1 confers resistance to cephalosporins in <i>Elizabethkingia</i> ( <i>Chryseobacterium</i> ) <i>meningoseptica</i> .  | GOB beta-lactamase  | carbapenem;cep<br>halosporin;pena<br>m                      | Beta-lactam | Antibioti<br>c inactivat<br>ion | 2    | 12   | 14   | 4    | 8     | 0    | 16   | 4    | 4     | 0     | 0     | 0     | 64     |  |
| ARO:3000<br>851 | THIN-B                      | THIN-B, isolated from <i>Janthinobacterium lividum</i> , hydrolyzes a broad spectrum of beta-lactams including penicillins, cephalosporins, and carbapenems.  | THIN-B beta-lactamase   | carbapenem;cep<br>halosporin;pena<br>m                      | Beta-lactam | Antibioti<br>c inactivat<br>ion | 0    | 2    | 2    | 0    | 0     | 2    | 32   | 8    | 0     | 0     | 0     | 0     | 46     |  |

|                 |         |   |                         |                                      |             |                         |     |     |     |      |     |    |      |      |     |     |     |     |      |
|-----------------|---------|---|-------------------------|--------------------------------------|-------------|-------------------------|-----|-----|-----|------|-----|----|------|------|-----|-----|-----|-----|------|
| ARO:3000<br>853 | AIM-1   | AIM-1 is an Ambler class B beta-lactamase that hydrolyzes most beta-lactams except aztreonam and ceftazidime. It was isolated from <i>Pseudomonas aeruginosa</i> and was the first subclass B3 mobile-elements encoded beta-lactamase discovered. | AIM beta-lactamase      | cephalosporin;cephamycin;penam       | Beta-lactam | Antibiotic inactivation | 4   | 4   | 2   | 8    | 12  | 8  | 28   | 22   | 14  | 52  | 40  | 10  | 204  |
| ARO:3000<br>854 | SMB-1   | SMB-1 can hydrolyze a variety of beta-lactams, including penicillins, cephalosporins, and carbapenems. It was identified in <i>Serratia marcescens</i> .  | SMB beta-lactamase      | carbapenem;cephalosporin;penam       | Beta-lactam | Antibiotic inactivation | 2   | 20  | 10  | 12   | 18  | 4  | 24   | 26   | 14  | 0   | 0   | 0   | 130  |
| ARO:3000<br>855 | CAU-1   | CAU-1 is a B3 metallo-beta-lactamase that is encoded by the <i>Caulobacter crescentus</i> chromosome  | CAU beta-lactamase      | carbapenem;penam                     | Beta-lactam | Antibiotic inactivation | 0   | 0   | 12  | 0    | 0   | 0  | 0    | 0    | 2   | 0   | 0   | 0   | 14   |
| ARO:3000<br>856 | BJP-1   | BJP-1 is a subclass B3 ortholog found in <i>Bradyrhizobium japonicum</i> that hydrolyzes most beta-lactams except aztreonam, ticarcillin, and temocillin.   | BJP beta-lactamase      | carbapenem                           | Beta-lactam | Antibiotic inactivation | 22  | 14  | 74  | 54   | 20  | 26 | 46   | 66   | 16  | 36  | 14  | 8   | 396  |
| ARO:3000<br>865 | oleD    | OleD is a glycotransferase found in <i>Streptomyces antibioticus</i> , a natural producer of oleandomycin. OleD can glycosylate a wide range of macrolides. Unlike oleI, oleD is not found in the oleandomycin biosynthetic cluster.              | ole glycosyltransferase | macrolide antibiotic                 | MLS         | Antibiotic inactivation | 4   | 24  | 16  | 0    | 36  | 14 | 6    | 12   | 48  | 16  | 0   | 4   | 180  |
| ARO:3000<br>866 | oleI    | OleI is a glycosyltransferase found in <i>Streptomyces antibioticus</i> , specifically the oleandomycin biosynthetic cluster. OleI glycosylates oleandomycin to confer self-resistance.   | ole glycosyltransferase | macrolide antibiotic                 | MLS         | Antibiotic inactivation | 8   | 68  | 46  | 100  | 66  | 38 | 62   | 110  | 58  | 26  | 22  | 6   | 610  |
| ARO:3000<br>873 | TEM-1   | TEM-1 is a broad-spectrum beta-lactamase found in many Gram-negative bacteria. Confers resistance to penicillins and first generation cephalosporins.   | TEM beta-lactamase      | cephalosporin;monobactam;penam;penem | Beta-lactam | Antibiotic inactivation | 670 | 230 | 198 | 1452 | 844 | 56 | 1932 | 1596 | 642 | 244 | 286 | 110 | 8260 |
| ARO:3000<br>968 | TEM-105 | TEM-105 is a beta-lactamase found in <i>E. coli</i> .   | TEM beta-lactamase      | cephalosporin;monobactam;penam;penem | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0   | 0    | 0   | 0  | 0    | 0    | 0   | 2   | 8   | 0   | 10   |

|             |          |   |  |  |              |                               |      |     |      |      |     |      |      |      |     |      |      |      |       |
|-------------|----------|---|--|--|--------------|-------------------------------|------|-----|------|------|-----|------|------|------|-----|------|------|------|-------|
| ARO:3001013 | TEM-146  | TEM-146 is a beta-lactamase found in <i>E. coli</i> .   | TEM beta-lactamase   | cephalosporin; monobactam; penam; penem  | Beta-lactam  | Antibiotic inactivation       | 0    | 0   | 6    | 0    | 0   | 0    | 0    | 0    | 0   | 72   | 70   | 122  | 270   |
| ARO:3001068 | SHV-9    | SHV-9 is an extended-spectrum beta-lactamase found in <i>Klebsiella pneumoniae</i> .  | SHV beta-lactamase   | carbapenem; cephalosporin; penam   | Beta-lactam  | Antibiotic inactivation       | 0    | 0   | 18   | 8    | 0   | 0    | 22   | 24   | 2   | 0    | 2    | 0    | 76    |
| ARO:3001205 | BRP(MBL) | A novel bleomycin resistance protein encoded by a metallo-beta-lactamase-associated ble gene. Expression of BRP(MBL) confers resistance to bleomycin and bleomycin-like antibiotics in Enterobacteriaceae and Acinetobacter, where it is co-expressed with an MBL and controlled by the same promoter region. | Bleomycin resistant protein                                | glycopeptide antibiotic  | Glycopeptide | Antibiotic inactivation       | 2    | 4   | 12   | 6    | 102 | 0    | 14   | 6    | 96  | 26   | 26   | 28   | 322   |
| ARO:3001209 | mecC     | A foreign PBP2a acquired by lateral gene transfer that able to perform peptidoglycan synthesis in the presence of beta-lactams.   | methicillin resistant PBP2                                 | carbapenem; cephalosporin; cephamycin; monobactam; penam   | Beta-lactam  | Antibiotic target replacement | 1026 | 850 | 1000 | 526  | 332 | 1076 | 488  | 574  | 300 | 1566 | 1434 | 1754 | 10926 |
| ARO:3001214 | mdtM     | Multidrug resistance protein MdtM   | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye; fluoroquinolone antibiotic; lincosamide antibiotic; nucleoside antibiotic; phenicol antibiotic | Multidrug    | Antibiotic efflux             | 610  | 320 | 206  | 1260 | 728 | 84   | 1906 | 1448 | 590 | 328  | 350  | 226  | 8056  |
| ARO:3001216 | mdtH     | Multidrug resistance protein MdtH   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic   | Multidrug    | Antibiotic efflux             | 394  | 186 | 150  | 930  | 404 | 76   | 1462 | 1040 | 372 | 158  | 178  | 72   | 5422  |
| ARO:3001265 | Erm(30)  | Erm(30) confers a MLSb resistant phenotype. Along with erm(31), these genes are responsible for self-resistance in the pikromycin/narbomycin/methylmycin/neomethylmycin   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic; macrolide antibiotic; streptogramin antibiotic                                       | MLS          | Antibiotic target alteration  | 954  | 152 | 240  | 196  | 840 | 1114 | 332  | 278  | 750 | 460  | 602  | 516  | 6434  |

|                 |   |   |   |  |     |   |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|---|---|---|--|-----|---|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3001<br>299 | tlrB<br>conferri<br>ng<br>tylosin<br>resistan<br>ce | producer, <i>Streptomyces venezuelae</i> .<br>TlrB is a methyltransferase found in <i>Streptomyces fradiae</i> and confers resistance to mycinamicin, tylosin and lincosamides. Specifically, this enzyme adds a methyl group to guanosine 748 (E. coli numbering). TlrB is found in the tylosin biosynthetic cluster and is one mechanism by which <i>S. fradiae</i> protects itself from self-destruction when producing this macrolide.  | non-erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase (G748) | lincosamide<br>antibiotic;macrol<br>ide antibiotic | MLS | Antibioti<br>c target<br>alteratio<br>n | 14   | 34   | 212  | 2    | 124  | 26   | 10   | 4    | 110  | 752  | 786  | 1056 | 3130  |
|                 |   | myrA is a methyltransferase found in <i>Micromonospora griseorubida</i> and confers resistance to mycinamicin, tylosin and lincosamides. Specifically, this enzyme adds a methyl group to guanosine 748 (E. coli numbering) of 23S ribosomal RNA. MyrA is found in the mycinamicin biosynthetic cluster and is one mechanism by which <i>M. griseorubida</i> protects itself from self-destruction when producing this macrolide.   | non-erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase (G748) | lincosamide<br>antibiotic;macrol<br>ide antibiotic | MLS | Antibioti<br>c target<br>alteratio<br>n | 42   | 64   | 88   | 186  | 206  | 60   | 210  | 164  | 220  | 854  | 1760 | 1338 | 5192  |
| ARO:3001<br>301 | RlmA(II)  | RlmA(II) is a methyltransferase found in <i>Streptococcus pneumoniae</i> and confers resistance to mycinamicin, tylosin and lincosamides. Specifically, this enzyme adds a methyl group to guanosine 748 (E. coli numbering) of 23S ribosomal RNA.<br>ChrB is a methyltransferase found in <i>Streptomyces bikiniensis</i> and confers resistance to chalcomycin, mycinamicin, tylosin and lincosamides. Specifically, this enzyme adds a methyl group to guanosine 748 (E. coli numbering). chrB is found in the | non-erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase (G748) | lincosamide<br>antibiotic;macrol<br>ide antibiotic | MLS | Antibioti<br>c target<br>alteratio<br>n | 2402 | 4038 | 3874 | 2156 | 1614 | 3788 | 1862 | 2724 | 2086 | 2306 | 1790 | 1822 | 30462 |
| ARO:3001<br>302 | chrB  |   | non-erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase (G748) | lincosamide<br>antibiotic;macrol<br>ide antibiotic | MLS | Antibioti<br>c target<br>alteratio<br>n | 766  | 1740 | 538  | 610  | 2602 | 1016 | 610  | 962  | 2510 | 1158 | 890  | 1262 | 14664 |



|                 |               |   |  |                                  |           |                              |     |     |     |     |     |     |      |      |     |     |     |     |      |
|-----------------|---------------|---|--|----------------------------------|-----------|------------------------------|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|------|
| ARO:3001<br>303 | ErmO-<br>srmA | chalcone biosynthetic cluster and is responsible for self-resistance in <i>S. bikiniensis</i> .<br>ErmO (gene <i>srmA</i> ) is a methyltransferase found in the spiramycin producer <i>Streptomyces ambofaciens</i> . Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. Specifically, this enzyme transfers only one methyl group. The gene is responsible for self-resistance to spiramycin. | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide | MLS       | Antibiotic target alteration | 44  | 16  | 8   | 2   | 2   | 28  | 4    | 0    | 2   | 2   | 6   | 0   | 114  |
| ARO:3001<br>304 | ErmS          | ErmS is a methyltransferase found in the tylosin producer <i>Streptomyces fradiae</i> . Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. Specifically, this enzyme transfers two methyl groups. The gene is found within the tylosin biosynthetic cluster and is responsible for self-resistance   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide | MLS       | Antibiotic target alteration | 0   | 0   | 44  | 0   | 36  | 0   | 6    | 0    | 32  | 60  | 86  | 148 | 412  |
| ARO:3001<br>306 | ErmW          | ErmW is a methyltransferase found in the mycinamicin producer <i>Micromonospora griseorubida</i> . Like other Erm enzymes, it catalyzes the methylation of A2058 of the 23S ribosomal RNA. The gene is found within the mycinamicin biosynthetic cluster and is responsible for self-resistance.  | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide | MLS       | Antibiotic target alteration | 2   | 22  | 168 | 30  | 172 | 10  | 8    | 40   | 226 | 338 | 292 | 398 | 1706 |
| ARO:3001<br>313 | facT          | Efflux protein <i>facT</i> confers resistance to factumycin. The gene has been heterologously expressed in <i>S. coelicolor</i> and its function was confirmed (Thaker et al. Med. Chem. Commun. 2012, 3: 1020). It is possible that this gene can efflux other kirromycin-like elfamycins, but this has not been tested.   | major facilitator superfamily (MFS) antibiotic efflux pump | elfamycin antibiotic             | Elfamycin | Antibiotic efflux            | 190 | 40  | 170 | 78  | 206 | 236 | 150  | 134  | 260 | 398 | 592 | 608 | 3062 |
| ARO:3001<br>327 | MdtK          | A multidrug and toxic compound extrusions (MATE)  | multidrug and toxic  | fluoroquinolone antibiotic       | Multidrug | Antibiotic efflux            | 984 | 786 | 642 | 932 | 744 | 528 | 1482 | 1134 | 780 | 208 | 202 | 98  | 8520 |

|             |                       |   |  |   |             |                         |      |      |     |      |     |      |      |      |     |     |     |     |      |
|-------------|-----------------------|---|--|---|-------------|-------------------------|------|------|-----|------|-----|------|------|------|-----|-----|-----|-----|------|
|             |                       | transporter conferring resistance to norfloxacin, doxorubicin and acriflavine.  | compound extrusion (MATE) transporter major facilitator superfamily (MFS) antibiotic efflux pump | benzalkonium chloride;rhodamine;tetracycline antibiotic | Multidrug   | Antibiotic efflux       | 928  | 1158 | 234 | 1076 | 586 | 576  | 1402 | 1088 | 450 | 326 | 312 | 320 | 8456 |
| ARO:3001328 | Escherichia coli mdxA | This multidrug efflux system was originally identified as the Cmr/CmlA chloramphenicol exporter.  |  |   |             |                         |      |      |     |      |     |      |      |      |     |     |     |     |      |
| ARO:3001329 | mdtG                  | The MdtG protein, also named YceE, appears to be a member of the major facilitator superfamily of transporters, and it has been reported, when overexpressed, to increase fosfomycin and deoxycholate resistances. mdtG is a member of the marA-soxS-rob regulon. | major facilitator superfamily (MFS) antibiotic efflux pump                                       | fosfomycin  | Fosfomycin  | Antibiotic efflux       | 1378 | 722  | 202 | 928  | 426 | 1420 | 1338 | 1028 | 388 | 126 | 122 | 30  | 8108 |
| ARO:3001392 | TEM-215               | From the Lahey list of beta-lactamases. Not yet released.   | TEM beta-lactamase   | cephalosporin;monobactam;penam;penem                    | Beta-lactam | Antibiotic inactivation | 24   | 132  | 0   | 28   | 8   | 86   | 10   | 14   | 14  | 46  | 22  | 46  | 430  |
| ARO:3001396 | OXA-1                 | OXA-1 is a beta-lactamase found in E. coli  | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 0    | 0    | 32  | 46   | 104 | 0    | 78   | 90   | 142 | 512 | 440 | 582 | 2026 |
| ARO:3001398 | OXA-3                 | OXA-3 is a beta-lactamase found in P. aeruginosa  | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 0    | 0    | 14  | 0    | 236 | 0    | 8    | 84   | 220 | 104 | 68  | 128 | 862  |
| ARO:3001405 | OXA-10                | OXA-10 is a beta-lactamase found in Acinetobacter baumannii and P. aeruginosa.  | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 6    | 6    | 24  | 56   | 12  | 0    | 42   | 132  | 4   | 124 | 120 | 238 | 764  |
| ARO:3001408 | OXA-13                | OXA-13 is a beta-lactamase found in P. aeruginosa.  | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 0    | 12   | 6   | 0    | 0   | 0    | 12   | 6    | 2   | 0   | 2   | 2   | 42   |
| ARO:3001413 | OXA-18                | OXA-18 is a beta-lactamase found in P. aeruginosa and Rickettsia.   | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 0    | 0    | 0   | 0    | 0   | 0    | 0    | 0    | 4   | 0   | 0   | 0   | 4    |
| ARO:3001416 | OXA-21                | OXA-21 is a beta-lactamase found in A. baumannii  | OXA beta-lactamase   | cephalosporin;penam                                     | Beta-lactam | Antibiotic inactivation | 0    | 4    | 186 | 30   | 162 | 12   | 66   | 26   | 276 | 402 | 360 | 526 | 2050 |

|                 |         |  |                    |                     |             |                         |     |     |     |     |      |     |     |     |     |     |     |     |      |
|-----------------|---------|--|--------------------|---------------------|-------------|-------------------------|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|------|
| ARO:3001<br>424 | OXA-29  | OXA-29 is a beta-lactamase found in <i>Legionella gormanii</i>           | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2   | 0   | 14   | 0   | 0   | 0   | 0   | 10  | 14  | 16  | 56   |
| ARO:3001<br>483 | OXA-205 | OXA-205 is a beta-lactamase. From the Lahey list of OXA beta-lactamases. | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 116 | 70  | 1086 | 2   | 58  | 444 | 986 | 274 | 234 | 288 | 3558 |
| ARO:3001<br>549 | OXA-362 | OXA-362 is a beta-lactamase. From the Lahey list of OXA beta-lactamases. | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 298 | 120 | 2   | 4   | 4    | 18  | 0   | 0   | 6   | 10  | 10  | 10  | 482  |
| ARO:3001<br>558 | OXA-372 | OXA-372 is a beta-lactamase. From the Lahey list of OXA beta-lactamases. | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0    | 0   | 4   | 4   | 0   | 40  | 24  | 54  | 126  |
| ARO:3001<br>611 | OXA-58  | OXA-58 is a beta-lactamase found in <i>A. baumannii</i>                  | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 48  | 140 | 6   | 122 | 18   | 94  | 126 | 154 | 14  | 36  | 20  | 30  | 808  |
| ARO:3001<br>676 | OXA-235 | OXA-235 is a beta-lactamase found in <i>A. baumannii</i>                 | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2   | 4   | 0    | 0   | 0   | 0   | 0   | 0   | 2   | 4   | 12   |
| ARO:3001<br>730 | OXA-274 | OXA-274 is a beta-lactamase found in <i>Acinetobacter</i> spp.           | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2   | 0   | 14   | 0   | 0   | 0   | 24  | 0   | 0   | 0   | 40   |
| ARO:3001<br>731 | OXA-275 | OXA-275 is a beta-lactamase found in <i>Acinetobacter</i> spp.           | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0   | 0   | 12   | 0   | 0   | 0   | 6   | 0   | 0   | 0   | 18   |
| ARO:3001<br>733 | OXA-277 | OXA-277 is a beta-lactamase found in <i>Acinetobacter</i> spp.           | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 26  | 176 | 2   | 12  | 24   | 114 | 10  | 10  | 24  | 26  | 4   | 34  | 462  |
| ARO:3001<br>773 | OXA-61  | OXA-61 is a beta-lactamase found in <i>Campylobacter jejuni</i>          | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 26  | 2   | 0   | 2   | 0    | 38  | 120 | 26  | 0   | 4   | 4   | 4   | 226  |
| ARO:3001<br>775 | OXA-119 | OXA-119 is a beta-lactamase found in Enterobacteriaceae                  | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2   | 8   | 4    | 0   | 78  | 36  | 0   | 96  | 60  | 126 | 410  |
| ARO:3001<br>777 | OXA-347 | OXA-347 is a beta-lactamase found in Enterobacteriaceae                  | OXA beta-lactamase | cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 6   | 40  | 52  | 12  | 4    | 50  | 48  | 16  | 22  | 706 | 414 | 582 | 1952 |

|             |         |  |                    |                                |             |                         |    |    |    |    |     |    |    |    |     |      |     |      |      |
|-------------|---------|--|--------------------|--------------------------------|-------------|-------------------------|----|----|----|----|-----|----|----|----|-----|------|-----|------|------|
| ARO:3001793 | OXA-320 | OXA-320 is a beta-lactamase found in <i>Proteus mirabilis</i>  | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 0  | 4  | 4  | 2  | 0   | 8  | 8  | 4  | 2   | 0    | 0   | 4    | 36   |
| ARO:3001797 | OXA-46  | OXA-46 is a beta-lactamase found in <i>Pseudomonas aeruginosa</i>  | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 0  | 0  | 0  | 0  | 0   | 0  | 0  | 0  | 0   | 24   | 100 | 58   | 182  |
| ARO:3001808 | OXA-60  | OXA-60 is a beta-lactamase found in <i>Ralstonia pickettii</i>   | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 0  | 0  | 0  | 2  | 0   | 0  | 2  | 6  | 2   | 10   | 10  | 2    | 34   |
| ARO:3001809 | OXA-209 | OXA-209 is a beta-lactamase found in <i>Riemerella anatipestifer</i>   | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 4  | 2  | 4  | 2  | 2   | 8  | 6  | 4  | 2   | 84   | 66  | 84   | 268  |
| ARO:3001810 | OXA-53  | OXA-53 is a beta-lactamase found in <i>Salmonella enterica</i>   | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 0  | 2  | 6  | 0  | 580 | 0  | 0  | 0  | 494 | 1268 | 740 | 1862 | 4952 |
| ARO:3001811 | OXA-129 | OXA-129 is a beta-lactamase found in <i>Salmonella enterica</i>  | OXA beta-lactamase | cephalosporin;penam            | Beta-lactam | Antibiotic inactivation | 0  | 0  | 0  | 0  | 0   | 0  | 0  | 0  | 0   | 0    | 4   | 0    | 4    |
| ARO:3001815 | ACC-1   | ACC-1 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>  | ACC beta-lactamase | cephalosporin;monobactam;penam | Beta-lactam | Antibiotic inactivation | 2  | 2  | 46 | 28 | 16  | 0  | 8  | 30 | 14  | 6    | 0   | 0    | 152  |
| ARO:3001816 | ACC-2   | ACC-2 is a beta-lactamase found in <i>Hafnia alvei</i>   | ACC beta-lactamase | cephalosporin;monobactam;penam | Beta-lactam | Antibiotic inactivation | 2  | 6  | 2  | 30 | 16  | 2  | 0  | 26 | 12  | 0    | 0   | 0    | 96   |
| ARO:3001817 | ACC-3   | ACC-3 is a beta-lactamase found in <i>Hafnia alvei</i>   | ACC beta-lactamase | cephalosporin;monobactam;penam | Beta-lactam | Antibiotic inactivation | 14 | 2  | 86 | 50 | 14  | 12 | 68 | 60 | 18  | 66   | 22  | 46   | 458  |
| ARO:3001818 | ACC-4   | ACC-4 is a beta-lactamase found in <i>Escherichia coli</i>   | ACC beta-lactamase | cephalosporin;monobactam;penam | Beta-lactam | Antibiotic inactivation | 0  | 10 | 2  | 8  | 0   | 2  | 8  | 12 | 0   | 60   | 46  | 32   | 180  |
| ARO:3001819 | ACC-5   | ACC-5 is a beta-lactamase. From the Lahey list of ACC beta-lactamases. It is detected among Gram-negative bacteria isolates (Gamma- and Alpha- | ACC beta-lactamase | cephalosporin;monobactam;penam | Beta-lactam | Antibiotic inactivation | 0  | 0  | 0  | 0  | 0   | 0  | 0  | 0  | 0   | 0    | 0   | 12   | 12   |

| proteobacteria) from urban water sources. |           |   |                      |   |             |                         |     |    |    |    |    |     |    |    |    |     |     |     |     |
|---|-----------|---|----------------------|---|-------------|-------------------------|-----|----|----|----|----|-----|----|----|----|-----|-----|-----|-----|
| ARO:3001825                               | ACT-6     | ACT-6 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>         | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0  | 2  | 0  | 0  | 0   | 0  | 0  | 0  | 126 | 162 | 138 | 428 |
| ARO:3001826                               | ACT-9     | ACT-9 is a beta-lactamase found in <i>Pantoea agglomerans</i>           | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 0   | 8  | 2  | 58 | 4  | 0   | 24 | 68 | 2  | 0   | 0   | 0   | 166 |
| ARO:3001834                               | ACT-12    | ACT-12 is a beta-lactamase. From the Lahey list of ACT beta-lactamases. | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0  | 0  | 24 | 0  | 8   | 4  | 4  | 2  | 2   | 2   | 0   | 46  |
| ARO:3001840                               | ACT-19    | ACT-19 is a beta-lactamase. From the Lahey list of ACT beta-lactamases. | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 2   | 14 | 28 | 4  | 4  | 2   | 6  | 18 | 2  | 2   | 0   | 0   | 82  |
| ARO:3001843                               | ACT-22    | ACT-22 is a beta-lactamase. From the Lahey list of ACT beta-lactamases. | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 14  | 2  | 0  | 4  | 0  | 8   | 12 | 10 | 2  | 0   | 0   | 2   | 54  |
| ARO:3001847                               | ACT-27    | ACT-27 is a beta-lactamase. From the Lahey list of ACT beta-lactamases. | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 156 | 8  | 0  | 0  | 0  | 118 | 0  | 0  | 8  | 0   | 0   | 0   | 290 |
| ARO:3001848                               | ACT-28    | ACT-28 is a beta-lactamase. From the Lahey list of ACT beta-lactamases. | ACT beta-lactamase   | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 8   | 2  | 0  | 0  | 0  | 18  | 0  | 0  | 0  | 8   | 4   | 22  | 62  |
| ARO:3001886                               | CTX-M-24  | CTX-M-24 is a beta-lactamase found in the Enterobacteriaceae family     | CTX-M beta-lactamase | cephalosporin                             | Beta-lactam | Antibiotic inactivation | 20  | 0  | 0  | 62 | 40 | 0   | 72 | 54 | 24 | 2   | 2   | 2   | 278 |
| ARO:3001917                               | CTX-M-55  | CTX-M-55 is a beta-lactamase found in the Enterobacteriaceae family     | CTX-M beta-lactamase | cephalosporin                             | Beta-lactam | Antibiotic inactivation | 0   | 0  | 4  | 52 | 14 | 0   | 38 | 18 | 2  | 10  | 0   | 0   | 138 |
| ARO:3001965                               | CTX-M-105 | CTX-M-105 is a beta-lactamase found in <i>Escherichia coli</i>          | CTX-M beta-lactamase | cephalosporin                             | Beta-lactam | Antibiotic inactivation | 0   | 0  | 0  | 0  | 0  | 0   | 0  | 0  | 0  | 2   | 16  | 4   | 22  |
| ARO:3001980                               | CTX-M-121 | CTX-M-121 is a beta-lactamase found in <i>Escherichia coli</i>          | CTX-M beta-lactamase | cephalosporin                             | Beta-lactam | Antibiotic inactivation | 0   | 0  | 6  | 2  | 0  | 4   | 10 | 4  | 0  | 0   | 0   | 0   | 26  |

|                 |         |  |                    |                          |             |                         |     |     |     |     |      |    |     |     |      |     |     |     |      |
|-----------------|---------|--|--------------------|--------------------------|-------------|-------------------------|-----|-----|-----|-----|------|----|-----|-----|------|-----|-----|-----|------|
| ARO:3002<br>012 | CMY-1   | CMY-1 is a beta-lactamase found in the Enterobacteriaceae family         | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 0   | 0   | 12  | 14  | 18   | 0  | 26  | 12  | 6    | 82  | 84  | 60  | 314  |
| ARO:3002<br>037 | CMY-26  | CMY-26 is a beta-lactamase found in the Enterobacteriaceae family        | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 0   | 0   | 44  | 0   | 88   | 0  | 0   | 0   | 166  | 70  | 26  | 56  | 450  |
| ARO:3002<br>062 | CMY-51  | CMY-51 is a beta-lactamase. From the Lahey list of CMY beta-lactamases.  | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 2   | 16  | 282 | 292 | 1688 | 20 | 294 | 564 | 1560 | 572 | 588 | 730 | 6608 |
| ARO:3002<br>086 | CMY-73  | CMY-73 is a beta-lactamase. From the Lahey list of CMY beta-lactamases.  | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 104 | 230 | 172 | 88  | 52   | 86 | 52  | 70  | 80   | 14  | 6   | 8   | 962  |
| ARO:3002<br>106 | CMY-93  | CMY-93 is a beta-lactamase. From the Lahey list of CMY beta-lactamases.  | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0    | 0  | 0   | 0   | 0    | 20  | 0   | 14  | 34   |
| ARO:3002<br>112 | CMY-100 | CMY-100 is a beta-lactamase. From the Lahey list of CMY beta-lactamases. | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 20  | 0   | 0   | 0   | 0    | 0  | 0   | 0   | 4    | 0   | 0   | 0   | 24   |
| ARO:3002<br>125 | CMY-114 | CMY-114 is a beta-lactamase. From the Lahey list of CMY beta-lactamases. | CMY beta-lactamase | cephamycin               | Beta-lactam | Antibiotic inactivation | 2   | 0   | 2   | 0   | 0    | 0  | 0   | 0   | 2    | 14  | 30  | 16  | 66   |
| ARO:3002<br>133 | DHA-2   | DHA-2 is a beta-lactamase found in Klebsiella pneumoniae                 | DHA beta-lactamase | cephalosporin;cephamycin | Beta-lactam | Antibiotic inactivation | 0   | 2   | 6   | 0   | 0    | 0  | 0   | 0   | 0    | 114 | 172 | 210 | 504  |
| ARO:3002<br>138 | DHA-5   | DHA-5 is a beta-lactamase. From the Lahey list of DHA beta-lactamases.   | DHA beta-lactamase | cephalosporin;cephamycin | Beta-lactam | Antibiotic inactivation | 66  | 2   | 0   | 0   | 2    | 16 | 12  | 0   | 0    | 0   | 0   | 0   | 98   |
| ARO:3002<br>140 | DHA-9   | DHA-9 is a beta-lactamase. From the Lahey list of DHA beta-lactamases.   | DHA beta-lactamase | cephalosporin;cephamycin | Beta-lactam | Antibiotic inactivation | 30  | 0   | 0   | 0   | 0    | 22 | 0   | 0   | 0    | 0   | 0   | 0   | 52   |
| ARO:3002<br>143 | DHA-12  | DHA-12 is a beta-lactamase. From the Lahey list of DHA beta-lactamases.  | DHA beta-lactamase | cephalosporin;cephamycin | Beta-lactam | Antibiotic inactivation | 8   | 20  | 16  | 0   | 2    | 24 | 0   | 0   | 10   | 6   | 2   | 6   | 94   |
| ARO:3002<br>147 | DHA-16  | DHA-16 is a beta-lactamase. From the Lahey list of DHA beta-lactamases.  | DHA beta-lactamase | cephalosporin;cephamycin | Beta-lactam | Antibiotic inactivation | 0   | 10  | 0   | 0   | 0    | 0  | 8   | 0   | 0    | 0   | 0   | 2   | 20   |

|                 |        |   |                    |                                |             |                         |     |     |    |    |    |     |     |    |    |     |     |     |     |
|-----------------|--------|---|--------------------|--------------------------------|-------------|-------------------------|-----|-----|----|----|----|-----|-----|----|----|-----|-----|-----|-----|
| ARO:3002<br>153 | DHA-22 | DHA-22 is a beta-lactamase. From the Lahey list of DHA beta-lactamases. | DHA beta-lactamase | cephalosporin;cephamycin       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 0  | 0  | 0   | 0   | 0  | 0  | 0   | 0   | 8   | 8   |
| ARO:3002<br>155 | FOX-1  | FOX-1 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>         | FOX beta-lactamase | cephalosporin;cephamycin       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 0  | 0  | 0   | 4   | 0  | 0  | 16  | 8   | 0   | 28  |
| ARO:3002<br>157 | FOX-3  | FOX-3 is a beta-lactamase found in <i>Klebsiella oxytoca</i>            | FOX beta-lactamase | cephalosporin;cephamycin       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 10 | 0  | 0   | 4   | 4  | 0  | 0   | 0   | 0   | 18  |
| ARO:3002<br>162 | FOX-10 | FOX-10 is a beta-lactamase. From the Lahey list of FOX beta-lactamases. | FOX beta-lactamase | cephalosporin;cephamycin       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 4  | 0  | 0   | 0   | 4  | 0  | 0   | 0   | 0   | 8   |
| ARO:3002<br>163 | FOX-9  | FOX-9 is a beta-lactamase. From the Lahey list of FOX beta-lactamases.  | FOX beta-lactamase | cephalosporin;cephamycin       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2  | 0  | 2  | 0   | 0   | 0  | 22 | 4   | 14  | 4   | 48  |
| ARO:3002<br>167 | MIR-4  | MIR-4 is a beta-lactamase found in <i>Escherichia coli</i>              | MIR beta-lactamase | cephalosporin;monobactam       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 20 | 0  | 0   | 112 | 14 | 0  | 0   | 10  | 0   | 156 |
| ARO:3002<br>169 | MIR-3  | MIR-3 is a beta-lactamase. From the Lahey list of MIR beta-lactamases.  | MIR beta-lactamase | cephalosporin;monobactam       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 8  | 6  | 10 | 0   | 16  | 22 | 8  | 96  | 82  | 56  | 304 |
| ARO:3002<br>177 | MIR-12 | MIR-12 is a beta-lactamase. From the Lahey list of MIR beta-lactamases. | MIR beta-lactamase | cephalosporin;monobactam       | Beta-lactam | Antibiotic inactivation | 0   | 0   | 20 | 0  | 0  | 0   | 0   | 0  | 0  | 96  | 122 | 100 | 338 |
| ARO:3002<br>182 | MOX-1  | MOX-1 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>         | MOX beta-lactamase | cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 6   | 0   | 4  | 8  | 4  | 30  | 4   | 8  | 4  | 2   | 0   | 6   | 76  |
| ARO:3002<br>183 | MOX-2  | MOX-2 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>         | MOX beta-lactamase | cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 164 | 148 | 84 | 32 | 12 | 252 | 38  | 46 | 14 | 8   | 0   | 4   | 802 |
| ARO:3002<br>184 | MOX-4  | MOX-4 is a beta-lactamase found in <i>Aeromonas caviae</i>              | MOX beta-lactamase | cephalosporin;cephamycin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 0  | 0  | 0   | 0   | 0  | 0  | 222 | 86  | 192 | 500 |

|                 |         |  |                     |   |             |                         |    |     |     |    |     |    |     |     |     |      |      |      |      |
|-----------------|---------|--|---------------------|---|-------------|-------------------------|----|-----|-----|----|-----|----|-----|-----|-----|------|------|------|------|
| ARO:3002<br>185 | MOX-6   | MOX-6 is a beta-lactamase found in <i>Klebsiella pneumoniae</i>          | MOX beta-lactamase  | cephalosporin;cephamycin;penam                  | Beta-lactam | Antibiotic inactivation | 14 | 8   | 26  | 0  | 2   | 8  | 8   | 0   | 14  | 0    | 2    | 2    | 84   |
| ARO:3002<br>186 | MOX-3   | MOX-3 is a beta-lactamase. From the Lahey list of MOX beta-lactamases.   | MOX beta-lactamase  | cephalosporin;cephamycin;penam                  | Beta-lactam | Antibiotic inactivation | 0  | 0   | 10  | 6  | 10  | 0  | 16  | 4   | 10  | 18   | 18   | 58   | 150  |
| ARO:3002<br>191 | MOX-9   | MOX-9 is a beta-lactamase found in <i>Citrobacter freundii</i> .         | MOX beta-lactamase  | cephalosporin;cephamycin;penam                  | Beta-lactam | Antibiotic inactivation | 0  | 0   | 0   | 28 | 0   | 0  | 14  | 112 | 0   | 0    | 0    | 0    | 154  |
| ARO:3002<br>226 | IMP-35  | IMP-35 is a beta-lactamase found in <i>Pseudomonas aeruginosa</i>        | IMP beta-lactamase  | carbapenem;cephalosporin;cephamycin;penam;penam | Beta-lactam | Antibiotic inactivation | 0  | 0   | 8   | 2  | 2   | 0  | 62  | 12  | 0   | 40   | 38   | 102  | 266  |
| ARO:3002<br>242 | CARB-3  | CARB-3 is a beta-lactamase found in <i>Pseudomonas aeruginosa</i>        | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 30 | 558 | 112 | 84 | 302 | 48 | 120 | 126 | 254 | 2254 | 1728 | 3376 | 8992 |
| ARO:3002<br>243 | CARB-4  | CARB-4 is a beta-lactamase found in <i>Pseudomonas aeruginosa</i>        | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 0  | 0   | 40  | 2  | 108 | 0  | 2   | 6   | 70  | 190  | 152  | 374  | 944  |
| ARO:3002<br>244 | CARB-5  | CARB-5 is a beta-lactamase found in <i>Acinetobacter calcoaceticus</i>   | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 0  | 0   | 0   | 2  | 0   | 0  | 8   | 2   | 0   | 22   | 28   | 28   | 90   |
| ARO:3002<br>248 | CARB-9  | CARB-9 is a beta-lactamase found in <i>Vibrio cholerae</i>               | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 0  | 0   | 94  | 54 | 756 | 0  | 40  | 434 | 860 | 268  | 168  | 212  | 2886 |
| ARO:3002<br>249 | CARB-10 | CARB-10 is a beta-lactamase found in <i>Acinetobacter baumannii</i>      | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 0  | 0   | 0   | 0  | 0   | 0  | 0   | 0   | 0   | 6    | 2    | 6    | 14   |
| ARO:3002<br>255 | CARB-16 | CARB-16 is a beta-lactamase. From the Lahey list of IMP beta-lactamases. | CARB beta-lactamase | penam   | Beta-lactam | Antibiotic inactivation | 8  | 2   | 12  | 24 | 44  | 2  | 14  | 42  | 170 | 66   | 60   | 46   | 490  |
| ARO:3002<br>327 | KPC-17  | KPC-17 is a beta-lactamase. From the Lahey list of KPC beta-lactamases.  | KPC beta-lactamase  | carbapenem;cephalosporin;monobactam;penam       | Beta-lactam | Antibiotic inactivation | 0  | 0   | 12  | 30 | 0   | 0  | 34  | 38  | 0   | 0    | 2    | 0    | 116  |
| ARO:3002<br>363 | PER-1   | PER-1 is a beta-lactamase found in <i>Pseudomonas aeruginosa</i>         | PER beta-lactamase  | carbapenem;cephalosporin;monobactam             | Beta-lactam | Antibiotic inactivation | 8  | 20  | 6   | 20 | 16  | 8  | 8   | 8   | 6   | 0    | 0    | 0    | 100  |



|                 |        |  |   |   |             |                            |     |    |    |    |    |    |    |    |   |     |     |     |     |
|-----------------|--------|--|---|---|-------------|----------------------------|-----|----|----|----|----|----|----|----|---|-----|-----|-----|-----|
| ARO:3002<br>364 | PER-2  | PER-2 is a beta-lactamase found in Salmonella typhimurium  | PER beta-lactamase  | bactam;penam;p<br>enem<br>carbapenem;cep<br>halosporin;mono<br>bactam;penam;p<br>enem | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 8  | 0  | 0  | 2  | 0  | 0  | 0 | 0   | 0   | 0   | 10  |
| ARO:3002<br>366 | PER-4  | PER-4 is a beta-lactamase. From the Lahey list of PER beta-lactamases.                               | PER beta-lactamase  | carbapenem;cep<br>halosporin;mono<br>bactam;penam;p<br>enem                           | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 2  | 12 | 0  | 0  | 4  | 8 | 0   | 2   | 0   | 28  |
| ARO:3002<br>372 | VEB-3  | VEB-3 is a beta-lactamase found in Enterobacter cloacae  | VEB beta-lactamase  | cephalosporin;m<br>onobactam  | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 8  | 6  | 0  | 2  | 0  | 0 | 0   | 0   | 0   | 16  |
| ARO:3002<br>373 | VEB-4  | VEB-4 is a beta-lactamase found in Proteus mirabilis   | VEB beta-lactamase  | cephalosporin;m<br>onobactam  | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 0  | 8  | 0  | 2  | 0  | 6 | 0   | 0   | 0   | 16  |
| ARO:3002<br>376 | VEB-7  | VEB-7 is a beta-lactamase. From the Lahey list of VEB beta-lactamases.                               | VEB beta-lactamase  | cephalosporin;m<br>onobactam  | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 2  | 0  | 0  | 2  | 4  | 0 | 166 | 114 | 190 | 478 |
| ARO:3002<br>387 | BEL-3  | BEL-3 is a beta-lactamase found in Pseudomonas aeruginosa  | BEL beta-lactamase  | cephalosporin;m<br>onobactam;pena<br>m  | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 0  | 0  | 0  | 6  | 0  | 0 | 0   | 0   | 0   | 6   |
| ARO:3002<br>481 | AER-1  | AER-1 is a beta-lactamase found in Aeromonas hydrophila  | AER beta-lactamase  | penam   | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 2  | 0  | 0  | 24 | 4  | 0 | 2   | 0   | 0   | 32  |
| ARO:3002<br>482 | LRA-1  | LRA-1 is a beta-lactamase isolated from soil samples in Alaska                                       | class A LRA<br>beta-lactamase                                   | cephalosporin;pe<br>nam   | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 0  | 10 | 0  | 0  | 52 | 10 | 4 | 50  | 48  | 40  | 214 |
| ARO:3002<br>483 | LRA-5  | LRA-5 is a beta-lactamase isolated from soil samples in Alaska                                       | class A LRA<br>beta-lactamase                                   | cephalosporin;pe<br>nam   | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 42 | 12 | 18 | 0  | 24 | 12 | 6 | 186 | 272 | 294 | 866 |
| ARO:3002<br>484 | LRA-13 | LRA-13 is a class D/class C fusion bifunctional beta-lactamase isolated from soil samples in Alaska. | class C LRA<br>beta-lactamase;<br>class D LRA<br>beta-lactamase | cephalosporin;pe<br>nam   | Beta-lactam | Antibiotic<br>inactivation | 0   | 0  | 22 | 0  | 0  | 0  | 0  | 0  | 0 | 42  | 86  | 92  | 242 |
| ARO:3002<br>485 | LRA-2  | LRA-2 is a beta-lactamase isolated from soil samples in Alaska                                       | subclass B3<br>LRA beta-lactamase                               | cephalosporin;pe<br>nam   | Beta-lactam | Antibiotic                 | 110 | 36 | 42 | 66 | 8  | 38 | 36 | 40 | 8 | 46  | 74  | 158 | 662 |

|                 |        |   |                                |                                     |             |                         |     |    |     |     |     |     |     |     |     |     |     |     |      |
|-----------------|--------|---|--------------------------------|-------------------------------------|-------------|-------------------------|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ARO:3002<br>487 | LRA-8  | LRA-8 is a beta-lactamase isolated from soil samples in Alaska  | subclass B3 LRA beta-lactamase | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 110 | 90 | 72  | 148 | 34  | 98  | 92  | 170 | 58  | 100 | 62  | 44  | 1078 |
| ARO:3002<br>488 | LRA-9  | LRA-9 is a beta-lactamase isolated from soil samples in Alaska  | subclass B3 LRA beta-lactamase | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 184 | 18 | 0   | 2   | 0   | 146 | 0   | 4   | 2   | 0   | 0   | 0   | 356  |
| ARO:3002<br>489 | LRA-10 | LRA-10 is a beta-lactamase isolated from soil samples in Alaska   | class C LRA beta-lactamase     | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 0   | 0  | 0   | 0   | 0   | 0   | 28  | 2   | 0   | 0   | 0   | 0   | 30   |
| ARO:3002<br>492 | LRA-18 | LRA-18 is a beta-lactamase isolated from soil samples in Alaska   | class C LRA beta-lactamase     | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 0   | 0  | 20  | 6   | 24  | 0   | 18  | 2   | 10  | 160 | 224 | 170 | 634  |
| ARO:3002<br>493 | SRT-1  | SRT-1, isolated from <i>Serratia marcescens</i> , confers resistance to cephalosporins but not carbapenems, penems and monobactams. | SRT beta-lactamase             | cephalosporin                       | Beta-lactam | Antibiotic inactivation | 2   | 6  | 22  | 8   | 10  | 20  | 2   | 8   | 48  | 160 | 180 | 192 | 658  |
| ARO:3002<br>494 | SRT-2  | SRT-2, isolated from <i>Serratia marcescens</i> , is a chromosomal beta-lactamase that confers resistance to cefotaxime             | SRT beta-lactamase             | cephalosporin                       | Beta-lactam | Antibiotic inactivation | 176 | 22 | 214 | 22  | 144 | 166 | 120 | 26  | 196 | 528 | 638 | 638 | 2890 |
| ARO:3002<br>498 | PDC-2  | PDC-2 is a extended-spectrum beta-lactamase found in <i>Pseudomonas aeruginosa</i> .  | PDC beta-lactamase             | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation | 60  | 6  | 0   | 0   | 0   | 106 | 0   | 0   | 0   | 0   | 0   | 0   | 172  |
| ARO:3002<br>507 | PDC-8  | PDC-8 is a extended-spectrum beta-lactamase found in <i>Pseudomonas aeruginosa</i> .  | PDC beta-lactamase             | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation | 0   | 38 | 6   | 0   | 0   | 10  | 0   | 2   | 0   | 4   | 0   | 0   | 60   |
| ARO:3002<br>509 | PDC-10 | PDC-10 is a extended-spectrum beta-lactamase found in <i>Pseudomonas aeruginosa</i> .   | PDC beta-lactamase             | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation | 0   | 0  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 6   | 88  | 32  | 126  |
| ARO:3002<br>510 | LRA-3  | LRA-3 is a beta-lactamase isolated from soil samples in Alaska  | subclass B3 LRA beta-lactamase | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 0   | 0  | 0   | 2   | 0   | 6   | 2   | 0   | 0   | 0   | 0   | 0   | 10   |
| ARO:3002<br>511 | LRA-12 | LRA-12 is a beta-lactamase isolated from soil samples in Alaska   | subclass B3 LRA beta-lactamase | cephalosporin;penam                 | Beta-lactam | Antibiotic inactivation | 0   | 14 | 0   | 0   | 6   | 4   | 4   | 4   | 18  | 4   | 8   | 2   | 64   |

|                 |            |   |   |   |                |                         |      |      |      |      |      |      |      |      |      |      |       |       |       |
|-----------------|------------|---|---|---|----------------|-------------------------|------|------|------|------|------|------|------|------|------|------|-------|-------|-------|
| ARO:3002<br>512 | LRA-17     | LRA-17 is a beta-lactamase isolated from soil samples in Alaska   | subclass B3<br>LRA beta-lactamase                 | cephalosporin;penam                             | Beta-lactam    | Antibiotic inactivation | 42   | 28   | 24   | 2    | 2    | 18   | 8    | 6    | 4    | 6    | 6     | 2     | 148   |
| ARO:3002<br>513 | LRA-19     | LRA-19 is a beta-lactamase isolated from soil samples in Alaska   | subclass B3<br>LRA beta-lactamase                 | cephalosporin;penam                             | Beta-lactam    | Antibiotic inactivation | 48   | 16   | 92   | 80   | 6    | 46   | 48   | 82   | 6    | 6    | 2     | 0     | 432   |
| ARO:3002<br>514 | OCH-1      | OCH-1 beta-lactamase is an Ambler class C chromosomal-encoded beta-lactamases in <i>Ochrobactrum anthropi</i>   | OCH beta-lactamase                                | cephalosporin;cephamycin;monobactam;penam;penem | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 2    | 4    | 2     | 4     | 12    |
| ARO:3002<br>516 | OCH-3      | OCH-3 beta-lactamase is an Ambler class C chromosomal-encoded beta-lactamases in <i>Ochrobactrum anthropi</i>   | OCH beta-lactamase                                | cephalosporin;cephamycin;monobactam;penam;penem | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 2    | 0    | 0    | 0    | 0    | 0    | 12   | 0    | 0     | 0     | 14    |
| ARO:3002<br>518 | OCH-5      | OCH-5 beta-lactamase is an Ambler class C chromosomal-encoded beta-lactamases in <i>Ochrobactrum anthropi</i>   | OCH beta-lactamase                                | cephalosporin;cephamycin;monobactam;penam;penem | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 10   | 0    | 0    | 0    | 0    | 0    | 6    | 0    | 0     | 0     | 16    |
| ARO:3002<br>522 | novA       | A type III ABC transporter, identified on the novobiocin biosynthetic gene cluster, involved in the transport and resistance of novobiocin. AAC(3)-Ia is an aminoglycoside acetyltransferase encoded by plasmids, transposons, integrons in <i>S. marcescens</i> , <i>E. coli</i> , <i>Acinetobacter baumannii</i> , <i>Klebsiella pneumoniae</i> , <i>Klebsiella oxytoca</i> , <i>P. aeruginosa</i> , <i>Salmonella typhimurium</i> and <i>Proteus mirabilis</i> | ATP-binding cassette (ABC) antibiotic efflux pump | aminocoumarin antibiotic                        | Aminocoumarin  | Antibiotic efflux       | 6542 | 6392 | 5888 | 3554 | 2742 | 7736 | 4392 | 3802 | 3776 | 8420 | 10378 | 10280 | 73902 |
| ARO:3002<br>528 | AAC(3)-Ia  | AAC(3)-Ic is an integron-encoded aminoglycoside acetyltransferase in <i>P. aeruginosa</i>   | AAC(3)  | aminoglycoside antibiotic                       | Aminoglycoside | Antibiotic inactivation | 8    | 30   | 76   | 16   | 0    | 6    | 4    | 14   | 4    | 0    | 0     | 0     | 158   |
| ARO:3002<br>531 | AAC(3)-Ic  | AAC(3)-IIa is a plasmid-encoded aminoglycoside acetyltransferase in <i>K. pneumoniae</i> , <i>E. cloacae</i> , <i>Actinobacillus pleuropneumoniae</i> , <i>S. typhimurium</i> , <i>Citrobacter freundii</i> , and <i>P. aeruginosa</i> .  | AAC(3)  | aminoglycoside antibiotic                       | Aminoglycoside | Antibiotic inactivation | 4    | 0    | 0    | 2    | 0    | 0    | 4    | 4    | 4    | 0    | 2     | 0     | 20    |
| ARO:3002<br>533 | AAC(3)-IIa |   | AAC(3)  | aminoglycoside antibiotic                       | Aminoglycoside | Antibiotic inactivation | 10   | 0    | 0    | 22   | 0    | 2    | 20   | 52   | 0    | 0    | 0     | 0     | 106   |

|              |              |  |         |                           |                |                         |     |     |    |     |     |     |    |     |     |    |     |     |      |
|--------------|--------------|--|---------|---------------------------|----------------|-------------------------|-----|-----|----|-----|-----|-----|----|-----|-----|----|-----|-----|------|
| ARO:3002-534 | AAC(3)-IIb   | AAC(3)-IIb is an aminoglycoside acetyltransferase in <i>E. coli</i> , <i>A. faecalis</i> and <i>S. marcescens</i>  | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0  | 0   | 0   | 0   | 0  | 0   | 2   | 0  | 16  | 0   | 18   |
| ARO:3002-535 | AAC(3)-IIc   | AAC(3)-IIc is a plasmid-encoded aminoglycoside acetyltransferase in <i>E. coli</i> and <i>P. aeruginosa</i>  | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 4  | 2   | 0   | 0   | 2  | 2   | 0   | 12 | 20  | 6   | 48   |
| ARO:3002-536 | AAC(3)-IIIa  | AAC(3)-IIIa is a chromosomal-encoded aminoglycoside acetyltransferase in <i>P. aeruginosa</i>  | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 708 | 10  | 2  | 0   | 0   | 926 | 0  | 0   | 36  | 0  | 0   | 4   | 1686 |
| ARO:3002-539 | AAC(3)-IV    | AAC(3)-IV is a plasmid-encoded aminoglycoside acetyltransferase in <i>E. coli</i> , <i>C. jejuni</i> and <i>P. stutzeri</i>  | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 96  | 218 | 40 | 134 | 42  | 186 | 58 | 154 | 94  | 50 | 140 | 102 | 1314 |
| ARO:3002-541 | AAC(3)-VIIa  | AAC(3)-VIIa is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Streptomyces rimosus</i>   | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 84  | 46  | 0  | 2   | 30  | 58  | 0  | 0   | 6   | 0  | 0   | 0   | 226  |
| ARO:3002-542 | AAC(3)-VIIIa | AAC(3)-VIIIa is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Streptomyces fradiae</i>  | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 10  | 38  | 0  | 0   | 0   | 22  | 0  | 0   | 2   | 0  | 0   | 2   | 74   |
| ARO:3002-543 | AAC(3)-IXa   | AAC(3)-IXa is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Micromonospora chalybeata</i>   | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 8   | 2   | 8  | 4   | 0   | 2   | 2  | 0   | 0   | 0  | 0   | 0   | 26   |
| ARO:3002-544 | AAC(3)-Xa    | AAC(3)-Xa is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Streptomyces griseus</i>   | AAC(3)  | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 4   | 34  | 18 | 8   | 420 | 30  | 4  | 16  | 382 | 0  | 0   | 0   | 916  |
| ARO:3002-545 | AAC(6')-Ia   | AAC(6')-Ia is an aminoglycoside acetyltransferase encoded by plasmids, transposons, integrons in <i>Citrobacter diversus</i> , <i>E. coli</i> , <i>K. pneumoniae</i> , <i>Shigella sonnei</i> , and <i>P. aeruginosa</i> . | AAC(6') | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 4   | 2   | 0  | 0   | 4   | 0   | 0  | 0   | 0   | 10 | 10  | 24  | 54   |
| ARO:3002-560 | AAC(6')-Iq   | AAC(6')-Iq is a aminoglycoside acetyltransferase encoded by plasmids and integrons in <i>K. pneumoniae</i>   | AAC(6') | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0  | 0   | 0   | 0   | 0  | 0   | 2   | 0  | 0   | 0   | 2    |
| ARO:3002-561 | AAC(6')-Ir   | AAC(6')-Ir is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Acinetobacter colistiniresistens</i>  | AAC(6') | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 14 | 0   | 0   | 4   | 0  | 0   | 0   | 4  | 0   | 0   | 22   |

|              |                        |  |                  |                           |                |                         |     |     |     |     |    |     |     |     |    |     |     |     |      |
|--------------|------------------------|--|------------------|---------------------------|----------------|-------------------------|-----|-----|-----|-----|----|-----|-----|-----|----|-----|-----|-----|------|
| ARO:3002-562 | AAC(6')-Is             | AAC(6')-Is is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Acinetobacter variabilis</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 2   | 8   | 6   | 0   | 0  | 10  | 2   | 0   | 4  | 12  | 6   | 18  | 68   |
| ARO:3002-572 | AAC(6')-lad            | AAC(6')-lad is a plasmid-encoded aminoglycoside acetyltransferase in <i>Acinetobacter genomosp. 3</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 276 | 166 | 274 | 138 | 90 | 268 | 134 | 196 | 92 | 160 | 80  | 62  | 1936 |
| ARO:3002-573 | AAC(6')-lae            | AAC(6')-lae is an integron-encoded aminoglycoside acetyltransferase in <i>P. aeruginosa</i> and <i>S. enterica</i>   | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 12  | 0   | 0   | 0   | 0  | 0   | 0   | 0   | 0  | 0   | 0   | 0   | 12   |
| ARO:3002-579 | AAC(6')-lb8            | AAC(6')-lb8 is a plasmid-encoded aminoglycoside acetyltransferase in <i>E. cloacae</i>   | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 2   | 10  | 0   | 0  | 0   | 0   | 0   | 0  | 2   | 6   | 6   | 26   |
| ARO:3002-584 | AAC(6')-29b            | AAC(6')-29b is an integron-encoded aminoglycoside acetyltransferase in <i>P. aeruginosa</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0  | 0   | 10  | 0   | 0  | 0   | 0   | 0   | 10   |
| ARO:3002-588 | AAC(6')-I30            | AAC(6')-I30 is an integron-encoded aminoglycoside acetyltransferase in <i>S. enterica</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 16  | 58  | 108 | 46  | 20 | 40  | 38  | 34  | 42 | 14  | 10  | 8   | 434  |
| ARO:3002-589 | AAC(6')-lid            | AAC(6')-lid is a chromosomal-encoded aminoglycoside acetyltransferase in <i>Enterococcus durans</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0  | 0   | 0   | 0   | 0  | 12  | 20  | 2   | 34   |
| ARO:3002-594 | AAC(6')-IIa            | AAC(6')-IIa is an aminoglycoside acetyltransferase encoded by plasmids and integrons in <i>P. aeruginosa</i> and <i>S. enterica</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0  | 0   | 14  | 2   | 0  | 0   | 4   | 0   | 20   |
| ARO:3002-595 | AAC(6')-IIb            | AAC(6')-IIb is an integron-encoded aminoglycoside acetyltransferase in <i>P. fluorescens</i>   | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0   | 0   | 0  | 0   | 2   | 0   | 0  | 0   | 2   | 0   | 4    |
| ARO:3002-596 | AAC(6')-IIc            | AAC(6')-IIc is an aminoglycoside acetyltransferase encoded by plasmids and integrons in <i>E. cloacae</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0   | 0   | 0   | 0   | 2  | 0   | 2   | 12  | 4  | 68  | 58  | 78  | 224  |
| ARO:3002-597 | AAC(6')-Ie-APH(2'')-Ia | AAC(6')-Ie-APH(2'')-Ia is an aminoglycoside acetyltransferase encoded by plasmids and transposons in <i>S. aureus</i> , <i>E. faecalis</i> , <i>E. faecium</i> and <i>Staphylococcus warneri</i> | AAC(6');APH(2'') | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 110 | 56  | 202 | 36  | 36 | 52  | 66  | 72  | 34 | 214 | 280 | 268 | 1426 |

|             |  |   |                  |                           |                |                         |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|--|---|------------------|---------------------------|----------------|-------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002598 | ANT(3'')-li-AAC(6')-Ild fusion protein | ANT(3'')-li-AAC(6')-Ild is an integron-encoded aminoglycoside acetyltransferase in <i>S. marcescens</i> .   | AAC(6');ANT(3'') | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 2    | 18   | 340  | 154  | 880  | 36   | 382  | 224  | 830  | 2390 | 2516 | 3938 | 11710 |
| ARO:3002599 | AAC(6')-30/AAC(6')-Ib' fusion protein  | AAC(6')-30/AAC(6')-Ib' is an integron-encoded aminoglycoside acetyltransferase in <i>P. aeruginosa</i>  | AAC(6')          | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 6    | 28   | 4    | 144  | 0    | 20   | 24   | 118  | 104  | 86   | 132  | 666   |
| ARO:3002602 | aadA2                                  | aadA2 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and integrons in <i>K. pneumoniae</i> , <i>Salmonella</i> spp., <i>Corynebacterium glutamicum</i> , <i>C. freundii</i> and <i>Aeromonas</i> spp. | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 400  | 798  | 312  | 1304 | 2484 | 160  | 2158 | 1432 | 2112 | 1288 | 1892 | 1702 | 16042 |
| ARO:3002604 | aadA4                                  | aadA4 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and chromosomes in <i>Bordetella parapertussis</i> and <i>E. coli</i>  | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 6    | 6    | 12    |
| ARO:3002605 | aadA5                                  | aadA5 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids, transposons and integrons in <i>E. coli</i> , <i>K. pneumoniae</i> , <i>Kluyvera georgiana</i> , <i>P. aeruginosa</i> and <i>E. cloacae</i>     | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 4    | 4    | 76   | 72   | 300  | 8    | 142  | 80   | 274  | 344  | 442  | 568  | 2314  |
| ARO:3002606 | aadA6                                  | aadA6 is an integron-encoded aminoglycoside nucleotidyltransferase gene in <i>P. aeruginosa</i>   | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 2    | 4    | 14   | 0    | 0    | 38   | 8    | 0    | 10   | 24   | 24   | 124   |
| ARO:3002607 | aadA7                                  | aadA7 is an integron-encoded aminoglycoside nucleotidyltransferase gene in <i>V. fluvialis</i> , <i>P. aeruginosa</i> , <i>E. coli</i> , <i>V. cholerae</i> and <i>S. enterica</i>  | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 4436 | 5306 | 3116 | 2016 | 838  | 5290 | 1958 | 2516 | 1266 | 934  | 532  | 474  | 28682 |
| ARO:3002609 | aadA9                                  | aadA9 is a plasmid-encoded aminoglycoside nucleotidyltransferase gene in <i>C. glutamicum</i>   | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 54   | 70   | 18   | 6    | 14   | 182  | 12   | 12   | 42   | 766  | 892  | 724  | 2792  |
| ARO:3002611 | aadA11                                 | aadA11 is an integron-encoded aminoglycoside nucleotidyltransferase gene in <i>E. coli</i> and <i>P. aeruginosa</i>   | ANT(3'')         | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 0    | 16   | 2    | 0    | 0    | 32   | 4    | 10   | 50   | 108  | 132  | 354   |

|                 |               |  |         |                           |                 |                                    |      |      |      |      |     |      |      |      |      |     |     |     |       |
|-----------------|---------------|--|---------|---------------------------|-----------------|------------------------------------|------|------|------|------|-----|------|------|------|------|-----|-----|-----|-------|
| ARO:3002<br>613 | aadA13        | aadA13 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and integrons in <i>Pseudomonas rettgeri</i> , <i>P. aeruginosa</i> , <i>Y. enterocolitica</i> and <i>E. coli</i>  | ANT(3") | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 412  | 602  | 926  | 292  | 256 | 512  | 206  | 354  | 422  | 566 | 474 | 442 | 5464  |
| ARO:3002<br>614 | aadA14        | aadA14 is a plasmid-encoded aminoglycoside nucleotidyltransferase gene in <i>Pasteurella multocida</i>   | ANT(3") | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 0    | 4    | 2    | 4    | 12  | 4    | 2    | 88   | 58   | 16  | 28  | 24  | 242   |
| ARO:3002<br>616 | aadA16        | aadA16 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and integrons in <i>E. coli</i> , <i>V. cholerae</i> and <i>K. pneumoniae</i>  | ANT(3") | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 0    | 12   | 12   | 24   | 140 | 10   | 34   | 40   | 190  | 152 | 164 | 212 | 990   |
| ARO:3002<br>620 | aadA23        | aadA23 is an integron-encoded aminoglycoside nucleotidyltransferase gene in <i>S. enterica</i>   | ANT(3") | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 0    | 0    | 0    | 0    | 0   | 0    | 0    | 0    | 0    | 0   | 0   | 6   | 6     |
| ARO:3002<br>626 | ANT(6)-<br>la | ANT(6)-la is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and chromosomes in <i>Staphylococcus epidermidis</i> , <i>E. faecium</i> , <i>Streptococcus suis</i> , <i>S. aureus</i> , <i>E. faecalis</i> and <i>Streptococcus mitis</i> | ANT(6)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 242  | 264  | 364  | 106  | 172 | 270  | 138  | 212  | 230  | 416 | 436 | 494 | 3344  |
| ARO:3002<br>627 | aadK          | aadK is a chromosomal-encoded aminoglycoside nucleotidyltransferase gene in <i>B. subtilis</i> and <i>Bacillus</i> spp.  | ANT(6)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 202  | 156  | 162  | 2    | 34  | 336  | 10   | 30   | 28   | 124 | 134 | 164 | 1382  |
| ARO:3002<br>628 | aad(6)        | aad(6) is a plasmid-encoded aminoglycoside nucleotidyltransferase gene in <i>E. faecalis</i> and <i>Streptococcus oralis</i>   | ANT(6)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 264  | 274  | 492  | 268  | 188 | 254  | 280  | 300  | 318  | 188 | 158 | 120 | 3104  |
| ARO:3002<br>629 | ANT(6)-<br>lb | ANT(6)-lb is an aminoglycoside nucleotidyltransferase gene encoded by transferable pathogenicity islands in <i>C. fetus</i> subsp. <i>fetus</i> and <i>B. subtilis</i>   | ANT(6)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 2534 | 3104 | 3046 | 1602 | 864 | 3136 | 1548 | 2100 | 1232 | 880 | 548 | 576 | 21170 |
| ARO:3002<br>630 | ANT(9)-<br>la | ANT(9)-la is an aminoglycoside nucleotidyltransferase encoded by plasmids and transposons in <i>S. aureus</i> , <i>Enterococcus</i> spp., <i>Staphylococcus sciuri</i> and <i>E. faecalis</i>  | ANT(9)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c<br>inactivat<br>ion | 0    | 0    | 8    | 0    | 22  | 0    | 2    | 2    | 2    | 4   | 0   | 0   | 40    |
| ARO:3002<br>631 | spd           | spd is a plasmid-encoded aminoglycoside  | ANT(9)  | aminoglycoside antibiotic | Aminoglyc oside | Antibioti<br>c                     | 4    | 0    | 4    | 6    | 60  | 22   | 0    | 2    | 146  | 54  | 88  | 84  | 470   |

|                 |                   |   |          |                              |                    |                                    |     |     |     |      |      |     |      |      |      |      |      |      |       |
|-----------------|-------------------|---|----------|------------------------------|--------------------|------------------------------------|-----|-----|-----|------|------|-----|------|------|------|------|------|------|-------|
|                 |                   | nucleotidyltransferase gene in <i>S. aureus</i>   |          |                              | inactivat<br>ion   |                                    |     |     |     |      |      |     |      |      |      |      |      |      |       |
| ARO:3002<br>634 | APH(2'')<br>-Ie   | APH(2'')-Ie is a plasmid or transposon-encoded aminoglycoside phosphotransferase in <i>E. faecium</i> and <i>E. casseliflavus</i>   | APH(2'') | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 0   | 0   | 0   | 0    | 0    | 0   | 0    | 2    | 0    | 32   | 42   | 16   | 92    |
| ARO:3002<br>635 | APH(2'')<br>-IIa  | APH(2'')-IIa is a chromosomal-encoded aminoglycoside phosphotransferase in <i>E. faecium</i> and <i>E. coli</i>   | APH(2'') | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 52  | 86  | 102 | 94   | 70   | 90  | 56   | 128  | 136  | 26   | 4    | 18   | 862   |
| ARO:3002<br>636 | APH(2'')<br>-IIIa | APH(2'')-IIIa is a plasmid-encoded aminoglycoside phosphotransferase in <i>Enterococcus gallinarum</i>  | APH(2'') | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 2   | 0   | 0   | 0    | 18   | 2   | 0    | 0    | 8    | 34   | 38   | 24   | 126   |
| ARO:3002<br>638 | APH(3'')<br>-Ia   | APH(3'')-Ia is a chromosomal-encoded aminoglycoside phosphotransferase in <i>S. griseus</i>   | APH(3'') | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 0   | 0   | 0   | 2    | 2    | 0   | 14   | 0    | 0    | 16   | 44   | 6    | 84    |
| ARO:3002<br>639 | APH(3'')<br>-Ib   | APH(3'')-Ib is an aminoglycoside phosphotransferase encoded by plasmids, transposons, integrative conjugative elements and chromosomes in <i>Enterobacteriaceae</i> and <i>Pseudomonas</i> spp.   | APH(3'') | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 498 | 606 | 968 | 1312 | 4000 | 614 | 1252 | 1928 | 3594 | 4530 | 4888 | 5838 | 30028 |
| ARO:3002<br>641 | APH(3')-<br>Ia    | APH(3')-Ia is a transposon-encoded aminoglycoside phosphotransferase in <i>E. coli</i> and <i>S. enterica</i> . It is identical at the protein sequence to APH(3')-Ic, an aminoglycoside phosphotransferase encoded by plasmids, transposons and genomic islands in <i>K. pneumoniae</i> , <i>A. baumannii</i> , <i>S. marcescens</i> , <i>Corynebacterium</i> spp., <i>Photobacterium</i> spp. and <i>Citrobacter</i> spp. | APH(3')  | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 200 | 886 | 176 | 428  | 598  | 370 | 630  | 578  | 842  | 1026 | 1072 | 1502 | 8308  |
| ARO:3002<br>642 | APH(3')-<br>Ib    | APH(3')-Ib is a plasmid-encoded aminoglycoside phosphotransferase in <i>E. coli</i>   | APH(3')  | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 0   | 0   | 6   | 14   | 2    | 0   | 10   | 12   | 6    | 6    | 12   | 6    | 74    |
| ARO:3002<br>644 | APH(3')-<br>IIa   | APH(3')-IIa is a transposon-encoded aminoglycoside phosphotransferase in <i>E. coli</i>   | APH(3')  | aminoglycoside<br>antibiotic | Aminoglyc<br>oside | Antibioti<br>c<br>inactivat<br>ion | 0   | 6   | 0   | 24   | 10   | 6   | 24   | 14   | 4    | 64   | 54   | 68   | 274   |



|              |              |  |                            |                           |                |                         |      |      |      |      |      |      |      |      |      |      |      |       |       |
|--------------|--------------|--|----------------------------|---------------------------|----------------|-------------------------|------|------|------|------|------|------|------|------|------|------|------|-------|-------|
| ARO:3002-647 | APH(3')-IIIa | APH(3')-IIIa is a plasmid-encoded aminoglycoside phosphotransferase in <i>S. aureus</i> and <i>Enterococcus</i> spp.   | APH(3')                    | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 1764 | 1724 | 6924 | 3592 | 2142 | 1730 | 3064 | 4058 | 2778 | 1550 | 1044 | 1200  | 31570 |
| ARO:3002-648 | APH(3')-IVa  | APH(3')-IVa is a chromosomal-encoded aminoglycoside phosphotransferase in <i>B. circulans</i>  | APH(3')                    | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 92   | 86   | 18   | 6    | 16   | 100  | 66   | 16   | 14   | 62   | 54   | 46    | 576   |
| ARO:3002-649 | APH(3')-Va   | APH(3')-Va is a chromosomal-encoded aminoglycoside phosphotransferase in <i>Streptomyces fradiae</i>   | APH(3')                    | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 2    | 24   | 0    | 22   | 2    | 22   | 58   | 32   | 6    | 36   | 48   | 12    | 264   |
| ARO:3002-652 | APH(3')-VIa  | APH(3')-VIa is a plasmid-encoded aminoglycoside phosphotransferase in <i>A. baumannii</i>  | APH(3')                    | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 8    | 6    | 368  | 80   | 1778 | 0    | 142  | 470  | 1536 | 1162 | 1110 | 1534  | 8194  |
| ARO:3002-654 | APH(3')-VIIa | APH(3')-VIIa is a plasmid-encoded aminoglycoside phosphotransferase in <i>C. jejuni</i>  | APH(3')                    | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 4    | 16   | 120  | 28   | 26   | 14   | 34   | 32   | 16   | 48   | 8    | 18    | 364   |
| ARO:3002-655 | APH(4)-Ia    | APH(4)-Ia is a plasmid-encoded aminoglycoside phosphotransferase in <i>E. coli</i>   | APH(4)                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 1470 | 844  | 1126 | 770  | 624  | 880  | 570  | 868  | 778  | 370  | 310  | 260   | 8870  |
| ARO:3002-657 | APH(6)-Ia    | APH(6)-Ia is a chromosomal-encoded aminoglycoside phosphotransferase in <i>S. griseus</i>  | APH(6)                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 0    | 0    | 0    | 0    | 0    | 20   | 10   | 0    | 8    | 10   | 6     | 54    |
| ARO:3002-659 | APH(6)-Ic    | APH(6)-Ic is a transposon-encoded aminoglycoside phosphotransferase in <i>S. enterica</i> , <i>P. aeruginosa</i> and <i>E. coli</i>  | APH(6)                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 8    | 2    | 22   | 0    | 6    | 8    | 10   | 6    | 56   | 44   | 56    | 218   |
| ARO:3002-660 | APH(6)-Id    | APH(6)-Id is an aminoglycoside phosphotransferase encoded by plasmids, integrative conjugative elements and chromosomal genomic islands in <i>K. pneumoniae</i> , <i>Salmonella</i> spp., <i>E. coli</i> , <i>Shigella flexneri</i> , <i>Providencia alcalifaciens</i> , <i>Pseudomonas</i> spp., <i>V. cholerae</i> , <i>Edwardsiella tarda</i> , <i>Pasteurella multocida</i> and <i>Aeromonas bestiarum</i> | APH(6)                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 850  | 798  | 1640 | 1924 | 8368 | 800  | 1986 | 3638 | 7668 | 7774 | 7856 | 10288 | 53590 |
| ARO:3002-666 | rmtF         | RmtF is a 16S rRNA methyltransferase found in  | 16S rRNA methyltransferase | aminoglycoside antibiotic | Aminoglycoside | Antibiotic target       | 10   | 0    | 14   | 6    | 10   | 24   | 16   | 8    | 8    | 6    | 4    | 0     | 106   |

|                 |                              |   |   |                           |                |                              |     |     |     |     |     |     |     |     |     |      |      |      |      |
|-----------------|------------------------------|---|---|---------------------------|----------------|------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|
| ARO:3002<br>667 | rmtD                         | Pseudomonas aeruginosa which methylates G1405 of the 16S rRNA. It confers high level resistance to many aminoglycosides. RmtD is a 16S rRNA methyltransferase found in Pseudomonas aeruginosa which methylates G1405 of the 16S rRNA. It confers high level resistance to many aminoglycosides. | 16S rRNA methyltransferase (G1405)      | aminoglycoside antibiotic | Aminoglycoside | Antibiotic target alteration | 4   | 0   | 8   | 0   | 4   | 8   | 0   | 0   | 6   | 0    | 0    | 4    | 34   |
| ARO:3002<br>672 | Bacillus pumilus cat86       | cat86 is a chromosome-encoded variant of the cat gene found in Bacillus pumilus   | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 0   | 0   | 18  | 8   | 0   | 0   | 8   | 20  | 2   | 40   | 12   | 34   | 142  |
| ARO:3002<br>674 | Clostridium butyricum catB   | catB is a chromosome-encoded variant of the cat gene found in Clostridium butyricum   | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 8   | 6   | 8   | 24  | 44  | 0   | 20  | 38  | 70  | 16   | 6    | 12   | 252  |
| ARO:3002<br>675 | catB2                        | catB2 is a plasmid-encoded variant of the cat gene found in Escherichia coli, Salmonella enteritidis and Pasteurella multocida  | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 12  | 118 | 90  | 12  | 184 | 12  | 38  | 42  | 184 | 62   | 36   | 76   | 866  |
| ARO:3002<br>676 | catB3                        | catB3 is a plasmid or chromosome-encoded variant of the cat gene found in Salmonella typhimurium, Acinetobacter baumannii and Escherichia coli  | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 354 | 382 | 452 | 140 | 280 | 470 | 206 | 154 | 472 | 730  | 566  | 856  | 5062 |
| ARO:3002<br>678 | Pseudomonas aeruginosa catB6 | catB6 is a plasmid-encoded variant of the cat gene found in Pseudomonas aeruginosa  | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 16  | 68  | 10  | 4   | 4   | 28  | 10  | 8   | 18  | 10   | 8    | 2    | 186  |
| ARO:3002<br>679 | Pseudomonas aeruginosa catB7 | catB7 is a chromosome-encoded variant of the cat gene found in Pseudomonas aeruginosa   | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 4   | 14  | 0   | 6   | 2   | 0   | 16  | 4   | 52  | 0    | 0    | 0    | 98   |
| ARO:3002<br>680 | catB8                        | catB8 is a plasmid or integron-encoded variant of the cat gene found in Klebsiella pneumoniae, Salmonella typhi and Pseudomonas aeruginosa  | chloramphenicol acetyltransferase (CAT) | phenicol antibiotic       | Phenicol       | Antibiotic inactivation      | 246 | 176 | 200 | 66  | 294 | 366 | 126 | 88  | 314 | 1106 | 1138 | 1610 | 5730 |

|                 |                            |   |  |                     |          |                         |     |     |     |     |     |     |     |     |     |      |     |      |      |
|-----------------|----------------------------|---|--|---------------------|----------|-------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|------|------|
| ARO:3002<br>681 | catB9                      | catB9 is a chromosome-encoded variant of the cat gene found in <i>Vibrio cholerae</i>   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 568 | 654 | 48  | 120 | 86  | 522 | 88  | 146 | 70  | 176  | 74  | 210  | 2762 |
| ARO:3002<br>683 | catI                       | catI is a chromosome and transposon-encoded variant of the cat gene found in <i>Escherichia coli</i> and <i>Acinetobacter baumannii</i>   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 126 | 108 | 80  | 12  | 94  | 94  | 34  | 16  | 100 | 8    | 2   | 0    | 674  |
| ARO:3002<br>684 | catII                      | catII is a plasmid-encoded variant of the cat gene found in <i>Haemophilus influenzae</i> , <i>Agrobacterium tumefaciens</i> and <i>Escherichia coli</i>                                  | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 44  | 0   | 2   | 0   | 0   | 0   | 4   | 0   | 0   | 0    | 0   | 0    | 50   |
| ARO:3002<br>685 | catIII                     | catIII is a plasmid-encoded variant of the cat gene found in <i>Shigella flexneri</i>   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 2   | 6   | 8   | 44  | 6   | 2   | 14  | 60  | 12  | 20   | 16  | 24   | 214  |
| ARO:3002<br>686 | catP                       | catP is a transposon and chromosome-encoded variant of the cat gene found in <i>Clostridium perfringens</i> and <i>Neisseria meningitidis</i>   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 40  | 52  | 78  | 52  | 12  | 40  | 46  | 46  | 22  | 4    | 8   | 6    | 406  |
| ARO:3002<br>687 | catQ                       | catQ is a chromosome-encoded variant of the cat gene found in <i>Clostridium perfringens</i>  | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic | Phenicol | Antibiotic inactivation | 88  | 246 | 154 | 92  | 64  | 170 | 100 | 96  | 104 | 78   | 38  | 24   | 1254 |
| ARO:3002<br>690 | Streptomyces lividans cmlR | cmlR is a plasmid or chromosome-encoded chloramphenicol resistance determinant (putative transmembrane protein) that is found in <i>Escherichia coli</i> and <i>Streptomyces lividans</i> | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 22  | 8   | 76  | 48  | 0   | 10  | 94  | 48  | 10  | 1508 | 942 | 2460 | 5226 |
| ARO:3002<br>691 | Salmonella enterica cmlA   | cmlA is a plasmid-encoded chloramphenicol exporter that is found in <i>Salmonella typhimurium</i>   | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 4    | 2   | 0    | 6    |
| ARO:3002<br>693 | cmlA1                      | cmlA1 is a plasmid or transposon-encoded chloramphenicol exporter that is found in <i>Pseudomonas aeruginosa</i> and <i>Klebsiella pneumoniae</i>   | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 110 | 354 | 50  | 438 | 108 | 32  | 516 | 472 | 100 | 116  | 92  | 136  | 2524 |

|                 |                          |  |  |                     |          |                         |      |     |     |      |     |     |      |      |     |      |      |      |       |
|-----------------|--------------------------|--|--|---------------------|----------|-------------------------|------|-----|-----|------|-----|-----|------|------|-----|------|------|------|-------|
| ARO:3002<br>694 | cmlA4                    | cmlA4 is a plasmid-encoded chloramphenicol exporter that is found in <i>Klebsiella pneumoniae</i>                                    | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 0    | 0   | 0   | 2    | 0   | 0   | 6    | 0    | 0   | 8    | 0    | 0    | 16    |
| ARO:3002<br>695 | cmlA5                    | cmlA5 is a plasmid or transposon-encoded chloramphenicol exporter that is found in <i>Escherichia coli</i>                           | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 104  | 388 | 24  | 564  | 132 | 28  | 672  | 540  | 110 | 102  | 104  | 120  | 2888  |
| ARO:3002<br>696 | cmlA6                    | cmlA6 is a plasmid-encoded chloramphenicol exporter that is found in <i>Pseudomonas aeruginosa</i>                                   | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 52   | 154 | 6   | 224  | 52  | 18  | 214  | 208  | 30  | 1846 | 1336 | 2784 | 6924  |
| ARO:3002<br>698 | cmlB                     | cmlB is a plasmid-encoded chloramphenicol exporter that is found in <i>Klebsiella aerogenes</i>                                      | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 704  | 218 | 162 | 754  | 372 | 368 | 1140 | 922  | 336 | 170  | 156  | 116  | 5418  |
| ARO:3002<br>699 | cmlB1                    | cmlB1 is a plasmid-encoded chloramphenicol exporter that is found in <i>Bordetella bronchiseptica</i>                                | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 0    | 6   | 0   | 18   | 4   | 0   | 86   | 22   | 0   | 18   | 20   | 64   | 238   |
| ARO:3002<br>700 | cmlv                     | cmlv is a chromosome-encoded chloramphenicol phosphotransferase that is found in <i>Streptomyces venezuelae</i>                      | chloramphenicol phosphotransferase                         | phenicol antibiotic | Phenicol | Antibiotic inactivation | 1270 | 366 | 298 | 1650 | 720 | 346 | 2304 | 1916 | 666 | 2074 | 1692 | 2900 | 16202 |
| ARO:3002<br>701 | Rhodococcus fascians cmr | cmr is a plasmid-encoded chloramphenicol exporter that is found in <i>Rhodococcus fascians</i> and <i>Corynebacterium glutamicum</i> | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 8    | 46  | 12  | 24   | 0   | 30  | 16   | 4    | 4   | 28   | 42   | 82   | 296   |
| ARO:3002<br>702 | cmrA                     | cmrA is a transposon-encoded chloramphenicol exporter that is found in <i>Rhodococcus rhodochrous</i>                                | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic | Phenicol | Antibiotic efflux       | 552  | 162 | 140 | 968  | 432 | 86  | 1382 | 1054 | 324 | 234  | 246  | 220  | 5800  |

|                 |        |  |   |                               |                     |   |      |      |      |      |       |      |      |      |       |       |       |       |       |
|-----------------|--------|--|---|-------------------------------|---------------------|---|------|------|------|------|-------|------|------|------|-------|-------|-------|-------|-------|
| ARO:3002<br>703 | cmx    | cmx is a plasmid or transposon-<br>encoded chloramphenicol<br>exporter that is found in<br>Corynebacterium striatum and<br>Pseudomonas aeruginosa.   | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump | phenicol<br>antibiotic        | Phenicol            | Antibioti<br>c efflux                   | 998  | 1678 | 844  | 472  | 758   | 1218 | 950  | 514  | 936   | 3814  | 5760  | 4506  | 22448 |
| ARO:3002<br>704 | fexA   | fexA is a plasmid-encoded<br>chloramphenicol exporter that<br>is found in Staphylococcus<br>lentus   | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump | phenicol<br>antibiotic        | Phenicol            | Antibioti<br>c efflux                   | 194  | 68   | 96   | 34   | 56    | 370  | 76   | 40   | 114   | 122   | 188   | 152   | 1510  |
| ARO:3002<br>705 | floR   | floR is a plasmid or<br>chromosome-encoded<br>chloramphenicol exporter that<br>is found in Bordetella<br>bronchiseptica, Escherichia coli,<br>Klebsiella pneumoniae,<br>Salmonella enterica subsp.<br>enterica serovar Typhimurium<br>str. DT104 and Vibrio cholerae | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump | phenicol<br>antibiotic        | Phenicol            | Antibioti<br>c efflux                   | 1870 | 3448 | 2890 | 4404 | 11560 | 1978 | 5540 | 6484 | 10168 | 14728 | 14542 | 19346 | 96958 |
| ARO:3002<br>707 | QnrA1  | QnrA1 is a plasmid-mediated<br>quinolone resistance protein<br>found in Klebsiella pneumoniae  | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 0    | 0    | 0    | 0    | 0     | 0    | 0    | 0    | 0     | 32    | 30    | 26    | 88    |
| ARO:3002<br>710 | QnrA4  | QnrA4 is a plasmid-mediated<br>quinolone resistance protein<br>found in Shewanella algae   | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 0    | 0    | 0    | 0    | 0     | 0    | 0    | 0    | 0     | 20    | 30    | 4     | 54    |
| ARO:3002<br>715 | QnrB2  | QnrB2 is a plasmid-mediated<br>quinolone resistance protein<br>found in Citrobacter koseri   | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 0    | 0    | 0    | 0    | 0     | 0    | 0    | 0    | 0     | 10    | 4     | 36    | 50    |
| ARO:3002<br>724 | QnrB10 | QnrB10 is a plasmid-mediated<br>quinolone resistance protein<br>found in Citrobacter freundii  | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 0    | 0    | 0    | 2    | 0     | 0    | 12   | 4    | 0     | 0     | 2     | 0     | 20    |
| ARO:3002<br>734 | QnrB19 | QnrB19 is a plasmid-mediated<br>quinolone resistance protein<br>found in Escherichia coli  | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 2    | 0    | 0    | 8    | 0     | 0    | 12   | 4    | 0     | 0     | 8     | 0     | 34    |
| ARO:3002<br>735 | QnrB20 | QnrB20 is a plasmid-mediated<br>quinolone resistance protein<br>found in Escherichia coli  | quinolone<br>resistance<br>protein (qnr)                                  | fluoroquinolone<br>antibiotic | Fluoroquin<br>olone | Antibioti<br>c target<br>protecti<br>on | 0    | 0    | 0    | 4    | 0     | 0    | 10   | 22   | 0     | 0     | 0     | 0     | 36    |

|                 |        |   |                                    |                            |                 |                              |     |     |    |     |     |     |      |      |     |     |     |     |      |
|-----------------|--------|---|------------------------------------|----------------------------|-----------------|------------------------------|-----|-----|----|-----|-----|-----|------|------|-----|-----|-----|-----|------|
| ARO:3002<br>744 | QnrB29 | QnrB29 is a plasmid-mediated quinolone resistance protein found in <i>Citrobacter freundii</i>      | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 4   | 0  | 0   | 4   | 0   | 0    | 0    | 0   | 6   | 12  | 4   | 30   |
| ARO:3002<br>747 | QnrB32 | QnrB32 is a plasmid-mediated quinolone resistance protein found in <i>Citrobacter freundii</i>      | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 0  | 4   | 0   | 0   | 20   | 0    | 0   | 2   | 0   | 6   | 32   |
| ARO:3002<br>750 | QnrB35 | QnrB35 is a plasmid-mediated quinolone resistance protein found in <i>Citrobacter freundii</i>      | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 0  | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 10  | 10   |
| ARO:3002<br>787 | QnrC   | QnrC is a plasmid-mediated quinolone resistance protein found in <i>Proteus mirabilis</i>           | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 12  | 2   | 0  | 0   | 0   | 24  | 4    | 0    | 0   | 0   | 0   | 4   | 46   |
| ARO:3002<br>790 | QnrS1  | QnrS1 is a plasmid-mediated quinolone resistance protein found in <i>Shigella flexneri</i>          | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 370 | 248 | 90 | 968 | 402 | 46  | 1180 | 1046 | 248 | 72  | 108 | 36  | 4814 |
| ARO:3002<br>795 | QnrS6  | QnrS6 is a plasmid-mediated quinolone resistance protein found in <i>Aeromonas hydrophila</i>       | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 0  | 8   | 0   | 0   | 0    | 14   | 0   | 0   | 0   | 0   | 22   |
| ARO:3002<br>799 | QnrVC1 | QnrVC1 is an integron-mediated quinolone resistance protein found in <i>Vibrio cholerae</i>         | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 12  | 0   | 0  | 0   | 0   | 6   | 0    | 0    | 0   | 0   | 0   | 0   | 18   |
| ARO:3002<br>800 | QnrVC3 | QnrVC3 is an integron-mediated quinolone resistance protein found in <i>Vibrio cholerae</i>         | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 2  | 0   | 0   | 0   | 2    | 0    | 0   | 78  | 68  | 62  | 212  |
| ARO:3002<br>801 | QnrVC4 | QnrVC4 is an integron-mediated quinolone resistance protein found in <i>Aeromonas punctata</i>      | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 0  | 10  | 0   | 0   | 0    | 30   | 0   | 118 | 198 | 190 | 546  |
| ARO:3002<br>802 | QnrVC5 | QnrVC5 is an integron-mediated quinolone resistance protein found in <i>Vibrio fluvialis</i>        | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 8  | 4   | 0   | 0   | 0    | 0    | 2   | 16  | 10  | 16  | 56   |
| ARO:3002<br>803 | QnrVC6 | QnrVC6 is an integron-mediated quinolone resistance protein found in <i>Acinetobacter baumannii</i> | quinolone resistance protein (qnr) | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic target protection | 0   | 0   | 0  | 0   | 0   | 0   | 6    | 0    | 0   | 344 | 282 | 348 | 980  |
| ARO:3002<br>812 | pp-flo | pp-flo is a plasmid chloramphenicol exporter that   | major facilitator superfamily      | phenicol antibiotic        | Phenicol        | Antibiotic efflux            | 98  | 110 | 64 | 14  | 92  | 108 | 16   | 22   | 26  | 112 | 228 | 202 | 1092 |

|                 |      |  |  |   |           |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|------|--|--|---|-----------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002<br>813 | lmrB | is found in <i>Photobacterium damsela</i> subsp. <i>piscicida</i><br><br>lmrB is a chromosomally-encoded efflux pump that confers resistance to lincosamides in <i>Bacillus subtilis</i> | (MFS) antibiotic efflux pump ATP-binding cassette (ABC) antibiotic efflux pump | lincosamide antibiotic  | MLS       | Antibiotic efflux            | 1160 | 290  | 480  | 258  | 1476 | 1376 | 506  | 518  | 1462 | 956  | 1510 | 1232 | 11224 |
| ARO:3002<br>814 | clbA | clbA is a plasmid-encoded cfr gene found in <i>Bacillus velezensis</i> ( <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> ).  | Cfr 23S ribosomal RNA methyltransferase  | lincosamide antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic lincosamide  | Multidrug | Antibiotic target alteration | 3234 | 3578 | 4176 | 1816 | 1180 | 3656 | 1732 | 2198 | 1642 | 1710 | 1266 | 1570 | 27758 |
| ARO:3002<br>815 | clbB | clbB is a plasmid-encoded cfr gene found in <i>Bacillus brevis</i>   | Cfr 23S ribosomal RNA methyltransferase  | antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic lincosamide  | Multidrug | Antibiotic target alteration | 120  | 226  | 292  | 266  | 86   | 184  | 156  | 230  | 92   | 154  | 176  | 166  | 2148  |
| ARO:3002<br>816 | clbC | clbC is a plasmid-encoded cfr gene found in <i>Bacillus clausii</i>  | Cfr 23S ribosomal RNA methyltransferase  | antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic lincosamide antibiotic;macrolide   | Multidrug | Antibiotic target alteration | 726  | 1048 | 250  | 248  | 88   | 554  | 218  | 274  | 114  | 248  | 422  | 426  | 4616  |
| ARO:3002<br>817 | carA | carA is an ABC-F subfamily protein involved in macrolide resistance. It is found in <i>Streptomyces thermotolerans</i>   | ABC-F ATP-binding cassette ribosomal protection protein                        | antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic lincosamide antibiotic;macrolide antibiotic;oxazolidinone | Multidrug | Antibiotic target protection | 2502 | 2234 | 2330 | 2548 | 2422 | 2060 | 3778 | 2918 | 2534 | 4544 | 4864 | 5352 | 38086 |
| ARO:3002<br>819 | msrC | msrC is a chromosomal-encoded ABC-F subfamily protein expressed in <i>Enterococcus faecium</i> that confers resistance to erythromycin and other   | ABC-F ATP-binding cassette ribosomal   | antibiotic;macrolide antibiotic;oxazolidinone   | Multidrug | Antibiotic target protection | 482  | 156  | 140  | 108  | 86   | 544  | 142  | 144  | 96   | 320  | 326  | 346  | 2890  |

|                 |      |   |   |   |           |                              |      |      |      |     |     |      |      |      |      |      |      |      |       |
|-----------------|------|---|---|---|-----------|------------------------------|------|------|------|-----|-----|------|------|------|------|------|------|------|-------|
|                 |      | macrolide and streptogramin B antibiotics.  | protection protein                                      | antibiotic;phenicol<br>antibiotic;pleuro mutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide   |           |                              |      |      |      |     |     |      |      |      |      |      |      |      |       |
| ARO:3002<br>823 | ErmH | ErmH is a plasmid-mediated methyltransferase found in Streptomyces thermotolerans   | Erm 23S ribosomal RNA methyltransferase                 | antibiotic;macrolide<br>antibiotic;streptogramin antibiotic<br>lincosamide  | MLS       | Antibiotic target alteration | 242  | 100  | 116  | 34  | 10  | 126  | 60   | 24   | 32   | 22   | 44   | 20   | 830   |
| ARO:3002<br>824 | ErmV | ErmV is a plasmid-mediated methyltransferase found in Streptomyces viridochromogenes  | Erm 23S ribosomal RNA methyltransferase                 | antibiotic;macrolide<br>antibiotic;streptogramin antibiotic<br>lincosamide  | MLS       | Antibiotic target alteration | 0    | 0    | 0    | 2   | 2   | 0    | 10   | 0    | 0    | 28   | 50   | 28   | 120   |
| ARO:3002<br>825 | ErmY | ErmY is a plasmid-mediated methyltransferase found in Staphylococcus aureus   | Erm 23S ribosomal RNA methyltransferase                 | antibiotic;macrolide<br>antibiotic;streptogramin antibiotic<br>lincosamide  | MLS       | Antibiotic target alteration | 0    | 20   | 0    | 0   | 0   | 0    | 0    | 0    | 0    | 0    | 24   | 4    | 48    |
| ARO:3002<br>827 | tlrC | tlrC is an ABC-F subfamily protein found in Streptomyces fradiae and confers resistance to mycinamicin, tylosin and lincosamides. tlrC is found in the tylosin biosynthetic cluster and is one mechanism by which S. fradiae protects itself from self-destruction when producing this macrolide. | ABC-F ATP-binding cassette ribosomal protection protein | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuro mutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide | Multidrug | Antibiotic target protection | 840  | 870  | 868  | 610 | 798 | 814  | 968  | 902  | 924  | 2788 | 2748 | 3680 | 16810 |
| ARO:3002<br>828 | srmB | srmB is an ABC-F subfamily protein found in Streptomyces ambofaciens that confers resistance to spiramycin  | ABC-F ATP-binding cassette ribosomal protection protein | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuro mutilin<br>antibiotic;streptogramin  | Multidrug | Antibiotic target protection | 1168 | 1610 | 1554 | 858 | 636 | 1340 | 1230 | 1028 | 1040 | 1940 | 2246 | 1892 | 16542 |



|                 |        |  |   |  |           |                              |     |     |     |     |      |     |     |     |      |      |      |     |      |  |
|-----------------|--------|--|---|--|-----------|------------------------------|-----|-----|-----|-----|------|-----|-----|-----|------|------|------|-----|------|--|
|                 |        |  | antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide |  |           |                              |     |     |     |     |      |     |     |     |      |      |      |     |      |  |
| ARO:3002<br>829 | vgaA   | vgaA is an ABC-F subfamily protein expressed in staphylococci that confers resistance to streptogramin A antibiotics and related compounds. It is associated with plasmid DNA.   | ABC-F ATP-binding cassette ribosomal protection protein                   | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide | Multidrug | Antibiotic target protection | 0   | 44  | 8   | 0   | 0    | 8   | 0   | 0   | 0    | 0    | 2    | 0   | 62   |  |
| ARO:3002<br>830 | vgaALC | vgaALC is an ABC-F subfamily protein expressed in staphylococci that confers resistance to streptogramin A antibiotics and related compounds. It is associated with plasmid DNA. | ABC-F ATP-binding cassette ribosomal protection protein                   | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide | Multidrug | Antibiotic target protection | 256 | 284 | 432 | 202 | 194  | 464 | 184 | 258 | 322  | 166  | 202  | 256 | 3220 |  |
| ARO:3002<br>831 | vgaC   | vgaC is an ABC-F subfamily protein expressed in staphylococci that confers resistance to streptogramin A antibiotics and related compounds. It is associated with plasmid DNA.   | ABC-F ATP-binding cassette ribosomal protection protein                   | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide | Multidrug | Antibiotic target protection | 154 | 408 | 358 | 428 | 1722 | 238 | 698 | 916 | 1790 | 1012 | 1280 | 982 | 9986 |  |
| ARO:3002<br>832 | vgaD   | vgaD is an ABC-F subfamily protein expressed in Enterococcus faecium that confers resistance to streptogramin A antibiotics and  | ABC-F ATP-binding cassette ribosomal protection protein                   | antibiotic;macrolide<br>antibiotic;oxazolidinone<br>antibiotic;phenic  | Multidrug | Antibiotic target protection | 314 | 404 | 406 | 290 | 92   | 322 | 224 | 230 | 154  | 316  | 284  | 320 | 3356 |  |

|             |      |   |   |  |           |                              |      |      |      |      |     |      |      |      |     |     |     |      |       |
|-------------|------|---|---|--|-----------|------------------------------|------|------|------|------|-----|------|------|------|-----|-----|-----|------|-------|
|             |      | related compounds. It is associated with plasmid DNA.   |   | ol antibiotic;pleuro mutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic lincosamide antibiotic;macrolide          |           |                              |      |      |      |      |     |      |      |      |     |     |     |      |       |
| ARO:3002833 | vgaE | vgaE is an ABC-F subfamily protein expressed in staphylococci that confers resistance to streptogramin A antibiotics and related compounds. It is associated with transposon DNA. | ABC-F ATP-binding cassette ribosomal protection protein | antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuro mutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic | Multidrug | Antibiotic target protection | 138  | 156  | 496  | 158  | 118 | 124  | 168  | 174  | 128 | 448 | 406 | 566  | 3080  |
| ARO:3002835 | InuA | InuA is a plasmid-mediated nucleotidyltransferase found in Staphylococcus chromogenes   | lincosamide nucleotidyltransferase (LNU)                | lincosamide antibiotic   | MLS       | Antibiotic inactivation      | 52   | 22   | 54   | 28   | 0   | 86   | 36   | 36   | 12  | 10  | 32  | 4    | 372   |
| ARO:3002837 | InuC | InuC is a transposon-mediated nucleotidyltransferase found in Streptococcus agalactiae  | lincosamide nucleotidyltransferase (LNU)                | lincosamide antibiotic   | MLS       | Antibiotic inactivation      | 2442 | 2712 | 2198 | 1230 | 636 | 2470 | 1032 | 1340 | 862 | 424 | 214 | 148  | 15708 |
| ARO:3002838 | InuD | InuD is a plasmid-mediated nucleotidyltransferase found in Streptococcus uberis   | lincosamide nucleotidyltransferase (LNU)                | lincosamide antibiotic   | MLS       | Antibiotic inactivation      | 6    | 46   | 8    | 16   | 8   | 12   | 24   | 28   | 16  | 118 | 106 | 82   | 470   |
| ARO:3002839 | InuF | InuF is an integron-mediated nucleotidyltransferase found in Escherichia coli   | lincosamide nucleotidyltransferase (LNU)                | lincosamide antibiotic   | MLS       | Antibiotic inactivation      | 14   | 14   | 10   | 88   | 190 | 4    | 124  | 90   | 166 | 566 | 446 | 1002 | 2714  |
| ARO:3002840 | vatA | vatA is a plasmid-mediated acetyltransferase found in Staphylococcus aureus   | streptogramin vat acetyltransferase                     | streptogramin antibiotic   | MLS       | Antibiotic inactivation      | 36   | 172  | 60   | 22   | 16  | 114  | 20   | 18   | 18  | 0   | 6   | 0    | 482   |
| ARO:3002841 | vatB | vatB is a plasmid-mediated acetyltransferase found in Staphylococcus aureus   | streptogramin vat acetyltransferase                     | streptogramin antibiotic   | MLS       | Antibiotic inactivation      | 2014 | 1330 | 990  | 608  | 492 | 1678 | 610  | 776  | 598 | 582 | 572 | 584  | 10834 |
| ARO:3002842 | vatC | vatC is a plasmid-mediated acetyltransferase found in Staphylococcus cohnii   | streptogramin vat                                       | streptogramin antibiotic   | MLS       | Antibiotic                   | 196  | 206  | 144  | 136  | 30  | 140  | 64   | 136  | 34  | 16  | 0   | 4    | 1106  |

|                 |        |  |   |                                 |                   |                                  |     |     |     |     |      |      |      |     |      |      |      |      |       |
|-----------------|--------|--|---|---------------------------------|-------------------|----------------------------------|-----|-----|-----|-----|------|------|------|-----|------|------|------|------|-------|
| ARO:3002<br>843 | vatD   | vatD is a transposon-mediated acetyltransferase found in <i>Enterococcus faecium</i>     | acetyltransferase<br>streptogramin vat<br>acetyltransferase | streptogramin<br>antibiotic     | MLS               | Antibiotic<br>inactivation       | 40  | 140 | 248 | 78  | 1442 | 68   | 46   | 490 | 1312 | 428  | 344  | 324  | 4960  |
| ARO:3002<br>844 | vatE   | vatE is a transposon-mediated acetyltransferase found in <i>Enterococcus faecium</i>     | acetyltransferase<br>streptogramin vat<br>acetyltransferase | streptogramin<br>antibiotic     | MLS               | Antibiotic<br>inactivation       | 822 | 262 | 306 | 218 | 60   | 1210 | 152  | 220 | 176  | 318  | 200  | 226  | 4170  |
| ARO:3002<br>845 | vatH   | vatH is a plasmid-mediated acetyltransferase found in <i>Enterococcus faecium</i>        | acetyltransferase<br>streptogramin vat<br>acetyltransferase | streptogramin<br>antibiotic     | MLS               | Antibiotic<br>inactivation       | 468 | 566 | 744 | 310 | 204  | 704  | 264  | 358 | 290  | 448  | 386  | 548  | 5290  |
| ARO:3002<br>846 | arr-1  | arr-1 is a chromosome-encoded ribosyltransferase found in <i>Mycobacterium smegmatis</i> | rifampin<br>ADP-ribosyltransferase (Arr)                    | rifampin<br>antibiotic          | Rifampicin        | Antibiotic<br>inactivation       | 14  | 6   | 2   | 0   | 4    | 10   | 10   | 2   | 0    | 54   | 50   | 60   | 212   |
| ARO:3002<br>848 | arr-3  | arr-3 is a plasmid-encoded ribosyltransferase found in <i>Vibrio fluvialis</i>           | rifampin<br>ADP-ribosyltransferase (Arr)                    | rifampin<br>antibiotic          | Rifampicin        | Antibiotic<br>inactivation       | 2   | 6   | 6   | 38  | 4    | 6    | 48   | 84  | 24   | 32   | 32   | 46   | 328   |
| ARO:3002<br>849 | arr-4  | arr-4 is an integron-encoded ribosyltransferase found in <i>Pseudomonas aeruginosa</i>   | rifampin<br>ADP-ribosyltransferase (Arr)                    | rifampin<br>antibiotic          | Rifampicin        | Antibiotic<br>inactivation       | 0   | 0   | 0   | 2   | 0    | 16   | 10   | 10  | 8    | 10   | 24   | 20   | 100   |
| ARO:3002<br>853 | arr-8  | arr-8 is an integron-encoded ribosyltransferase found in <i>Klebsiella oxytoca</i>       | rifampin<br>ADP-ribosyltransferase (Arr)                    | rifampin<br>antibiotic          | Rifampicin        | Antibiotic<br>inactivation       | 0   | 0   | 0   | 0   | 0    | 0    | 0    | 0   | 0    | 8    | 2    | 2    | 12    |
| ARO:3002<br>854 | dfrA1  | dfrA1 is an integron-encoded dihydrofolate reductase                                     | trimethoprim resistant<br>dihydrofolate reductase<br>dfr    | diaminopyrimidine<br>antibiotic | Diaminopyrimidine | Antibiotic<br>target replacement | 46  | 116 | 270 | 224 | 1066 | 58   | 228  | 408 | 1102 | 2142 | 1814 | 2810 | 10284 |
| ARO:3002<br>857 | dfrA26 | dfrA26 is an integron-encoded dihydrofolate reductase found in <i>Escherichia coli</i>   | trimethoprim resistant<br>dihydrofolate reductase<br>dfr    | diaminopyrimidine<br>antibiotic | Diaminopyrimidine | Antibiotic<br>target replacement | 510 | 542 | 392 | 268 | 188  | 644  | 302  | 294 | 418  | 1532 | 1204 | 2144 | 8438  |
| ARO:3002<br>858 | dfrA12 | dfrA12 is an integron-encoded dihydrofolate reductase found in <i>Vibrio cholerae</i>    | trimethoprim resistant<br>dihydrofolate reductase<br>dfr    | diaminopyrimidine<br>antibiotic | Diaminopyrimidine | Antibiotic<br>target replacement | 480 | 196 | 174 | 900 | 384  | 56   | 1212 | 906 | 236  | 200  | 250  | 212  | 5206  |

|                 |        |  |  |                              |                   |                               |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----------------|--------|--|--|------------------------------|-------------------|-------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ARO:3002<br>859 | dfrA14 | dfrA14 is an integron-encoded dihydrofolate reductase found in <i>Escherichia coli</i>                                       | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 12  | 6   | 40  | 106 | 24  | 4   | 94  | 134 | 22  | 100 | 140 | 198 | 880  |
| ARO:3002<br>860 | dfrA17 | dfrA17 is an integron-encoded dihydrofolate reductase found in <i>Escherichia coli</i>                                       | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 0   | 0   | 24  | 30  | 54  | 0   | 120 | 50  | 46  | 94  | 140 | 204 | 762  |
| ARO:3002<br>861 | dfrA5  | dfrA5 is an integron-encoded dihydrofolate reductase found in <i>Vibrio cholerae</i>   | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 0   | 0   | 4   | 0   | 0   | 0   | 14  | 6   | 0   | 14  | 22  | 26  | 86   |
| ARO:3002<br>863 | dfrA8  | dfrA8 is a transposon-encoded dihydrofolate reductase found in <i>Salmonella enterica</i>                                    | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 224 | 54  | 6   | 6   | 2   | 86  | 14  | 10  | 4   | 0   | 2   | 2   | 410  |
| ARO:3002<br>864 | dfrB1  | A plasmid-associated trimethoprim-resistant dihydrofolate reductase detected in <i>Bordetella bronchiseptica</i> on pKBB958. | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 0   | 0   | 8   | 6   | 0   | 0   | 0   | 0   | 0   | 6   | 6   | 0   | 26   |
| ARO:3002<br>865 | dfrC   | dfrC is a chromosome-encoded dihydrofolate reductase found in <i>Staphylococcus aureus</i>                                   | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 162 | 158 | 284 | 122 | 58  | 274 | 68  | 106 | 146 | 58  | 54  | 28  | 1518 |
| ARO:3002<br>866 | dfrD   | dfrD is a plasmid-encoded dihydrofolate reductase found in <i>Listeria monocytogenes</i>                                     | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 524 | 488 | 232 | 76  | 78  | 364 | 82  | 92  | 64  | 240 | 198 | 288 | 2726 |
| ARO:3002<br>867 | dfrF   | dfrF is a chromosome-encoded dihydrofolate reductase found in <i>Streptococcus pyogenes</i>                                  | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 130 | 232 | 194 | 110 | 166 | 108 | 102 | 150 | 204 | 48  | 36  | 28  | 1508 |
| ARO:3002<br>868 | dfrG   | dfrG is a plasmid-encoded dihydrofolate reductase found in <i>Staphylococcus aureus</i>                                      | trimethoprim resistant dihydrofolate reductase dfr | diaminopyrimidine antibiotic | Diaminopyrimidine | Antibiotic target replacement | 106 | 42  | 90  | 42  | 106 | 70  | 48  | 48  | 94  | 160 | 156 | 186 | 1148 |

|                 |       |  |   |   |                   |                               |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|-------|--|---|---|-------------------|-------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002<br>869 | dfrK  | dfrK is a plasmid-encoded dihydrofolate reductase found in <i>Staphylococcus aureus</i>  | trimethoprim resistant dihydrofolate reductase dfr      | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 52   | 50   | 44   | 16   | 4    | 2    | 38   | 12   | 6    | 2    | 14   | 20   | 260   |
| ARO:3002<br>871 | tet37 | tet37 is a chromosome-encoded oxidoreductase isolated from an uncultured bacterium that confers resistance to tetracycline<br>An enzyme that confers resistance to fosfomycin in <i>Escherichia coli</i> by breaking the epoxide ring of the molecule. It depends on the cofactors Manganese (II) and Potassium and uses Glutathione (GSH) as the nucleophilic molecule. A thiol transferase that leads to the resistance of fosfomycin in <i>Enterococcus faecium</i> . | tetracycline inactivation enzyme                        | tetracycline antibiotic   | Tetracycline      | Antibiotic inactivation       | 486  | 704  | 786  | 340  | 184  | 700  | 240  | 324  | 290  | 834  | 532  | 860  | 6280  |
| ARO:3002<br>872 | FosA3 | Contrasting FosA, FosB is dependent on the cofactor Magnesium (II) and uses either bacillithiol to open up the epoxide ring of fosfomycin. FosC2 is an enzyme that phosphorylates fosfomycin to confer resistance in <i>Escherichia coli</i>   | fosfomycin thiol transferase                            | fosfomycin  | Fosfomycin        | Antibiotic inactivation       | 0    | 0    | 0    | 6    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 6     |
| ARO:3002<br>873 | FosB3 |  | fosfomycin thiol transferase                            | fosfomycin  | Fosfomycin        | Antibiotic inactivation       | 20   | 36   | 14   | 0    | 0    | 10   | 8    | 2    | 0    | 0    | 0    | 0    | 90    |
| ARO:3002<br>874 | FosC2 |  | fosC phosphotransferase family                          | fosfomycin  | Fosfomycin        | Antibiotic inactivation       | 18   | 0    | 0    | 0    | 0    | 6    | 16   | 0    | 0    | 26   | 38   | 54   | 158   |
| ARO:3002<br>875 | dfrE  | dfrE is a chromosome-encoded dihydrofolate reductase found in <i>Enterococcus faecalis</i>   | trimethoprim resistant dihydrofolate reductase dfr      | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 246  | 164  | 46   | 20   | 8    | 454  | 8    | 16   | 36   | 56   | 36   | 26   | 1116  |
| ARO:3002<br>878 | BclI  | <i>Bacillus cereus</i> beta-lactamase II is a zinc metallo-beta-lactamase that hydrolyzes a large number of penicillins and cephalosporins in the <i>Bacillus cereus</i> strain 5/B/6  | Bc beta-lactamase                                       | cephalosporin;penam   | Beta-lactam       | Antibiotic inactivation       | 2    | 0    | 2    | 0    | 4    | 2    | 0    | 0    | 20   | 2    | 20   | 14   | 66    |
| ARO:3002<br>881 | ImrC  | ImrC is an ABC-F subfamily protein that confers resistance to lincosamides in <i>Streptomyces lincolnensis</i> and <i>Lactococcus lactis</i> . It can dimerize with ImrD   | ABC-F ATP-binding cassette ribosomal protection protein | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenic | Multidrug         | Antibiotic target protection  | 4322 | 6276 | 8288 | 4200 | 3030 | 5572 | 4014 | 4590 | 4128 | 7822 | 8596 | 8168 | 69006 |

|                 |         |  |   |  |                  |   |      |      |      |      |      |      |       |      |      |      |      |      |       |  |
|-----------------|---------|--|---|--|------------------|---|------|------|------|------|------|------|-------|------|------|------|------|------|-------|--|
|                 |         |  |   | ol<br>antibiotic;pleuro<br>mutilin<br>antibiotic;strepto<br>gramin<br>antibiotic;tetracy<br>cline antibiotic |                  |   |      |      |      |      |      |      |       |      |      |      |      |      |       |  |
| ARO:3002<br>882 | ImrD    | ImrD is a chromosomally-<br>encoded efflux pump that<br>confers resistance to<br>lincosamides in Streptomyces<br>lincolnensis and Lactococcus<br>lactis. It can dimerize with ImrC | ATP-binding<br>cassette<br>(ABC)<br>antibiotic<br>efflux pump                   | lincosamide<br>antibiotic  | MLS              | Antibioti<br>c efflux                   | 9104 | 8998 | 6370 | 8428 | 7584 | 8836 | 10484 | 9454 | 7740 | 4716 | 4606 | 4780 | 91100 |  |
| ARO:3002<br>883 | rgt1438 | rgt1438 is a glycosyltransferase<br>that confers rifampin resistance<br>in Streptomyces  | rifampin<br>glycosyltrans<br>ferase   | rifamycin<br>antibiotic  | Rifamycin        | Antibioti<br>c inactivat<br>ion         | 248  | 46   | 40   | 42   | 18   | 152  | 132   | 70   | 8    | 6    | 18   | 8    | 788   |  |
| ARO:3002<br>884 | iri     | iri is a monooxygenase that<br>confers resistance to rifampin<br>found in Rhodococcus hoagii   | rifampin<br>monooxygen<br>ase   | rifamycin<br>antibiotic  | Rifamycin        | Antibioti<br>c inactivat<br>ion         | 1032 | 1604 | 328  | 1256 | 600  | 770  | 2026  | 1288 | 566  | 594  | 712  | 864  | 11640 |  |
| ARO:3002<br>891 | otr(A)  | otr(A) is an oxytetracycline<br>resistance ribosomal protection<br>protein found in Streptomyces<br>rimosus  | tetracycline-<br>resistant<br>ribosomal<br>protection<br>protein<br>major       | tetracycline<br>antibiotic   | Tetracyclin<br>e | Antibioti<br>c target<br>protecti<br>on | 5326 | 5354 | 5714 | 3892 | 4994 | 5398 | 4598  | 4274 | 4930 | 5994 | 6594 | 6392 | 63460 |  |
| ARO:3002<br>892 | otr(B)  | otr(B) is a tetracycline resistance<br>efflux pump found in<br>Streptomyces rimosus  | facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump<br>major       | tetracycline<br>antibiotic   | Tetracyclin<br>e | Antibioti<br>c efflux                   | 178  | 16   | 26   | 90   | 48   | 94   | 258   | 104  | 64   | 710  | 1040 | 928  | 3556  |  |
| ARO:3002<br>893 | tcr3    | tcr3 is a tetracycline efflux<br>pump that confers self-<br>resistance to Kitasatospora<br>aureofaciens  | facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump<br>ATP-binding | tetracycline<br>antibiotic   | Tetracyclin<br>e | Antibioti<br>c efflux                   | 582  | 178  | 386  | 1142 | 2200 | 78   | 1612  | 1462 | 1724 | 826  | 690  | 748  | 11628 |  |
| ARO:3002<br>894 | otrC    | otrC is a tetracycline resistance<br>efflux pump found in<br>Streptomyces rimosus  | cassette<br>(ABC)<br>antibiotic<br>efflux pump                                  | tetracycline<br>antibiotic   | Tetracyclin<br>e | Antibioti<br>c efflux                   | 290  | 378  | 202  | 100  | 110  | 272  | 120   | 138  | 134  | 230  | 268  | 222  | 2464  |  |
| ARO:3002<br>895 | SAT-2   | SAT-2 is a plasmid-mediated<br>streptothricin acetyltransferase,<br>which confers resistance to<br>streptothricin, a nucleoside  | streptothrici<br>n<br>acetyltransfe<br>rase (SAT)                               | nucleoside<br>antibiotic   | Nucleosid<br>e   | Antibioti<br>c inactivat<br>ion         | 124  | 302  | 58   | 114  | 110  | 162  | 92    | 86   | 84   | 106  | 94   | 182  | 1514  |  |

|                 |       |  |                         |              |                              |      |      |      |      |      |      |      |      |      |      |      |     |       |
|-----------------|-------|--|-------------------------|--------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|-----|-------|
| ARO:3002<br>897 | SAT-4 | antibiotic. Originally described from an E. coli plasmid sequence by Heim et al., 1989. SAT-4 is a plasmid-mediated streptothricin acetyltransferase and streptothricin (a nucleoside streptothricin antibiotic) resistant determinant. Originally described from a Campylobacter coli BE/G4 plasmid gene sequence by Jacob et al, 1994. SAT-3 is a plasmid-mediated streptothricin acetyltransferase and streptothricin resistance determinant. Originally described from an E. coli plasmid gene by Tietze and Brevet, 1995. | nucleoside antibiotic   | Nucleoside   | Antibiotic inactivation      | 690  | 348  | 910  | 436  | 354  | 438  | 374  | 430  | 452  | 248  | 240  | 174 | 5094  |
| ARO:3002<br>898 | SAT-3 | VanE is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity in Enterococcus faecalis. VanF is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is associated with both vancomycin and teicoplanin resistance in Paenibacillus popilliae.  | nucleoside antibiotic   | Nucleoside   | Antibiotic inactivation      | 0    | 16   | 4    | 0    | 0    | 12   | 2    | 4    | 16   | 0    | 6    | 2   | 62    |
| ARO:3002<br>907 | vanE  | VanG is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity in Enterococcus faecalis. VanL is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces  | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 732  | 752  | 844  | 376  | 246  | 956  | 286  | 388  | 424  | 612  | 622  | 662 | 6900  |
| ARO:3002<br>908 | vanF  | VanG is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity in Enterococcus faecalis. VanL is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces  | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 42   | 56   | 124  | 110  | 22   | 114  | 86   | 160  | 74   | 468  | 312  | 332 | 1900  |
| ARO:3002<br>909 | vanG  | VanL is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces  | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 2260 | 2438 | 1204 | 2550 | 1398 | 1692 | 3052 | 2616 | 1342 | 1006 | 1050 | 872 | 21480 |
| ARO:3002<br>910 | vanL  | VanL is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces  | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 1166 | 512  | 558  | 818  | 450  | 716  | 1284 | 1078 | 396  | 228  | 266  | 142 | 7614  |

|             |       |   |  |                         |              |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|-------|---|--|-------------------------|--------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002911 | vanM  | vancomycin binding affinity in <i>Enterococcus faecalis</i> . VanM is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is associated with both vancomycin and teicoplanin resistance.  | glycopeptide resistance gene cluster;van ligase        | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 118  | 304  | 198  | 76   | 18   | 242  | 92   | 78   | 40   | 154  | 268  | 158  | 1746  |
| ARO:3002912 | vanN  | VanN is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Ser, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity in <i>Enterococcus faecium</i> . VanO is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is associated with both vancomycin and teicoplanin resistance. | glycopeptide resistance gene cluster;van ligase        | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 502  | 614  | 1344 | 210  | 420  | 464  | 212  | 210  | 724  | 1106 | 850  | 1570 | 8226  |
| ARO:3002913 | vanO  | VanO is a D-Ala-D-Ala ligase homolog that can synthesize D-Ala-D-Lac, an alternative substrate for peptidoglycan synthesis that reduces vancomycin binding affinity. It is associated with both vancomycin and teicoplanin resistance.  | glycopeptide resistance gene cluster;van ligase        | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 108  | 100  | 168  | 126  | 80   | 138  | 118  | 100  | 90   | 54   | 98   | 90   | 1270  |
| ARO:3002919 | vanRA | vanRA, also known as vanR, is a vanR variant found in the vanA gene cluster   | glycopeptide resistance gene cluster;vanR glycopeptide | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 1560 | 1256 | 1108 | 1596 | 866  | 968  | 2196 | 1726 | 930  | 472  | 398  | 218  | 13294 |
| ARO:3002921 | vanRB | vanRB is a vanR variant found in the vanB gene cluster  | glycopeptide resistance gene cluster;vanR glycopeptide | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 1676 | 1488 | 1652 | 1568 | 1044 | 1576 | 1836 | 1568 | 1176 | 3748 | 3164 | 5180 | 25676 |
| ARO:3002922 | vanRC | vanRC is a vanR variant found in the vanC gene cluster  | glycopeptide resistance gene cluster;vanR glycopeptide | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 438  | 102  | 226  | 72   | 74   | 290  | 66   | 156  | 138  | 194  | 168  | 300  | 2224  |
| ARO:3002923 | vanRD | vanRD is a mutated vanR variant found in the vanD gene cluster that caused constitutive expression of vanD peptidoglycan synthesis  | glycopeptide resistance gene cluster;vanR glycopeptide | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 194  | 66   | 154  | 40   | 70   | 152  | 56   | 40   | 72   | 58   | 106  | 68   | 1076  |
| ARO:3002924 | vanRE | vanRE is a vanR variant found in the vanE gene cluster  | glycopeptide resistance                                | glycopeptide antibiotic | Glycopeptide | Antibiotic target            | 1732 | 904  | 656  | 654  | 584  | 1458 | 564  | 944  | 798  | 738  | 654  | 498  | 10184 |



|                 |       |  |  |                         |                                |      |      |      |      |      |      |      |      |      |       |      |       |       |
|-----------------|-------|--|--|-------------------------|--------------------------------|------|------|------|------|------|------|------|------|------|-------|------|-------|-------|
| ARO:3002<br>925 | vanRF | vanRF is a vanR variant found in the vanF gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 8216 | 7794 | 6122 | 3502 | 8104 | 7234 | 3604 | 5234 | 8908 | 10510 | 9236 | 12420 | 90884 |
| ARO:3002<br>926 | vanRG | vanRG is a vanR variant found in the vanG gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 1216 | 1052 | 884  | 470  | 496  | 1050 | 418  | 500  | 566  | 710   | 576  | 932   | 8870  |
| ARO:3002<br>927 | vanRL | vanRL is a vanR variant found in the vanL gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 96   | 202  | 120  | 156  | 112  | 96   | 172  | 180  | 104  | 716   | 652  | 780   | 3386  |
| ARO:3002<br>928 | vanRM | vanRM is a vanR variant found in the vanM gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 3332 | 2582 | 2058 | 1386 | 1158 | 3456 | 1396 | 1530 | 1380 | 2692  | 2684 | 3386  | 27040 |
| ARO:3002<br>929 | vanRN | vanRN is a vanR variant found in the vanN gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 102  | 216  | 388  | 142  | 80   | 204  | 220  | 128  | 140  | 164   | 106  | 62    | 1952  |
| ARO:3002<br>930 | vanRO | vanRO is a vanR variant found in the vanO gene cluster   | gene cluster;vanR glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 282  | 738  | 1468 | 1076 | 6974 | 478  | 1514 | 2192 | 6908 | 3380  | 3266 | 3298  | 31574 |
| ARO:3002<br>931 | vanSA | vanSA, also known as vanS, is a vanS variant found in the vanA gene cluster  | gene cluster;vanS glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 1890 | 1724 | 1588 | 886  | 1436 | 1612 | 1218 | 1238 | 1316 | 1940  | 2000 | 2430  | 19278 |
| ARO:3002<br>932 | vanSB | vanSB is a vanS variant found in the vanB gene cluster   | gene cluster;vanS glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 1432 | 2170 | 440  | 1554 | 628  | 1172 | 2058 | 1472 | 560  | 876   | 908  | 1142  | 14412 |
| ARO:3002<br>933 | vanSC | vanSC is a vanS variant found in the vanC gene cluster   | gene cluster;vanS glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 266  | 726  | 356  | 240  | 180  | 384  | 144  | 188  | 490  | 378   | 408  | 400   | 4160  |
| ARO:3002<br>934 | vanSD | vanSD is a mutated vanS variant found in the vanD gene cluster that caused constitutive expression of vanD peptidoglycan synthesis | gene cluster;vanS glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 4    | 32   | 42   | 10   | 12   | 20   | 14   | 14   | 4    | 8     | 26   | 8     | 194   |
| ARO:3002<br>935 | vanSE | vanSE is a vanS variant found in the vanE gene cluster   | gene cluster;vanS glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 1654 | 1286 | 1078 | 538  | 342  | 1250 | 560  | 656  | 448  | 738   | 692  | 810   | 10052 |

|                 |       |   |  |                         |                                |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|-------|---|--|-------------------------|--------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002<br>936 | vanSF | vanSF is a vanS variant found in the vanF gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 2002 | 2138 | 1078 | 780  | 524  | 2056 | 658  | 816  | 706  | 1388 | 1224 | 1546 | 14916 |
| ARO:3002<br>937 | vanSG | vanSG is a vanS variant found in the vanG gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 4186 | 4656 | 4932 | 3244 | 3282 | 3490 | 4410 | 3872 | 3882 | 2776 | 2396 | 2722 | 43848 |
| ARO:3002<br>938 | vanSL | vanSL is a vanS variant found in the vanL gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 596  | 450  | 248  | 1034 | 546  | 254  | 1298 | 1042 | 410  | 260  | 344  | 216  | 6698  |
| ARO:3002<br>939 | vanSM | vanSM is a vanS variant found in the vanM gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 2422 | 2974 | 1898 | 1762 | 858  | 1868 | 2174 | 2060 | 1182 | 764  | 570  | 540  | 19072 |
| ARO:3002<br>940 | vanSN | vanSN is a vanS variant found in the vanN gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 510  | 890  | 1458 | 930  | 5960 | 976  | 1372 | 1768 | 5946 | 5650 | 4708 | 6368 | 36536 |
| ARO:3002<br>941 | vanSO | vanSO is a vanS variant found in the vanO gene cluster                | glycopeptide resistance gene cluster;vanS glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 266  | 444  | 976  | 382  | 348  | 554  | 554  | 450  | 492  | 1024 | 1220 | 1288 | 7998  |
| ARO:3002<br>942 | vanHA | vanHA, also known as vanH, is a vanH variant in the vanA gene cluster | glycopeptide resistance gene cluster;vanH glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 1796 | 1724 | 1886 | 560  | 552  | 2222 | 570  | 654  | 1028 | 570  | 656  | 532  | 12750 |
| ARO:3002<br>943 | vanHB | vanHB is a vanH variant in the vanB gene cluster                      | glycopeptide resistance gene cluster;vanH glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 1692 | 2516 | 1626 | 1286 | 646  | 1922 | 1312 | 1228 | 864  | 4208 | 4108 | 6280 | 27688 |
| ARO:3002<br>944 | vanHD | vanHD is a vanH variant in the vanD gene cluster                      | glycopeptide resistance gene cluster;vanH glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 3244 | 3340 | 2766 | 2868 | 2986 | 2648 | 3346 | 3064 | 3054 | 3502 | 3160 | 4138 | 38116 |
| ARO:3002<br>945 | vanHF | vanHF is a vanH variant in the vanF gene cluster                      | glycopeptide resistance gene cluster;vanH glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 1530 | 2738 | 2366 | 1212 | 5150 | 2072 | 1434 | 1856 | 4484 | 2786 | 2722 | 3100 | 31450 |
| ARO:3002<br>947 | vanHM | vanHM is a vanH variant in the vanM gene cluster                      | glycopeptide resistance gene cluster;vanH glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 1348 | 1412 | 1878 | 676  | 802  | 1116 | 688  | 782  | 1044 | 414  | 390  | 294  | 10844 |
| ARO:3002<br>948 | vanHO | vanHO is a vanH variant in the vanO gene cluster                      | glycopeptide resistance                                | glycopeptide antibiotic | Glycopepti c target            | 3414 | 2690 | 2056 | 2032 | 1364 | 3880 | 2578 | 2170 | 1396 | 2110 | 2070 | 2462 | 28222 |

|             |        |   |  |                         |                                |     |      |      |     |     |     |     |     |     |     |     |     |      |
|-------------|--------|---|--|-------------------------|--------------------------------|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ARO:3002949 | vanXA  | vanXA, also known as vanX, is a vanX variant found in the vanA gene cluster | gene cluster;vanH glycopeptide resistance gene | glycopeptide antibiotic | Glycopeptide target alteration | 6   | 30   | 4    | 24  | 4   | 4   | 18  | 12  | 8   | 0   | 0   | 0   | 110  |
| ARO:3002950 | vanXB  | vanXB is a vanX variant found in the vanB gene cluster                      | cluster;vanX glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 192 | 124  | 80   | 24  | 28  | 196 | 26  | 52  | 42  | 8   | 16  | 14  | 802  |
| ARO:3002952 | vanXF  | vanXF is a vanX variant found in the vanF gene cluster                      | cluster;vanX glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 0   | 0    | 0    | 8   | 0   | 0   | 40  | 12  | 0   | 16  | 4   | 18  | 98   |
| ARO:3002953 | vanXM  | vanXM is a vanX variant found in the vanM gene cluster                      | cluster;vanX glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 104 | 418  | 220  | 110 | 88  | 250 | 124 | 106 | 122 | 46  | 64  | 12  | 1664 |
| ARO:3002954 | vanXO  | vanXO is a vanX variant found in the vanO gene cluster                      | cluster;vanX glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 398 | 122  | 250  | 228 | 86  | 218 | 288 | 224 | 144 | 94  | 126 | 50  | 2228 |
| ARO:3002955 | vanYA  | vanYA, also known as vanY, is a vanY variant found in the vanA gene cluster | cluster;vanY glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 430 | 356  | 170  | 74  | 50  | 178 | 68  | 36  | 70  | 68  | 78  | 60  | 1638 |
| ARO:3002956 | vanYB  | vanYB is a vanY variant found in the vanB gene cluster                      | cluster;vanY glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 366 | 1326 | 1426 | 626 | 378 | 738 | 542 | 584 | 498 | 296 | 180 | 154 | 7114 |
| ARO:3002958 | vanYF  | vanYF is a vanY variant found in the vanF gene cluster                      | cluster;vanY glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 202 | 468  | 194  | 160 | 86  | 176 | 220 | 214 | 120 | 128 | 50  | 42  | 2060 |
| ARO:3002959 | vanYG1 | vanYG1 is a vanY variant found in the vanG gene cluster                     | cluster;vanY glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 12  | 102  | 168  | 40  | 48  | 66  | 46  | 46  | 48  | 18  | 20  | 0   | 614  |
| ARO:3002961 | vanYM  | vanYM is a vanY variant found in the vanM gene cluster                      | cluster;vanY glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 26  | 182  | 166  | 152 | 40  | 90  | 150 | 156 | 38  | 36  | 26  | 24  | 1086 |
| ARO:3002962 | vanZA  | vanZA, also known as vanZ, is a vanZ variant found in the vanA gene cluster | cluster;vanZ glycopeptide resistance gene      | glycopeptide antibiotic | Glycopeptide target alteration | 46  | 6    | 10   | 6   | 14  | 22  | 10  | 4   | 28  | 10  | 12  | 20  | 188  |

|                 |        |   |  |                         |                                |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|--------|---|--|-------------------------|--------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3002<br>963 | vanZF  | vanZF is a vanZ variant found in the vanF gene cluster                      | glycopeptide resistance gene cluster;vanZ glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 586  | 118  | 92   | 66   | 30   | 490  | 108  | 154  | 84   | 48   | 66   | 46   | 1888  |
| ARO:3002<br>964 | vanWB  | vanWB, also known as vanW, is a vanW variant found in the vanB gene cluster | glycopeptide resistance gene cluster;vanW              | glycopeptide antibiotic | Glycopepti c target alteration | 234  | 362  | 392  | 266  | 124  | 316  | 190  | 294  | 106  | 66   | 98   | 66   | 2514  |
| ARO:3002<br>965 | vanWG  | vanWG is a vanW variant found in the vanG gene cluster                      | glycopeptide resistance gene cluster;vanW              | glycopeptide antibiotic | Glycopepti c target alteration | 230  | 364  | 220  | 194  | 206  | 280  | 118  | 208  | 228  | 152  | 78   | 50   | 2328  |
| ARO:3002<br>966 | vanXYC | vanXYC is a vanXY variant found in the vanC gene cluster                    | glycopeptide resistance gene cluster;vanX Y            | glycopeptide antibiotic | Glycopepti c target alteration | 74   | 6    | 0    | 2    | 2    | 16   | 12   | 4    | 0    | 4    | 18   | 0    | 138   |
| ARO:3002<br>967 | vanXE  | vanXE is a vanXY variant found in the vanE gene cluster                     | glycopeptide resistance gene cluster;vanX Y            | glycopeptide antibiotic | Glycopepti c target alteration | 316  | 124  | 86   | 20   | 76   | 108  | 30   | 24   | 72   | 76   | 32   | 28   | 992   |
| ARO:3002<br>968 | vanXYL | vanXYL is a vanXY variant found in the vanL gene cluster                    | glycopeptide resistance gene cluster;vanX Y            | glycopeptide antibiotic | Glycopepti c target alteration | 46   | 48   | 196  | 80   | 18   | 52   | 80   | 56   | 54   | 14   | 24   | 8    | 676   |
| ARO:3002<br>969 | vanXYN | vanXYN is a vanXY variant found in the vanN gene cluster                    | glycopeptide resistance gene cluster;vanX Y            | glycopeptide antibiotic | Glycopepti c target alteration | 66   | 110  | 338  | 188  | 62   | 148  | 134  | 146  | 72   | 274  | 280  | 290  | 2108  |
| ARO:3002<br>970 | vanTC  | vanTC is a vanT variant found in the vanC gene cluster                      | glycopeptide resistance gene cluster;vanT glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 1102 | 852  | 860  | 514  | 308  | 1348 | 450  | 660  | 462  | 676  | 740  | 698  | 8670  |
| ARO:3002<br>971 | vanTE  | vanTE is a vanT variant found in the vanE gene cluster                      | glycopeptide resistance gene cluster;vanT glycopeptide | glycopeptide antibiotic | Glycopepti c target alteration | 436  | 990  | 1146 | 138  | 396  | 720  | 166  | 106  | 398  | 362  | 500  | 516  | 5874  |
| ARO:3002<br>972 | vanTG  | vanTG is a vanT variant found in the vanG gene cluster                      | glycopeptide resistance gene cluster;vanT              | glycopeptide antibiotic | Glycopepti c target alteration | 3112 | 4972 | 3218 | 1782 | 1542 | 3772 | 1252 | 1744 | 1594 | 2176 | 2038 | 2388 | 29590 |

|                 |        |   |  |                           |                                       |       |       |       |       |       |       |       |       |       |       |       |       |        |
|-----------------|--------|---|--|---------------------------|---------------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| ARO:3002<br>974 | vanTrL | vanTrL is a vanT variant found in the vanL gene cluster. vanTrL codes for the racemase component of vanT  | glycopeptide resistance gene cluster;vanT glycopeptide           | glycopeptide antibiotic   | Glycopepti c target alteration        | 116   | 282   | 756   | 820   | 5318  | 172   | 1056  | 1520  | 4630  | 1656  | 1626  | 1454  | 19406  |
| ARO:3002<br>975 | vanTN  | vanTN is a vanT variant found in the vanN gene cluster  | glycopeptide resistance gene cluster;vanT                        | glycopeptide antibiotic   | Glycopepti c target alteration        | 470   | 522   | 340   | 132   | 84    | 694   | 276   | 138   | 126   | 234   | 200   | 204   | 3420   |
| ARO:3002<br>982 | amrA   | amrA is the efflux pump subunit of the AmrAB-OprM multidrug efflux complex. amrA corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic | Multidrug Antibioti c efflux          | 2     | 156   | 38    | 20    | 26    | 40    | 22    | 30    | 28    | 38    | 26    | 38    | 464    |
| ARO:3002<br>983 | amrB   | amrB is the membrane fusion protein of the AmrAB-OprM multidrug efflux complex.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic | Multidrug Antibioti c efflux          | 12    | 16    | 34    | 18    | 56    | 18    | 28    | 22    | 30    | 226   | 270   | 130   | 860    |
| ARO:3002<br>985 | arnA   | arnA modifies lipid A with 4-amino-4-deoxy-L-arabinose (Ara4N) which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin. arnA is found in E. coli and P. aeruginosa. | pmr phosphoethanolamine transferase                              | peptide antibiotic        | Peptide Antibioti c target alteration | 3380  | 4130  | 3342  | 2808  | 1404  | 4016  | 2856  | 2938  | 1858  | 2136  | 1806  | 2246  | 32920  |
| ARO:3002<br>986 | bacA   | The bacA gene product (BacA) recycles undecaprenyl pyrophosphate during cell wall biosynthesis which confers resistance to bacitracin.  | undecaprenyl pyrophosphate related proteins                      | peptide antibiotic        | Peptide Antibioti c target alteration | 4312  | 6050  | 5260  | 3402  | 2732  | 4930  | 4152  | 3852  | 3250  | 5068  | 4834  | 5882  | 53724  |
| ARO:3002<br>987 | bcrA   | bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance   | ATP-binding cassette (ABC) antibiotic efflux pump                | peptide antibiotic        | Peptide Antibioti c efflux            | 22656 | 18684 | 19686 | 13056 | 14480 | 23500 | 15208 | 14622 | 15230 | 14496 | 14500 | 14264 | 200382 |
| ARO:3002<br>988 | bcrB   | bcrB is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance   | ATP-binding cassette (ABC) antibiotic efflux pump                | peptide antibiotic        | Peptide Antibioti c efflux            | 174   | 178   | 138   | 60    | 38    | 232   | 28    | 56    | 28    | 8     | 2     | 20    | 962    |

|             |        |   |  |  |                   |                               |     |     |      |      |     |     |      |      |     |      |      |      |      |
|-------------|--------|---|--|--|-------------------|-------------------------------|-----|-----|------|------|-----|-----|------|------|-----|------|------|------|------|
| ARO:3002993 | AQU-1  | AQU-1 is a chromosomal class C beta-lactamase found in clinical <i>Aeromonas dhakensis</i> isolates   | AQU beta-lactamase   | cephalosporin  | Beta-lactam       | Antibiotic inactivation       | 158 | 220 | 128  | 86   | 98  | 198 | 66   | 110  | 146 | 28   | 12   | 14   | 1264 |
| ARO:3002999 | CblA-1 | CblA-1 beta-lactamase is a class A beta-lactamase found in <i>Bacteroides uniformis</i> that is species-specific.   | CblA beta-lactamase  | cephalosporin  | Beta-lactam       | Antibiotic inactivation       | 38  | 72  | 20   | 66   | 4   | 82  | 30   | 102  | 16  | 4    | 2    | 0    | 436  |
| ARO:3003002 | CfxA2  | cfxA2 beta-lactamase is a class A beta-lactamase found in <i>Prevotella intermedia</i>  | CfxA beta-lactamase  | cephamycin   | Beta-lactam       | Antibiotic inactivation       | 132 | 64  | 134  | 68   | 16  | 162 | 52   | 72   | 40  | 22   | 4    | 4    | 770  |
| ARO:3003003 | CfxA3  | cfxA3 beta-lactamase is a class A beta-lactamase found in <i>Capnocytophaga ochracea</i>  | CfxA beta-lactamase  | cephamycin   | Beta-lactam       | Antibiotic inactivation       | 414 | 570 | 898  | 248  | 202 | 544 | 194  | 336  | 350 | 48   | 34   | 36   | 3874 |
| ARO:3003006 | blt    | blt is an MFS efflux pump that confers resistance to multiple drugs such as rhodamine and acridine dyes, and fluoroquinolone antibiotics                            | major facilitator superfamily (MFS) antibiotic efflux pump       | acridine dye; fluoroquinolone antibiotic   | Multidrug         | Antibiotic efflux             | 190 | 210 | 390  | 40   | 194 | 174 | 40   | 42   | 188 | 1776 | 1346 | 2788 | 7378 |
| ARO:3003007 | bmr    | bmr is an MFS antibiotic efflux pump that confers resistance to multiple drugs including acridine dyes, fluoroquinolone antibiotics, chloramphenicol, and puromycin | major facilitator superfamily (MFS) antibiotic efflux pump       | acridine dye; fluoroquinolone antibiotic; nucleoside antibiotic; phenicol antibiotic | Multidrug         | Antibiotic efflux             | 122 | 78  | 6    | 2    | 4   | 296 | 2    | 24   | 6   | 54   | 102  | 84   | 780  |
| ARO:3003009 | ceoA   | ceoA is a periplasmic linker subunit of the CeoAB-OpcM efflux pump  | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic; fluoroquinolone antibiotic                                | Multidrug         | Antibiotic efflux             | 516 | 228 | 172  | 1014 | 482 | 120 | 1302 | 1022 | 332 | 122  | 158  | 52   | 5520 |
| ARO:3003010 | ceoB   | ceoB is a cytoplasmic membrane component of the CeoAB-OpcM efflux pump  | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic; fluoroquinolone antibiotic                                | Multidrug         | Antibiotic efflux             | 714 | 930 | 1024 | 926  | 414 | 856 | 612  | 914  | 452 | 288  | 332  | 272  | 7734 |
| ARO:3003013 | dfrA15 | dfrA15 is an integron-encoded dihydrofolate reductase found in <i>Vibrio cholerae</i>   | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic   | Diaminopyrimidine | Antibiotic target replacement | 0   | 2   | 22   | 22   | 148 | 0   | 56   | 20   | 184 | 176  | 166  | 236  | 1032 |

|             |        |   |  |   |                   |                               |      |     |     |      |     |     |      |      |     |      |      |      |       |
|-------------|--------|---|--|---|-------------------|-------------------------------|------|-----|-----|------|-----|-----|------|------|-----|------|------|------|-------|
| ARO:3003014 | dfrA16 | dfrA16 is an integron-encoded dihydrofolate reductase found in <i>Salmonella enterica</i>                               | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 20   | 292 | 126 | 148  | 724 | 36  | 214  | 166  | 730 | 440  | 416  | 478  | 3790  |
| ARO:3003016 | dfrA20 | dfrA20 is a plasmid-encoded dihydrofolate reductase found in <i>Pasteurella multocida</i>                               | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 152  | 276 | 190 | 120  | 44  | 166 | 134  | 112  | 92  | 696  | 778  | 850  | 3610  |
| ARO:3003017 | dfrA21 | dfrA21 is an integron-encoded dihydrofolate reductase found in <i>Salmonella enterica</i>                               | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 0    | 0   | 0   | 0    | 0   | 0   | 0    | 0    | 0   | 22   | 22   | 18   | 62    |
| ARO:3003018 | dfrA22 | dfrA22 is an integron-encoded dihydrofolate reductase found in <i>Salmonella enterica</i>                               | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 4    | 18  | 26  | 24   | 4   | 12  | 32   | 16   | 14  | 32   | 64   | 52   | 298   |
| ARO:3003020 | dfrA25 | dfrA25 is an integron-encoded dihydrofolate reductase found in <i>Salmonella agona</i>                                  | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 0    | 0   | 0   | 2    | 0   | 0   | 12   | 12   | 0   | 0    | 0    | 0    | 26    |
| ARO:3003021 | dfrB2  | dfrB2 is an integron-encoded dihydrofolate reductase found in an uncultured bacterium from a wastewater treatment plant | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 0    | 0   | 0   | 0    | 0   | 0   | 0    | 2    | 0   | 0    | 8    | 0    | 10    |
| ARO:3003022 | dfrB3  | dfrB3 is an integron-encoded dihydrofolate reductase found in <i>Klebsiella oxytoca</i>                                 | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 0    | 0   | 0   | 0    | 0   | 0   | 0    | 0    | 0   | 0    | 8    | 6    | 14    |
| ARO:3003023 | dfrB6  | dfrB6 is an integron-encoded dihydrofolate reductase found in <i>Salmonella enterica</i>                                | trimethoprim resistant dihydrofolate reductase dfr               | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 0    | 0   | 0   | 0    | 0   | 0   | 0    | 0    | 0   | 12   | 12   | 30   | 54    |
| ARO:3003030 | MexV   | MexV is the membrane fusion protein of the MexVW-OprM multidrug efflux complex.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye;fluoroquinolone antibiotic;macrolide antibiotic;phenicol | Multidrug         | Antibiotic efflux             | 1066 | 564 | 474 | 2056 | 902 | 112 | 3176 | 2228 | 912 | 2808 | 3168 | 3446 | 20912 |

|             |      |  |  |   |                 |                              |      |      |      |     |      |      |      |      |      |      |      |      |       |
|-------------|------|--|--|---|-----------------|------------------------------|------|------|------|-----|------|------|------|------|------|------|------|------|-------|
| ARO:3003031 | MexW | MexW is the RND-type membrane protein of the efflux complex MexVW-OprM.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | antibiotic;tetracycline antibiotic acridine dye;fluoroquinolone antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic acridine dye;aminoglycoside       | Multidrug       | Antibiotic efflux            | 2076 | 1358 | 3446 | 876 | 1222 | 1426 | 956  | 1062 | 1136 | 6092 | 6620 | 7864 | 34134 |
| ARO:3003033 | mexY | MexY is the RND-type membrane protein of the efflux complex MexXY-OprM.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | antibiotic;carbapenem;cephalosporin;cephamycin; fluoroquinolone antibiotic;macrolide antibiotic;penam;phenicol antibiotic;tetracycline antibiotic acridine dye;aminoglycoside | Multidrug       | Antibiotic efflux            | 52   | 58   | 80   | 28  | 32   | 108  | 32   | 42   | 50   | 290  | 264  | 556  | 1592  |
| ARO:3003034 | mexX | MexX is the membrane fusion protein of the MexXY-OprM multidrug efflux complex.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | antibiotic;carbapenem;cephalosporin;cephamycin; fluoroquinolone antibiotic;macrolide antibiotic;penam;phenicol antibiotic;tetracycline antibiotic                             | Multidrug       | Antibiotic efflux            | 0    | 0    | 2    | 4   | 4    | 0    | 4    | 10   | 2    | 0    | 4    | 4    | 34    |
| ARO:3003035 | mfpA | mfpA is a qnr homolog and a pentapeptide repeat protein that confers resistance to fluoroquinolones in Mycolicibacterium smegmatis | quinolone resistance protein (qnr)                               | fluoroquinolone antibiotic  | Fluoroquinolone | Antibiotic target protection | 0    | 8    | 16   | 6   | 0    | 0    | 24   | 4    | 6    | 176  | 164  | 36   | 440   |
| ARO:3003036 | oleB | oleB is an ABC-F subfamily protein in Streptomyces antibioticus and is involved in oleandomycin secretion                          | ABC-F ATP-binding cassette ribosomal                             | lincosamide antibiotic;macrolide antibiotic;oxazolidinone   | Multidrug       | Antibiotic target protection | 566  | 780  | 1118 | 978 | 2668 | 828  | 1722 | 1402 | 3072 | 3382 | 4682 | 3880 | 25078 |



|                 |      |  |   |   |           |                       |     |     |     |      |     |     |      |      |     |     |     |     |       |  |
|-----------------|------|--|---|---|-----------|-----------------------|-----|-----|-----|------|-----|-----|------|------|-----|-----|-----|-----|-------|--|
|                 |      |  | protection protein  | antibiotic;phenicol<br>antibiotic;pleuro<br>mutilin<br>antibiotic;strepto<br>gramin<br>antibiotic;tetracy<br>cline antibiotic         |           |                       |     |     |     |      |     |     |      |      |     |     |     |     |       |  |
| ARO:3003<br>037 | opcM | OpcM is an outer membrane factor protein found in Burkholderia cepacia. It is part of the CeoAB-OpcM complex.  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | aminoglycoside<br>antibiotic;fluoro<br>quinolone<br>antibiotic  | Multidrug | Antibioti<br>c efflux | 222 | 72  | 180 | 70   | 54  | 116 | 50   | 74   | 28  | 76  | 124 | 74  | 1140  |  |
| ARO:3003<br>039 | OprA | OprA is an outer membrane factor protein found in Pseudomonas aeruginosa. It is part of the MexXY-OprA complex.  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | aminoglycoside<br>antibiotic;carbap<br>enem;fluoroquin<br>olone<br>antibiotic;macrol<br>ide<br>antibiotic;tetracy<br>cline antibiotic | Multidrug | Antibioti<br>c efflux | 628 | 308 | 234 | 784  | 288 | 234 | 1146 | 814  | 268 | 508 | 500 | 402 | 6114  |  |
| ARO:3003<br>046 | qacA | qacA is a subunit of the qac multidrug efflux pump   | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump         | fluoroquinolone<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 646 | 24  | 38  | 92   | 26  | 556 | 88   | 100  | 208 | 42  | 60  | 24  | 1904  |  |
| ARO:3003<br>047 | qacB | qacB is a subunit of the qac multidrug efflux pump   | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump         | fluoroquinolone<br>antibiotic   | Multidrug | Antibioti<br>c efflux | 0   | 0   | 4   | 4    | 0   | 0   | 18   | 2    | 2   | 64  | 94  | 98  | 286   |  |
| ARO:3003<br>048 | rosA | rosA is part of an efflux pump/potassium antiporter system (RosAB) in Yersinia that confers resistance to cationic antimicrobial peptides such as polymyxin B. | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump         | peptide<br>antibiotic   | Peptide   | Antibioti<br>c efflux | 714 | 286 | 238 | 900  | 492 | 378 | 1452 | 1204 | 556 | 628 | 700 | 632 | 8180  |  |
| ARO:3003<br>049 | rosB | rosB is part of an efflux pump/potassium antiporter system (RosAB) in Yersinia that confers resistance to cationic antimicrobial peptides such as polymyxin B. | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump         | peptide<br>antibiotic   | Peptide   | Antibioti<br>c efflux | 886 | 840 | 446 | 1548 | 650 | 664 | 2224 | 1648 | 616 | 452 | 530 | 522 | 11026 |  |

|             |      |   |  |   |            |                                    |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|------|---|--|---|------------|------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003051 | smeA | smeA is the membrane fusion protein of the smeABC multidrug efflux complex in <i>Stenotrophomonas maltophilia</i> | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic;cephalosporin;cephamycin;penam  | Multidrug  | Antibiotic efflux                  | 1418 | 3208 | 3126 | 1190 | 1246 | 1854 | 918  | 1212 | 1442 | 1568 | 1254 | 1632 | 20068 |
| ARO:3003052 | smeB | smeB is the inner membrane multidrug exporter of the efflux complex smeABC in <i>Stenotrophomonas maltophilia</i> | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic;cephalosporin;cephamycin;penam  | Multidrug  | Antibiotic efflux                  | 276  | 746  | 132  | 352  | 116  | 344  | 264  | 320  | 128  | 228  | 176  | 338  | 3420  |
| ARO:3003053 | smeC | smeC is an outer membrane multidrug efflux protein of the smeABC complex in <i>Stenotrophomonas maltophilia</i>   | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminoglycoside antibiotic;cephalosporin;cephamycin;penam  | Multidrug  | Antibiotic efflux                  | 282  | 114  | 198  | 184  | 68   | 112  | 224  | 204  | 78   | 100  | 104  | 84   | 1752  |
| ARO:3003055 | smeD | smeD is the membrane fusion protein of the smeDEF multidrug efflux complex in <i>Stenotrophomonas maltophilia</i> | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic;fluoroquinolone antibiotic;macrolide antibiotic | Multidrug  | Antibiotic efflux                  | 42   | 54   | 226  | 178  | 138  | 58   | 456  | 110  | 76   | 3900 | 3252 | 5916 | 14406 |
| ARO:3003056 | smeE | smeE is the RND protein of the efflux complex smeDEF in <i>Stenotrophomonas maltophilia</i>                       | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic;fluoroquinolone antibiotic;macrolide antibiotic   | Multidrug  | Antibiotic efflux                  | 40   | 96   | 128  | 162  | 58   | 102  | 304  | 194  | 92   | 654  | 880  | 748  | 3458  |
| ARO:3003057 | smeF | smeF is an outer membrane multidrug efflux protein of the smeDEF complex in <i>Stenotrophomonas maltophilia</i>   | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic   | Multidrug  | Antibiotic efflux                  | 658  | 534  | 516  | 1182 | 570  | 420  | 1958 | 1602 | 630  | 872  | 1136 | 1128 | 11206 |
| ARO:3003059 | tmrB | tmrB is an ATP-binding tunicamycin resistance protein found in <i>Bacillus subtilis</i>                           | tunicamycin resistance protein                                   | nucleoside antibiotic   | Nucleoside | Reduced permeability to antibiotic | 30   | 2    | 0    | 0    | 0    | 22   | 0    | 18   | 0    | 8    | 8    | 26   | 114   |
| ARO:3003060 | tsnR | tsnR is a 23S ribosomal RNA methyltransferase that methylates adenosine-1067 to                                   | non-erm 23S ribosomal RNA  | peptide antibiotic  | Peptide    | Antibiotic target                  | 290  | 714  | 856  | 154  | 176  | 400  | 192  | 204  | 260  | 276  | 274  | 310  | 4106  |

|                 |        |   |   |   |  |   |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|--------|---|---|---|--|---|------|------|------|------|------|------|------|------|------|------|------|------|-------|
|                 |        | confer resistance to<br>thiostrepton  | methyltransf<br>erase<br>(A1067)<br>small<br>multidrug<br>resistance<br>(SMR)<br>antibiotic<br>efflux pump  | aminoglycoside<br>antibiotic;phenic<br>ol<br>antibiotic;tetracy<br>cline antibiotic | Multidrug                                | Antibioti<br>c efflux                   | 392  | 176  | 214  | 594  | 262  | 238  | 884  | 706  | 272  | 262  | 308  | 204  | 4512  |
| ARO:3003<br>063 | ykkC   | ykkC is an SMR-type protein<br>that is a subunit of the ykkCD<br>efflux pump  |   |   |  |   |      |      |      |      |      |      |      |      |      |      |      |      |       |
| ARO:3003<br>064 | ykkD   | ykkD is an SMR-type protein<br>that is a subunit of the ykkCD<br>efflux pump  | antibiotic<br>efflux pump<br>small<br>multidrug<br>resistance<br>(SMR)<br>antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND) | aminoglycoside<br>antibiotic;phenic<br>ol<br>antibiotic;tetracy<br>cline antibiotic | Multidrug                                | Antibioti<br>c efflux                   | 318  | 586  | 22   | 104  | 66   | 330  | 62   | 80   | 78   | 144  | 116  | 182  | 2088  |
| ARO:3003<br>066 | smeR   | smeR is the responder<br>component of a two component<br>signal transduction system that<br>includes smeS   | antibiotic<br>efflux pump<br>resistance-<br>nodulation-<br>cell division<br>(RND)   | aminoglycoside<br>antibiotic;cephal<br>osporin;cephamy<br>cin;penam                 | Multidrug                                | Antibioti<br>c efflux                   | 1662 | 2202 | 1342 | 2340 | 1454 | 1270 | 3062 | 2622 | 1422 | 1120 | 1132 | 1304 | 20932 |
| ARO:3003<br>067 | smeS   | smeS is the protein kinase<br>sensor component of a two<br>component signal transduction<br>system that includes smeR   | antibiotic<br>efflux pump<br>glycopeptide<br>resistance<br>gene<br>cluster;vanX<br>Y  | aminoglycoside<br>antibiotic;cephal<br>osporin;cephamy<br>cin;penam                 | Multidrug                                | Antibioti<br>c efflux                   | 6410 | 6574 | 6598 | 5726 | 8860 | 6040 | 7754 | 7298 | 8408 | 5816 | 6304 | 5914 | 81702 |
| ARO:3003<br>069 | vanXYG | vanXYG is a vanXY variant found<br>in the vanG gene cluster   | glycopeptide<br>resistance<br>gene<br>cluster;vanX<br>Y   | glycopeptide<br>antibiotic  | Glycopepti<br>c target<br>alteratio<br>n | Antibioti<br>c target<br>alteratio<br>n | 34   | 98   | 90   | 24   | 28   | 68   | 18   | 10   | 34   | 44   | 68   | 32   | 548   |
| ARO:3003<br>070 | vanXD  | vanXD is a vanX variant found in<br>the vanD gene cluster   | glycopeptide<br>resistance<br>gene<br>cluster;vanX<br>Y   | glycopeptide<br>antibiotic  | Glycopepti<br>c target<br>alteratio<br>n | Antibioti<br>c target<br>alteratio<br>n | 0    | 6    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 6     |
| ARO:3003<br>071 | mphF   | mphF is a macrolide<br>phosphotransferase and<br>resistance gene identified on<br>the IncP plasmid pRSB111<br>CEPH-A3 is an Ambler Class B<br>MBL; subclass B2 originally<br>isolated from Aeromonas<br>veronii. This enzyme has specific<br>activity against carbapenems<br>and is active as a mono-zinc<br>protein. | macrolide<br>phosphotran<br>sferase<br>(MPH)  | macrolide<br>antibiotic   | MLS                                      | Antibioti<br>c inactivat<br>ion         | 6    | 6    | 68   | 74   | 1244 | 2    | 166  | 92   | 828  | 546  | 706  | 598  | 4336  |
| ARO:3003<br>093 | cphA3  |   | CphA beta-<br>lactamase   | carbapenem  | Beta-<br>lactam                          | Antibioti<br>c inactivat<br>ion         | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 2    | 114  | 150  | 170  | 436   |

|             |         |  |  |   |                   |                               |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|---------|--|--|---|-------------------|-------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003096 | CfxA5   | cfxA5 beta-lactamase is a class A beta-lactamase found in <i>Bacteroides distasonis</i>  | CfxA beta-lactamase  | cephamycin  | Beta-lactam       | Antibiotic inactivation       | 8    | 44   | 48   | 26   | 8    | 32   | 12   | 30   | 12   | 10   | 0    | 0    | 230   |
| ARO:3003097 | CfxA6   | cfxA6 beta-lactamase is a class A beta-lactamase found in an uncultured bacterium  | CfxA beta-lactamase  | cephamycin  | Beta-lactam       | Antibiotic inactivation       | 136  | 346  | 220  | 84   | 16   | 228  | 68   | 90   | 76   | 4    | 4    | 4    | 1276  |
| ARO:3003105 | dfrA3   | dfrA3 is an integron-encoded dihydrofolate reductase found in <i>Escherichia coli</i>  | trimethoprim resistant dihydrofolate reductase dfr         | diaminopyrimidine antibiotic  | Diaminopyrimidine | Antibiotic target replacement | 1156 | 1328 | 1190 | 1300 | 1286 | 796  | 1784 | 1400 | 1200 | 1858 | 2118 | 2402 | 17818 |
| ARO:3003106 | Erm(42) | Erm42 confers MLSb phenotype in <i>Pasteurella multocida</i>   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide  | MLS               | Antibiotic target alteration  | 74   | 390  | 666  | 262  | 1796 | 180  | 356  | 748  | 1632 | 4314 | 3798 | 6356 | 20572 |
| ARO:3003107 | mef(B)  | mef(B) is a macrolide efflux gene located in the vicinity of sul3 in <i>Escherichia coli</i> . There is also a mefB found in <i>Streptococcus agalactiae</i> that confers resistance to macrolides.  | major facilitator superfamily (MFS) antibiotic efflux pump | macrolide antibiotic  | MLS               | Antibiotic efflux             | 142  | 70   | 32   | 368  | 166  | 84   | 510  | 334  | 130  | 46   | 82   | 24   | 1988  |
| ARO:3003109 | msrE    | MsrE is an ABC-F subfamily protein expressed to <i>Klebsiella pneumoniae</i> that confers resistance to erythromycin and streptogramin B antibiotics. It is associated with plasmid DNA. It is also 100% identical to ABC-F type ribosomal protection protein Msr(E) which is in multiple species. | ABC-F ATP-binding cassette ribosomal protection protein    | lincosamide antibiotic;macrolide<br>antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic | Multidrug         | Antibiotic target protection  | 3762 | 7446 | 728  | 1242 | 3416 | 4302 | 1292 | 1256 | 3468 | 3222 | 3066 | 4338 | 37538 |
| ARO:3003110 | catB10  | catB10 is an integron-encoded variant of the cat gene found in <i>P. aeruginosa</i>  | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic   | Phenicol          | Antibiotic inactivation       | 2    | 18   | 52   | 26   | 28   | 14   | 0    | 48   | 14   | 22   | 36   | 70   | 330   |
| ARO:3003111 | lsaB    | LsaB is an ABC-F subfamily protein expressed in <i>Staphylococcus sciuri</i> . It confers resistance to clindamycin.   | ABC-F ATP-binding cassette ribosomal                       | lincosamide antibiotic;macrolide<br>antibiotic;oxazolidinone  | Multidrug         | Antibiotic target protection  | 2612 | 4288 | 3810 | 3478 | 1786 | 3096 | 3638 | 3768 | 2130 | 1458 | 1026 | 624  | 31714 |

|             |             |  |   |   |                |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|-------------|--|---|---|----------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
|             |             |  | protection protein                                      | antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic<br>lincosamide<br>antibiotic;macrolide<br>antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuromutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic | Multidrug      | Antibiotic target protection | 3886 | 4298 | 2252 | 2404 | 1684 | 4098 | 2680 | 2610 | 2082 | 2844 | 2072 | 3226 | 34136 |
| ARO:3003112 | IsaC        | LsaC is an ABC-F subfamily protein expressed in <i>Streptococcus agalactiae</i> . It confers resistance to lincomycin, clindamycin, dalbopristin, and tiamulin                           | ABC-F ATP-binding cassette ribosomal protection protein |   |                |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
| ARO:3003115 | OXA-427     | From the Lahey list of beta-lactamases. Not yet released.  | OXA beta-lactamase                                      | cephalosporin;penam   | Beta-lactam    | Antibiotic inactivation      | 0    | 0    | 0    | 16   | 0    | 0    | 6    | 58   | 0    | 0    | 0    | 0    | 80    |
| ARO:3003171 | ACT-36      | From the Lahey list of beta-lactamases.  | ACT beta-lactamase                                      | carbapenem;cephalosporin;cephamycin;penam   | Beta-lactam    | Antibiotic inactivation      | 0    | 0    | 0    | 12   | 2    | 8    | 2    | 4    | 0    | 4    | 0    | 0    | 32    |
| ARO:3003172 | ACT-37      | From the Lahey list of beta-lactamases.  | ACT beta-lactamase                                      | carbapenem;cephalosporin;cephamycin;penam   | Beta-lactam    | Antibiotic inactivation      | 170  | 6    | 16   | 2    | 4    | 126  | 0    | 0    | 36   | 82   | 64   | 124  | 630   |
| ARO:3003183 | NDM-14      | NDM-14 is a beta-lactamase found in <i>Acinetobacter lwoffii</i> .   | NDM beta-lactamase                                      | carbapenem;cephalosporin;cephamycin;penam   | Beta-lactam    | Antibiotic inactivation      | 0    | 0    | 2    | 72   | 0    | 0    | 76   | 74   | 0    | 2    | 2    | 0    | 228   |
| ARO:3003197 | aadA25      | streptomycin/spectinomycin resistance gene found in <i>Pasteurella multocida</i> isolated from bovine respiratory tract  | ANT(3'')  | aminoglycoside antibiotic   | Aminoglycoside | Antibiotic inactivation      | 606  | 1234 | 1126 | 534  | 278  | 1118 | 294  | 572  | 450  | 144  | 70   | 40   | 6466  |
| ARO:3003200 | AAC(6')-lan | AAC(6')-lan is an amikacin acetyltransferase gene found on a transferable plasmid of the <i>Serratia marcescens</i> strain NUBL-11663. It catalyzes the transfer of an acetyl group from | AAC(6')   | aminoglycoside antibiotic   | Aminoglycoside | Antibiotic inactivation      | 70   | 2    | 34   | 32   | 0    | 38   | 30   | 28   | 4    | 6    | 0    | 0    | 244   |

|                 |         |  |   |  |             |                              |    |     |     |    |    |    |    |    |    |     |    |    |     |
|-----------------|---------|--|---|--|-------------|------------------------------|----|-----|-----|----|----|----|----|----|----|-----|----|----|-----|
| ARO:3003<br>202 | TLA-1   | acetyl coenzyme A onto an amine at the 6'-position of various aminoglycosides. TLA-1 is a beta-lactamase found in plasmids of clinical isolates of Escherichia coli strain R170 in Latin America. It preferentially hydrolyzed cephaloridine, cefotaxime, cephalothin, benzylpenicillin, and ceftazidime. The enzyme was markedly inhibited by sulbactam, tazobactam, and clavulanic acid. | TLA beta-lactamase                                      | cephalosporin; fluoroquinolone antibiotic; monobactam  | Beta-lactam | Antibiotic inactivation      | 2  | 10  | 0   | 4  | 0  | 14 | 4  | 8  | 4  | 0   | 0  | 0  | 46  |
| ARO:3003<br>203 | TLA-2   | TLA-2 is a beta-lactamase is present on a plasmid isolated from an unidentified bacterial strain from a waste water treatment plant. The enzyme mostly hydrolyzes cephalosporins.  | TLA beta-lactamase                                      | cephalosporin; fluoroquinolone antibiotic; monobactam  | Beta-lactam | Antibiotic inactivation      | 0  | 0   | 54  | 36 | 6  | 0  | 22 | 20 | 4  | 2   | 0  | 0  | 144 |
| ARO:3003<br>204 | TLA-3   | TLA-3 is a beta-lactamase found in a transferable plasmid of Serratia marcescens clinical isolate. It confers resistance to ceftazidime, cefotaxime and cefepime, but not to cefmetazole and meropenem   | TLA beta-lactamase                                      | cephalosporin; fluoroquinolone antibiotic; monobactam  | Beta-lactam | Antibiotic inactivation      | 40 | 158 | 158 | 38 | 34 | 78 | 30 | 72 | 32 | 2   | 2  | 2  | 646 |
| ARO:3003<br>205 | Erm(43) | Erm(43) is a macrolide, lincosamide, and streptogramin B resistance gene found in Staphylococcus lentus chromosome isolated from human, dog and chicken.   | Erm 23S ribosomal RNA methyltransferase                 | lincosamide antibiotic; macrolide antibiotic; streptogramin antibiotic   | MLS         | Antibiotic target alteration | 0  | 0   | 0   | 2  | 0  | 0  | 0  | 6  | 0  | 0   | 0  | 0  | 8   |
| ARO:3003<br>206 | IsaE    | IsaE is an ABC-F subfamily protein found in porcine MRSA isolates. It confers resistance to pleuromutilin, lincosamide, and streptogramin A  | ABC-F ATP-binding cassette ribosomal protection protein | lincosamide antibiotic; macrolide antibiotic; oxazolidinone antibiotic; phenicol antibiotic; pleuromutilin antibiotic; streptogramin antibiotic; tetracycline antibiotic | Multidrug   | Antibiotic target protection | 16 | 22  | 44  | 10 | 6  | 34 | 34 | 30 | 10 | 144 | 96 | 74 | 520 |

|                 |  |   |   |  |               |                               |       |       |       |       |       |       |       |       |       |       |       |       |        |
|-----------------|--|---|---|--|---------------|-------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| ARO:3003<br>207 | FosK   | FosK is a fosfomycin thiol transferase isolated from <i>Acinetobacter soli</i> . It is integron-mediated. It confers a high level of resistance to fosfomycin.  | fosfomycin thiol transferase                | fosfomycin   | Fosfomycin    | Antibiotic inactivation       | 0     | 0     | 2     | 0     | 0     | 0     | 0     | 0     | 0     | 34    | 30    | 54    | 120    |
| ARO:3003<br>250 | bcrC   | The bcrC gene product (BcrC) is an undecaprenyl pyrophosphatase originally isolated from <i>Bacillus subtilis</i> . When overexpressed it can confer resistance to bacitracin.  | undecaprenyl pyrophosphate related proteins | peptide antibiotic   | Peptide       | Antibiotic target alteration  | 0     | 0     | 0     | 0     | 0     | 0     | 6     | 0     | 0     | 0     | 0     | 0     | 6      |
| ARO:3003<br>318 | <i>Streptomyces rishirien</i> sis parY mutant conferring resistance to aminocoumarin | point mutation on the <i>Streptomyces rishirien</i> sis parY resulting in aminocoumarin resistance  | aminocoumarin resistant parY                | aminocoumarin antibiotic   | Aminocoumarin | Antibiotic target alteration  | 13148 | 16746 | 12802 | 10130 | 11774 | 14428 | 11428 | 12328 | 12870 | 16848 | 15228 | 19320 | 167050 |
| ARO:3003<br>324 | <i>Bacillus subtilis</i> mprF  | MprF is a integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface. This confers resistance to cationic peptides that disrupt the cell membrane, including defensins. Additionally, large-scale mutations causing loss of function of the gene result in increased susceptibility to daptomycin. | defensin resistant mprF                     | peptide antibiotic   | Peptide       | Antibiotic target alteration  | 0     | 0     | 30    | 0     | 0     | 0     | 0     | 0     | 2     | 2     | 6     | 0     | 40     |
| ARO:3003<br>440 | mecB   | A foreign PBP2 acquired by lateral gene transfer that able to perform peptidoglycan synthesis in the presence of beta-lactams.  | methicillin resistant PBP2                  | carbapenem;cephalosporin;cephamycin;monobactam;penam   | Beta-lactam   | Antibiotic target replacement | 1380  | 1076  | 1618  | 2234  | 4344  | 1246  | 3026  | 2894  | 4330  | 2462  | 2586  | 2640  | 29836  |
| ARO:3003<br>441 | cfrA   | CfrA is a chloramphenicol-florfenicol resistance gene and methyltransferase enzyme. Methylation of position 8 of A2503 in 23S rRNA confers resistance to chloramphenicol antibiotics first identified by  | Cfr 23S ribosomal RNA methyltransferase     | lincosamide antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic | Multidrug     | Antibiotic target alteration  | 812   | 1192  | 980   | 1524  | 856   | 700   | 2026  | 1520  | 648   | 2050  | 1930  | 2752  | 16990  |

|                 |      |  |  |                                    |              |                         |      |     |     |      |     |     |      |      |     |     |     |     |       |
|-----------------|------|--|--|------------------------------------|--------------|-------------------------|------|-----|-----|------|-----|-----|------|------|-----|-----|-----|-----|-------|
|                 |      | Schwarz 2000 as cfr from <i>Staphylococcus sciuri</i> . Additional Oxazolidinone resistance mediated by the cfr gene in a human isolated was first reported from Colombia in linezolid- and methicillin-resistant <i>Staphylococcus aureus</i> (PMID: 10952608). Described by Arias et al. 2008. Chandela T. et al. (PMID: 28663118) grouped Cfr with ClbA in the Cfr Group. |  |                                    |              |                         |      |     |     |      |     |     |      |      |     |     |     |     |       |
| ARO:3003<br>548 | mdtN | Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.  | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye;nucleoside antibiotic | Multidrug    | Antibiotic efflux       | 1192 | 642 | 534 | 1890 | 986 | 446 | 2638 | 1968 | 844 | 660 | 552 | 494 | 12846 |
| ARO:3003<br>549 | mdtO | Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride   | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye;nucleoside antibiotic | Multidrug    | Antibiotic efflux       | 424  | 198 | 108 | 940  | 558 | 38  | 1520 | 1054 | 482 | 174 | 176 | 80  | 5752  |
| ARO:3003<br>550 | mdtP | Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride   | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye;nucleoside antibiotic | Multidrug    | Antibiotic efflux       | 1032 | 380 | 242 | 1904 | 908 | 294 | 2684 | 1920 | 640 | 298 | 280 | 130 | 10712 |
| ARO:3003<br>551 | emeA | A multidrug efflux pump from <i>Enterococcus faecalis</i> . There exist efflux activity of several antimicrobial agents such as DAPI, Hoechst 33342 and acriflavine. Efflux of DAPI via EmeA was strongly inhibited by reserpine.  | multidrug and toxic compound extrusion (MATE) transporter  | acridine dye                       | Multidrug    | Antibiotic efflux       | 38   | 20  | 108 | 10   | 4   | 62  | 42   | 14   | 10  | 34  | 66  | 110 | 518   |
| ARO:3003<br>552 | fusB | FusB encodes a 2-domain zinc-binding protein that binds the ribosomal translocase EF-G, causing it to dissociate from the ribosome. This action increases the ribosomal turnover rate and confers resistance to fusidic acid.  | fusidic acid inactivation enzyme                           | fusidic acid                       | Fusidic acid | Antibiotic inactivation | 2    | 8   | 0   | 0    | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 10    |



|                 |       |  |                                     |                      |             |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|-------|--|-------------------------------------|----------------------|-------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003<br>553 | CepS  | CEPS is a typical class C cephalosporinase found in <i>Aeromonas sobria</i> , first isolated from strain 163a.   | CepS beta-lactamase                 | cephalosporin        | Beta-lactam | Antibiotic inactivation      | 0    | 24   | 14   | 0    | 10   | 6    | 0    | 0    | 10   | 6    | 4    | 8    | 82    |
| ARO:3003<br>557 | SFB-1 | This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.   | SHW beta-lactamase                  | cephalosporin; penam | Beta-lactam | Antibiotic inactivation      | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 54   | 22   | 54   | 130   |
| ARO:3003<br>559 | cepA  | A beta-lactamase found in <i>Bacteroides fragilis</i> producing either low or high levels of the endogenous cephalosporinase activity  | cepA beta-lactamase                 | cephalosporin        | Beta-lactam | Antibiotic inactivation      | 370  | 926  | 782  | 482  | 222  | 564  | 386  | 490  | 354  | 104  | 76   | 44   | 4800  |
| ARO:3003<br>563 | RCP-1 | RCP is a class A beta-lactamase found in <i>Rhodopseudomonas capsulata</i> .   | RCP beta-lactamase                  | penam                | Beta-lactam | Antibiotic inactivation      | 0    | 0    | 0    | 0    | 0    | 0    | 24   | 0    | 0    | 32   | 38   | 26   | 120   |
| ARO:3003<br>576 | eptA  | PmrC mediates the modification of Lipid A by the addition of 4-amino-4-deoxy-L-arabinose (L-Ara4N) and phosphoethanolamine, resulting in a less negative cell membrane and decreased binding of polymyxin B.   | pmr phosphoethanolamine transferase | peptide antibiotic   | Peptide     | Antibiotic target alteration | 1076 | 794  | 570  | 1254 | 706  | 408  | 1998 | 1590 | 740  | 368  | 344  | 218  | 10066 |
| ARO:3003<br>577 | ugd   | PmrE is required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A, which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin   | pmr phosphoethanolamine transferase | peptide antibiotic   | Peptide     | Antibiotic target alteration | 3268 | 3672 | 5382 | 2950 | 5352 | 3042 | 2882 | 3518 | 5254 | 3938 | 4158 | 4786 | 48202 |
| ARO:3003<br>578 | PmrF  | PmrF is required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A, which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin. pmrF corresponds to 1 locus in <i>Pseudomonas aeruginosa</i> PAO1 and 1 locus in <i>Pseudomonas aeruginosa</i> LESB58. | pmr phosphoethanolamine transferase | peptide antibiotic   | Peptide     | Antibiotic target alteration | 5112 | 4910 | 4456 | 2464 | 1836 | 5728 | 2154 | 2568 | 2042 | 1736 | 1424 | 1742 | 36172 |

|                 |             |  |   |   |                |   |      |      |      |      |      |      |      |      |      |       |       |       |       |
|-----------------|-------------|--|---|---|----------------|---|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|
| ARO:3003<br>583 | basS        | Histidine protein kinase sensor Lipid A modification gene; part of a two-component system involved in polymyxin resistance that senses high extracellular Fe(2+)   | pmr phosphoethanolamine transferase       | peptide antibiotic                        | Peptide        | Antibiotic efflux; antibiotic target alteration | 3896 | 6870 | 2734 | 4372 | 7368 | 3764 | 5950 | 5774 | 7350 | 11468 | 10406 | 15916 | 85868 |
| ARO:3003<br>605 | OXA-449     | Assigned by Lahey's list of beta-lactamases, no accessions or other information available  | OXA beta-lactamase                        | cephalosporin;penam                       | Beta-lactam    | Antibiotic inactivation                         | 0    | 0    | 30   | 36   | 4    | 0    | 20   | 50   | 4    | 4     | 0     | 0     | 148   |
| ARO:3003<br>617 | OXA-461     | Assigned by Lahey's list of beta-lactamases, no accessions or other information available  | OXA beta-lactamase                        | cephalosporin;penam                       | Beta-lactam    | Antibiotic inactivation                         | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0     | 6     | 0     | 6     |
| ARO:3003<br>620 | OXA-464     | Assigned by Lahey's list of beta-lactamases, no accessions or other information available  | OXA beta-lactamase                        | cephalosporin;penam                       | Beta-lactam    | Antibiotic inactivation                         | 0    | 0    | 6    | 0    | 8    | 0    | 0    | 0    | 4    | 98    | 38    | 68    | 222   |
| ARO:3003<br>643 | OXA-486     | Assigned by Lahey's list of beta-lactamases, no accessions or other information available  | OXA beta-lactamase                        | cephalosporin;penam                       | Beta-lactam    | Antibiotic inactivation                         | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 4     | 10    | 0     | 14    |
| ARO:3003<br>645 | OXA-488     | Assigned by Lahey's list of beta-lactamases, no accessions or other information available  | OXA beta-lactamase                        | cephalosporin;penam                       | Beta-lactam    | Antibiotic inactivation                         | 0    | 0    | 64   | 2    | 22   | 0    | 0    | 4    | 12   | 26    | 48    | 44    | 222   |
| ARO:3003<br>665 | NmcR        | NmcR is a homolog of the LysR regulator found in Enterobacter cloacae that contribute to the regulation of NmcA beta-lactamase   | NmcA beta-lactamase                       | carbapenem;cephalosporin;cephamycin;penam | Beta-lactam    | Antibiotic inactivation                         | 2558 | 1510 | 1876 | 3104 | 5474 | 1936 | 4244 | 4152 | 4936 | 4362  | 4458  | 5012  | 43622 |
| ARO:3003<br>670 | PEDO-1      | PEDO-1 is a subclass B3 metallo-beta lactamase isolated from Pedobacter roseus exhibiting resistance to carbapenems. AAC(6')-Iaj is a functional acetyltransferase that modifies the amino groups at the 6' positions of aminoglycosides and contributes to aminoglycoside resistance of P. aeruginosa | subclass B3 PEDO beta-lactamase           | carbapenem                                | Beta-lactam    | Antibiotic inactivation                         | 50   | 232  | 56   | 10   | 2    | 140  | 62   | 34   | 20   | 12    | 12    | 6     | 636   |
| ARO:3003<br>677 | AAC(6')-Iaj | AAC(6')-Iaj is a functional acetyltransferase that modifies the amino groups at the 6' positions of aminoglycosides and contributes to aminoglycoside resistance of P. aeruginosa  | AAC(6')                                   | aminoglycoside antibiotic                 | Aminoglycoside | Antibiotic inactivation                         | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 4     | 12    | 14    | 30    |
| ARO:3003<br>679 | TriA        | TriA is a membrane protein that is fused to TriB and both are required for the triclosan efflux  | resistance-nodulation-cell division (RND) | triclosan                                 | Triclosan      | Antibiotic efflux                               | 1196 | 2230 | 458  | 624  | 1478 | 1490 | 646  | 850  | 1112 | 2266  | 1766  | 3788  | 17904 |

|                 |      |  |   |   |           |                   |      |      |      |      |       |      |      |      |       |      |      |      |       |
|-----------------|------|--|---|---|-----------|-------------------|------|------|------|------|-------|------|------|------|-------|------|------|------|-------|
| ARO:3003<br>680 | TriB | pump function of TriABC-OpmH in <i>P. aeruginosa</i> .<br><br>TriB is a membrane protein that is fused to TriA and both are required for the triclosan efflux pump function of TriABC-OpmH in <i>P. aeruginosa</i> . | antibiotic efflux pump resistance-nodulation-cell division (RND) antibiotic efflux pump resistance-nodulation-cell division (RND) | triclosan   | Triclosan | Antibiotic efflux | 276  | 28   | 218  | 90   | 34    | 196  | 72   | 124  | 78    | 188  | 372  | 308  | 1984  |
| ARO:3003<br>681 | TriC | TriC is a resistance nodulation-cell division (RND) transporter that is a part of TriABC-OpmH, a triclosan-specific efflux protein.  | antibiotic efflux pump resistance-nodulation-cell division (RND)  | triclosan   | Triclosan | Antibiotic efflux | 370  | 384  | 1158 | 810  | 5284  | 332  | 1192 | 1090 | 5068  | 2624 | 2336 | 3072 | 23720 |
| ARO:3003<br>682 | OpmH | OpmH is an outer membrane efflux protein required for triclosan-specific efflux pump function.   | antibiotic efflux pump resistance-nodulation-cell division (RND)  | triclosan   | Triclosan | Antibiotic efflux | 1070 | 2078 | 1080 | 912  | 5928  | 1202 | 1304 | 1690 | 5398  | 6368 | 5868 | 8934 | 41832 |
| ARO:3003<br>692 | MexJ | mexJ is the membrane fusion protein of the MexJK multidrug efflux protein.   | antibiotic efflux pump resistance-nodulation-cell division (RND)  | macrolide antibiotic;tetracycline antibiotic;triclosan  | Multidrug | Antibiotic efflux | 1102 | 2594 | 2488 | 1842 | 12350 | 1522 | 2186 | 3150 | 11656 | 5872 | 5480 | 6376 | 56618 |
| ARO:3003<br>693 | MexK | mexK is the inner membrane resistance-nodulation-cell division (RND) transporter in the MexJK multidrug efflux protein.  | antibiotic efflux pump resistance-nodulation-cell division (RND)  | macrolide antibiotic;tetracycline antibiotic;triclosan  | Multidrug | Antibiotic efflux | 1460 | 2616 | 1594 | 1402 | 4430  | 1616 | 1840 | 2032 | 3984  | 6640 | 6206 | 8738 | 42558 |
| ARO:3003<br>698 | mexP | MexP is the membrane fusion protein of the MexPQ-OpmE multidrug efflux complex   | antibiotic efflux pump resistance-nodulation-cell division (RND)  | acridine dye;carbapenem;diaminopyrimidine antibiotic;macrolide antibiotic;phenicol antibiotic;tetracycline antibiotic | Multidrug | Antibiotic efflux | 36   | 158  | 198  | 92   | 84    | 76   | 70   | 72   | 84    | 90   | 110  | 118  | 1188  |
| ARO:3003<br>699 | mexQ | MexQ is the inner membrane transporter of the multidrug efflux pump MexPQ-OpmE.  | resistance-nodulation-cell division (RND)   | acridine dye;carbapenem;diaminopyrimidine antibiotic;macrol   | Multidrug | Antibiotic efflux | 44   | 122  | 100  | 96   | 16    | 70   | 112  | 104  | 22    | 1270 | 828  | 1272 | 4056  |

|                 |        |   |  |   |             |                         |     |      |     |     |     |     |     |     |     |      |      |      |       |
|-----------------|--------|---|--|---|-------------|-------------------------|-----|------|-----|-----|-----|-----|-----|-----|-----|------|------|------|-------|
| ARO:3003<br>700 | opmE   | opmE is an outer membrane factor protein that is part of the multidrug efflux pump MexPQ-OpmE.                          | antibiotic efflux pump<br>antibiotic;phenicol<br>antibiotic;tetracycline antibiotic<br>acridine dye;carbapenem resistance-;diaminopyrimidine<br>nodulation-cell division (RND)<br>antibiotic efflux pump | antibiotic;macrolide<br>antibiotic;phenicol<br>antibiotic;tetracycline antibiotic | Multidrug   | Antibiotic efflux       | 98  | 38   | 110 | 44  | 24  | 50  | 36  | 78  | 22  | 366  | 388  | 442  | 1696  |
| ARO:3003<br>704 | mexM   | mexM is the membrane fusion protein of the MexMN-OprM multidrug efflux complex.   | antibiotic efflux pump<br>resistance-nodulation-cell division (RND)<br>antibiotic efflux pump  | phenicol antibiotic   | Multidrug   | Antibiotic efflux       | 184 | 120  | 112 | 70  | 288 | 144 | 94  | 108 | 408 | 900  | 642  | 1002 | 4072  |
| ARO:3003<br>705 | mexN   | MexN is the inner membrane transporter of the MexMN-OprM multidrug efflux complex.                                      | antibiotic efflux pump<br>resistance-nodulation-cell division (RND)<br>antibiotic efflux pump  | phenicol antibiotic   | Multidrug   | Antibiotic efflux       | 352 | 480  | 468 | 328 | 500 | 410 | 384 | 392 | 428 | 3982 | 3440 | 5376 | 16540 |
| ARO:3003<br>710 | MexL   | MexL is a specific repressor of mexJK transcription and autoregulates its own expression.                               | antibiotic efflux pump<br>resistance-nodulation-cell division (RND)<br>antibiotic efflux pump  | macrolide antibiotic;tetracycline antibiotic;triclosan                            | Multidrug   | Antibiotic efflux       | 712 | 1566 | 440 | 428 | 874 | 888 | 450 | 480 | 730 | 1984 | 2182 | 2540 | 13274 |
| ARO:3003<br>714 | PEDO-2 | PEDO-2 is a subclass B3 metallo-beta lactamase isolated from Pedobacter borealis exhibiting carbapenem resistance.      | subclass B3 PEDO beta-lactamase  | carbapenem  | Beta-lactam | Antibiotic inactivation | 68  | 14   | 14  | 76  | 30  | 36  | 54  | 106 | 26  | 16   | 20   | 4    | 464   |
| ARO:3003<br>715 | PEDO-3 | PEDO-3 is a class B1 metallo-beta lactamase isolated from Pedobacter kyunghensis exhibiting resistance to carbapenems.  | subclass B1 PEDO beta-lactamase  | carbapenem  | Beta-lactam | Antibiotic inactivation | 0   | 0    | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 86   | 120  | 122  | 328   |
| ARO:3003<br>717 | ESP-1  | ESP-1 is a subclass B3 metallo-beta lactamase isolated from Epilithonimonas tenax conferring resistance to carbapenems. | ESP beta-lactamase   | carbapenem  | Beta-lactam | Antibiotic inactivation | 0   | 8    | 4   | 2   | 4   | 4   | 0   | 0   | 18  | 6    | 4    | 6    | 56    |

|                 |  |  |   |                         |              |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|--|--|---|-------------------------|--------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003<br>718 | MSI-1  | MSI-1 is a subclass B3 metallo-beta lactamase isolated from <i>Massilia oculi</i> conferring resistance to carbapenems.  | MSI beta-lactamase                                    | carbapenem              | Beta-lactam  | Antibiotic inactivation      | 86   | 96   | 216  | 188  | 68   | 174  | 128  | 118  | 42   | 40   | 60   | 32   | 1248  |
| ARO:3003<br>720 | SPG-1  | SPG-1 is a subclass B3 metallo-beta lactamase isolated from <i>Sphingomonas</i> sp.  | SPG beta-lactamase                                    | carbapenem              | Beta-lactam  | Antibiotic inactivation      | 10   | 48   | 8    | 12   | 8    | 20   | 14   | 18   | 2    | 32   | 16   | 16   | 204   |
| ARO:3003<br>723 | vanI   | VanI is a D-Ala-D-Lac ligase that reduces vancomycin binding affinity, helping to confer vancomycin resistance as part of the VanI resistance gene cluster in <i>Desulfitobacterium</i> spp. and <i>Desulfosporosinus</i> spp. | glycopeptide resistance gene cluster; van ligase      | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 116  | 124  | 138  | 136  | 140  | 66   | 190  | 174  | 114  | 164  | 132  | 152  | 1646  |
| ARO:3003<br>724 | vanWI  | VanWI is a vanW variant found in the vanI gene cluster   | glycopeptide resistance gene cluster; vanW            | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 586  | 494  | 1016 | 668  | 322  | 782  | 676  | 664  | 450  | 708  | 586  | 524  | 7476  |
| ARO:3003<br>725 | vanXI  | VanXI is a vanX variant found in the VanI glycopeptide resistance gene cluster. It is a D-Ala-D-Ala dipeptidase.   | glycopeptide resistance gene cluster; vanX            | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 280  | 328  | 614  | 4    | 154  | 180  | 12   | 18   | 172  | 12   | 26   | 16   | 1816  |
| ARO:3003<br>727 | vanKI  | VanKI is a peptidoglycan bridge formation protein also known as FemAB that is part of the VanI glycopeptide resistance gene cluster.   | glycopeptide resistance gene cluster; vanK            | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 22   | 344  | 68   | 96   | 36   | 78   | 66   | 80   | 42   | 14   | 8    | 6    | 860   |
| ARO:3003<br>728 | vanRI  | VanRI is the regulatory transcriptional activator in the VanSR regulator within the VanI glycopeptide resistance gene cluster.   | glycopeptide resistance gene cluster; vanR            | glycopeptide antibiotic | Glycopeptide | Antibiotic target alteration | 3782 | 5120 | 3182 | 2368 | 1752 | 3284 | 2696 | 2500 | 1702 | 2412 | 2176 | 2422 | 33396 |
| ARO:3003<br>730 | <i>Bifidobacterium</i> ileS conferring resistance to mupirocin | <i>Bifidobacteria</i> have an intrinsically resistant form of ileS (isoleucyl-tRNA synthetase) that confers resistance to mupirocin.   | antibiotic-resistant isoleucyl-tRNA synthetase (ileS) | mupirocin               | Mupirocin    | Antibiotic target alteration | 1528 | 800  | 906  | 660  | 492  | 1150 | 698  | 702  | 656  | 810  | 1310 | 770  | 10482 |
| ARO:3003<br>733 | fusC   | FusC is a fusidic acid resistance gene enabling ribosomal translocase EF-G dissociation from the ribosome that has   | fusidic acid inactivation enzyme                      | fusidic acid            | Fusidic acid | Antibiotic inactivation      | 48   | 2    | 0    | 0    | 0    | 14   | 0    | 0    | 0    | 0    | 2    | 0    | 66    |

|             |       |  |  |  |           |                              |      |       |       |      |       |       |      |       |       |       |       |       |        |
|-------------|-------|--|--|--|-----------|------------------------------|------|-------|-------|------|-------|-------|------|-------|-------|-------|-------|-------|--------|
|             |       | been detected in <i>Staphylococcus aureus</i> and <i>Staphylococcus intermedius</i> . Its mechanism is believed to be similar to <i>fusB</i> due to its high level of sequence homology.   |  |  |           |                              |      |       |       |      |       |       |      |       |       |       |       |       |        |
| ARO:3003741 | mphE  | mphE is a macrolide phosphotransferase and resistance gene identified on a plasmid, pRSB105  | macrolide phosphotransferase (MPH)   | macrolide antibiotic   | MLS       | Antibiotic inactivation      | 3500 | 8130  | 590   | 1212 | 3140  | 4098  | 1114 | 1220  | 3046  | 6082  | 4860  | 8146  | 45138  |
| ARO:3003742 | mphG  | The mphG gene encodes a macrolide 2'-phosphotransferase found in <i>Photobacterium damsela</i> sharing sequence similarity to mphA in <i>E. coli</i> .   | macrolide phosphotransferase (MPH)   | macrolide antibiotic   | MLS       | Antibiotic inactivation      | 2    | 12    | 24    | 10   | 40    | 0     | 46   | 8     | 26    | 474   | 334   | 492   | 1468   |
| ARO:3003744 | vatF  | vatF is a streptogramin A acetyltransferase gene isolated from the chromosome of <i>Yersinia enterocolitica</i> .  | streptogramin vat acetyltransferase major facilitator superfamily (MFS) antibiotic efflux pump | streptogramin antibiotic   | MLS       | Antibiotic inactivation      | 736  | 1628  | 576   | 442  | 1260  | 904   | 342  | 834   | 1148  | 920   | 862   | 1072  | 10724  |
| ARO:3003745 | mefC  | mefC is a macrolide efflux gene isolated from a plasmid in <i>Photobacterium damsela</i> .   | antibiotic efflux pump   | macrolide antibiotic   | MLS       | Antibiotic efflux            | 280  | 630   | 232   | 80   | 84    | 422   | 114  | 164   | 80    | 826   | 564   | 738   | 4214   |
| ARO:3003746 | optrA | Optra is a member of the ABC-F protein subfamily that confers resistance to oxazolidinones. The gene encoding the protein was originally isolated from a plasmid in <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> . | ABC-F ATP-binding cassette ribosomal protection protein  | lincosamide antibiotic; macrolide antibiotic; oxazolidinone antibiotic; phenicol antibiotic; pleuromutilin antibiotic; streptogramin antibiotic; tetracycline antibiotic | Multidrug | Antibiotic target protection | 9408 | 10976 | 11092 | 7732 | 9312  | 10010 | 8936 | 9436  | 10108 | 12988 | 12400 | 15096 | 127494 |
| ARO:3003748 | oleC  | oleC is an ABC transporter isolated from <i>Streptomyces antibioticus</i> and is involved in oleandomycin secretion.   | ATP-binding cassette (ABC) antibiotic efflux pump  | macrolide antibiotic   | MLS       | Antibiotic efflux            | 8042 | 7810  | 11676 | 7094 | 20156 | 8550  | 9290 | 10138 | 20622 | 13974 | 14650 | 14546 | 146548 |
| ARO:3003749 | salA  | salA is an ABC-F subfamily protein gene isolated from the chromosome of <i>Staphylococcus</i>  | ABC-F ATP-binding cassette   | lincosamide antibiotic; macrolide  | Multidrug | Antibiotic target            | 790  | 1012  | 548   | 450  | 230   | 914   | 280  | 414   | 326   | 828   | 826   | 1100  | 7718   |

|             |                              |   |  |  |            |                              |     |     |     |     |     |     |     |     |     |     |    |     |      |
|-------------|------------------------------|---|--|--|------------|------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|------|
|             |                              | sciuri conferring resistance to lincosamides and streptogramins.  | ribosomal protection protein             | antibiotic;oxazolidinone<br>antibiotic;phenicol<br>antibiotic;pleuro mutilin<br>antibiotic;streptogramin<br>antibiotic;tetracycline antibiotic | protection |                              |     |     |     |     |     |     |     |     |     |     |    |     |      |
| ARO:3003762 | InuE                         | InuE encodes a lincosamide resistance gene isolated from Streptococcus suis that was truncated by an ISEnf5-cfr-ISEnf5 segment insertion. It shares the closest sequence similarity to InuA.                              | lincosamide nucleotidyltransferase (LNU) | lincosamide antibiotic   | MLS        | Antibiotic inactivation      | 268 | 570 | 460 | 306 | 158 | 504 | 230 | 270 | 180 | 120 | 64 | 52  | 3182 |
| ARO:3003767 | mphM                         | mphM is a chromosomally-encoded macrolide phosphotransferases that inactivate 14-, 15- and 16-membered macrolides.  | macrolide phosphotransferase (MPH)       | macrolide antibiotic   | MLS        | Antibiotic inactivation      | 14  | 38  | 32  | 50  | 6   | 78  | 36  | 64  | 66  | 74  | 70 | 100 | 628  |
| ARO:3003770 | Listeria monocytogenes mprF  | MprF is an integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface. This confers resistance to cationic peptides that disrupt the cell membrane, including defensins. | defensin resistant mprF                  | peptide antibiotic   | Peptide    | Antibiotic target alteration | 72  | 66  | 4   | 0   | 10  | 162 | 12  | 4   | 120 | 28  | 26 | 8   | 512  |
| ARO:3003772 | Brucella suis mprF           | MprF is an integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface. This confers resistance to cationic peptides that disrupt the cell membrane, including defensins. | defensin resistant mprF                  | peptide antibiotic   | Peptide    | Antibiotic target alteration | 218 | 14  | 40  | 0   | 12  | 222 | 58  | 8   | 34  | 2   | 8  | 4   | 620  |
| ARO:3003773 | Clostridium perfringens mprF | MprF is an integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface. This confers resistance to cationic peptides that disrupt the cell membrane, including defensins. | defensin resistant mprF                  | peptide antibiotic   | Peptide    | Antibiotic target alteration | 0   | 18  | 4   | 0   | 6   | 26  | 0   | 0   | 4   | 2   | 16 | 2   | 78   |

|             |  |  |  |   |              |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|--|--|--|---|--------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003774 | Streptococcus agalactiae mprF                                  | MprF is a integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface. This confers resistance to cationic peptides that disrupt the cell membrane, including defensins.                                 | defensin resistant mprF  | peptide antibiotic                      | Peptide      | Antibiotic target alteration | 0    | 0    | 6    | 2    | 2    | 0    | 4    | 12   | 4    | 16   | 50   | 12   | 108   |
| ARO:3003785 | Chlamydia trachomatis murA conferring resistance to fosfomycin | Chlamydia murA confers intrinsic resistance to fosfomycin. The presence of an aspartic acid residue in place of the critical cysteine at position 119 that enables fosfomycin binding is believed to be responsible for this intrinsic resistance.       | antibiotic-resistant murA transferase                            | fosfomycin                              | Fosfomycin   | Antibiotic target alteration | 5530 | 7940 | 5304 | 3764 | 2732 | 6718 | 4240 | 4020 | 3186 | 5282 | 5090 | 6628 | 60434 |
| ARO:3003801 | bcr-1  | Transmembrane protein which expels bicyclomycin from the cell, leading to bicyclomycin resistance. Identified in Pseudomonas aeruginosa strains responsible for outbreaks in Brazil, often appearing with blaSPM-1, another bicyclomycin resistance gene | major facilitator superfamily (MFS) antibiotic efflux pump       | bicyclomycin                            | Bicyclomycin | Antibiotic efflux            | 2420 | 2100 | 1108 | 2168 | 1638 | 2028 | 3064 | 2276 | 1732 | 2522 | 2654 | 3516 | 27226 |
| ARO:3003811 | adeC   | AdeC is the outer membrane factor of the AdeABC multidrug efflux complex. It can be replaced by other outer membrane channels, and is not essential for antibiotic resistance.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | glycylcycline;tetracycline antibiotic   | Multidrug    | Antibiotic efflux            | 0    | 0    | 10   | 0    | 2    | 14   | 20   | 0    | 0    | 452  | 282  | 286  | 1066  |
| ARO:3003835 | cdeA   | Clostridioides difficile and Escherichia coli multidrug efflux transporter with antiporter function. Confers resistance to fluoroquinolones in E. coli and acriflavin in Clostridioides difficile.   | multidrug and toxic compound extrusion (MATE) transporter        | acridine dye;fluoroquinolone antibiotic | Multidrug    | Antibiotic efflux            | 1420 | 2338 | 2550 | 884  | 998  | 1722 | 948  | 998  | 1238 | 1142 | 776  | 866  | 15880 |
| ARO:3003836 | qacH   | qacH is a subunit of the qac multidrug efflux pump in Vibrio cholerae  | small multidrug resistance                                       | fluoroquinolone antibiotic              | Multidrug    | Antibiotic efflux            | 112  | 390  | 382  | 614  | 1152 | 68   | 1122 | 916  | 1418 | 4602 | 4464 | 6576 | 21816 |



|                 |        |   |  |                                      |                |                         |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|--------|---|--|--------------------------------------|----------------|-------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
|                 |        |   | (SMR)<br>antibiotic<br>efflux pump                               |                                      |                |                         |      |      |      |      |      |      |      |      |      |      |      |      |       |
| ARO:3003<br>838 | gadW   | GadW is an AraC-family regulator that promotes mdtEF expression to confer multidrug resistance. GadW inhibits GadX-dependent activation. GadW clearly represses gadX and, in situations where GadX is missing, activates gadA and gadBC.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide | Multidrug      | Antibiotic efflux       | 860  | 226  | 184  | 1414 | 650  | 150  | 1950 | 1758 | 552  | 232  | 270  | 66   | 8312  |
| ARO:3003<br>841 | kdpE   | kdpE is a transcriptional activator that is part of the two-component system KdpD/KdpE that is studied for its regulatory role in potassium transport and has been identified as an adaptive regulator involved in the virulence and intracellular survival of pathogenic bacteria. kdpE regulates a range of virulence loci through direct promoter binding. | kdpDE  | aminoglycoside antibiotic            | Aminoglycoside | Antibiotic efflux       | 3560 | 3854 | 3178 | 2758 | 1738 | 3256 | 3464 | 3158 | 2052 | 2548 | 2278 | 2606 | 34450 |
| ARO:3003<br>842 | MUS-2  | MUS-2 is a chromosome-encoded beta-lactamase from Myroides odoratimimus.  | MUS beta-lactamase   | carbapenem                           | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 0    | 4    | 0    | 0    | 68   | 4    | 0    | 0    | 0    | 0    | 76    |
| ARO:3003<br>852 | ADC-6  | ADC-6 is a beta-lactamase found in Acinetobacter baumannii.   | ADC beta-lactamase without carbapenemase activity                | cephalosporin                        | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 0    | 2    | 0    | 0    | 20   | 2    | 0    | 2    | 0    | 0    | 26    |
| ARO:3003<br>862 | ADC-18 | ADC-18 is a beta-lactamase found in Acinetobacter pittii.   | ADC beta-lactamase without carbapenemase activity                | cephalosporin                        | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 6    | 8    | 10   | 0    | 12   | 12   | 6    | 82   | 88   | 40   | 264   |
| ARO:3003<br>863 | ADC-19 | ADC-19 is a beta-lactamase found in Acinetobacter pittii.   | ADC beta-lactamase without carbapenemase activity                | cephalosporin                        | Beta-lactam    | Antibiotic inactivation | 0    | 2    | 2    | 2    | 0    | 8    | 2    | 0    | 0    | 2    | 0    | 0    | 18    |
| ARO:3003<br>867 | ADC-23 | ADC-23 is a beta-lactamase found in Acinetobacter pittii.   | ADC beta-lactamase without                                       | cephalosporin                        | Beta-lactam    | Antibiotic inactivation | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 4    | 18   | 4    | 26    |

|                 |                |  |   |  |                    |   |      |     |     |      |      |     |      |      |     |      |      |      |       |  |
|-----------------|----------------|--|---|--|--------------------|---|------|-----|-----|------|------|-----|------|------|-----|------|------|------|-------|--|
|                 |                |  |   | carbapenem<br>ase activity   |                    |   |      |     |     |      |      |     |      |      |     |      |      |      |       |  |
| ARO:3003<br>905 | ANT(4')-<br>lb | Kanamycin<br>nucleotidyltransferase sequence<br>from Staphylococcus aureus<br>plasmid. Confers resistance to<br>kanamycin, neomycin and other<br>aminoglycosides | ANT(4')   | aminoglycoside<br>antibiotic   | Aminoglyc<br>oside | Antibioti<br>c inactivat<br>ion         | 40   | 122 | 52  | 2    | 80   | 132 | 12   | 10   | 58  | 344  | 496  | 448  | 1796  |  |
| ARO:3003<br>907 | cipA           | Cfr-like methyltransferase<br>enzyme conferring resistance to<br>multiple clinically relevant<br>antibiotic classes.   | Cfr 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase                              | lincosamide<br>antibiotic;phenic<br>ol<br>antibiotic;pleuro<br>mutilin<br>antibiotic;strepto<br>gramin antibiotic    | Multidrug          | Antibioti<br>c target<br>alteratio<br>n | 236  | 312 | 192 | 332  | 224  | 336 | 406  | 292  | 506 | 556  | 1100 | 594  | 5086  |  |
| ARO:3003<br>908 | Erm(47)        | Chromosome-encoded gene<br>conferring MLSB resistance.<br>Identified from Helcococcus<br>kunzii.   | Erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase                              | lincosamide<br>antibiotic;macrol<br>ide<br>antibiotic;strepto<br>gramin antibiotic                                   | MLS                | Antibioti<br>c target<br>alteratio<br>n | 570  | 552 | 486 | 64   | 94   | 634 | 92   | 134  | 142 | 138  | 114  | 60   | 3080  |  |
| ARO:3003<br>918 | apmA           | Plasmid-borne apramycin-<br>resistant aminocyclitol<br>acetyltransferase gene<br>identified from bovine MRSA.  | amp<br>acetyltransfe<br>rase  | aminoglycoside<br>antibiotic   | Aminoglyc<br>oside | Antibioti<br>c inactivat<br>ion         | 306  | 378 | 210 | 168  | 194  | 266 | 138  | 246  | 176 | 296  | 166  | 138  | 2682  |  |
| ARO:3003<br>920 | pgpB           | A gene that produces the<br>protein lipid A 4'-phosphatase   | lipid A<br>phosphatase  | peptide<br>antibiotic  | Peptide            | Antibioti<br>c target<br>alteratio<br>n | 192  | 232 | 204 | 86   | 70   | 244 | 50   | 96   | 64  | 462  | 352  | 666  | 2718  |  |
| ARO:3003<br>922 | oqxA           | RND efflux pump conferring<br>resistance to fluoroquinolone  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | diaminopyrimidi<br>ne<br>antibiotic;fluoro<br>quinolone<br>antibiotic;glycyl<br>cine;nitrofurant<br>cline antibiotic | Multidrug          | Antibioti<br>c efflux                   | 1246 | 920 | 822 | 1460 | 918  | 842 | 1874 | 1650 | 792 | 2906 | 2136 | 3952 | 19518 |  |
| ARO:3003<br>923 | oqxB           | RND efflux pump conferring<br>resistance to fluoroquinolone  | resistance-<br>nodulation-<br>cell division<br>(RND)<br>antibiotic<br>efflux pump | antibiotic;fluoro<br>quinolone<br>antibiotic;glycyl<br>cine;nitrofurant<br>cline antibiotic                          | Multidrug          | Antibioti<br>c efflux                   | 1018 | 796 | 680 | 1988 | 1070 | 296 | 3124 | 3124 | 932 | 1594 | 1612 | 2028 | 18262 |  |
| ARO:3003<br>942 | abcA           | AbcA is a multidrug resistant<br>ABC transporter that confers<br>resistance to methicillin,  | ATP-binding<br>cassette<br>(ABC)  | cephalosporin;pe<br>nam;peptide<br>antibiotic  | Multidrug          | Antibioti<br>c efflux                   | 234  | 496 | 376 | 138  | 114  | 358 | 110  | 140  | 178 | 1416 | 1354 | 1602 | 6516  |  |

|                 |      |   |  |   |           |                   |       |       |       |           |       |       |       |       |       |       |       |       |        |
|-----------------|------|---|--|---|-----------|-------------------|-------|-------|-------|-----------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| ARO:3003<br>948 | efrA | daptomycin, cefotaxime, and moenomycin.<br><br>efrA is a part of the EfrAB efflux pump, and both efrA and efrB are necessary to confer drug resistance.   | antibiotic efflux pump<br>ATP-binding cassette (ABC)<br>antibiotic efflux pump | fluoroquinolone antibiotic;macrolide<br>antibiotic;rifamycin antibiotic | Multidrug | Antibiotic efflux | 12022 | 9976  | 9344  | 6834      | 8696  | 12718 | 8478  | 8498  | 9484  | 6038  | 5760  | 4940  | 102788 |
| ARO:3003<br>949 | efrB | efrB is a part of the EfrAB efflux pump, and both efrA and efrB are necessary to confer multidrug resistance.   | ATP-binding cassette (ABC)<br>antibiotic efflux pump                           | fluoroquinolone antibiotic;macrolide<br>antibiotic;rifamycin antibiotic | Multidrug | Antibiotic efflux | 2582  | 3130  | 3714  | 2460      | 3400  | 2742  | 2944  | 2806  | 3788  | 7214  | 5942  | 8682  | 49404  |
| ARO:3003<br>950 | msbA | MsbA is a multidrug resistance transporter homolog from E. coli and belongs to a superfamily of transporters that contain an adenosine triphosphate (ATP) binding cassette (ABC) which is also called a nucleotide-binding domain (NBD). MsbA is a member of the MDR-ABC transporter group by sequence homology. MsbA transports lipid A, a major component of the bacterial outer cell membrane, and is the only bacterial ABC transporter that is essential for cell viability. | ATP-binding cassette (ABC)<br>antibiotic efflux pump                           | nitroimidazole antibiotic   | Multidrug | Antibiotic efflux | 23286 | 19502 | 14692 | 1742<br>2 | 21564 | 21232 | 23002 | 21012 | 21140 | 22716 | 22970 | 26294 | 254832 |
| ARO:3003<br>952 | Yojl | Yojl mediates resistance to the peptide antibiotic microcin J25 when it is expressed from a multicopy vector. Yojl is capable of pumping out microcin molecules. The outer membrane protein TolC in addition to Yojl is required for export of microcin J25 out of the cell. Microcin J25 is thus the first known substrate for Yojl.   | ATP-binding cassette (ABC)<br>antibiotic efflux pump                           | peptide antibiotic  | Peptide   | Antibiotic efflux | 3418  | 2798  | 2408  | 3494      | 1920  | 2918  | 5014  | 4292  | 2424  | 1416  | 1524  | 1072  | 32698  |
| ARO:3003<br>953 | hmrM | hmrM is a multidrug efflux pump belonging to the MATE family and functions as a Na <sup>+</sup> /drug antiporter.   | multidrug and toxic compound extrusion (MATE) transporter                      | acridine dye;fluoroquinolone antibiotic                                 | Multidrug | Antibiotic efflux | 432   | 424   | 190   | 968       | 436   | 160   | 1298  | 1208  | 402   | 1030  | 938   | 1228  | 8714   |

|                 |              |   |  |  |                 |                              |       |       |       |       |       |       |       |       |       |       |       |       |        |
|-----------------|--------------|---|--|--|-----------------|------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| ARO:3003<br>954 | efmA         | efmA is an MFS transporter permease in <i>E. faecium</i> .  | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic;macrolide antibiotic                              | Multidrug       | Antibiotic efflux            | 440   | 348   | 138   | 24    | 174   | 464   | 62    | 34    | 162   | 390   | 350   | 524   | 3110   |
| ARO:3003<br>955 | efpA         | efpA is an MFS transporter found in <i>Mycobacterium tuberculosis</i> .   | major facilitator superfamily (MFS) antibiotic efflux pump | isoniazid;rifamycin antibiotic   | Multidrug       | Antibiotic efflux            | 706   | 1746  | 108   | 228   | 200   | 840   | 182   | 228   | 144   | 686   | 684   | 1010  | 6762   |
| ARO:3003<br>961 | farA         | farA is the membrane fusion protein that is part of the farAB efflux pump.  | major facilitator superfamily (MFS) antibiotic efflux pump | antibacterial free fatty acids   | Multidrug       | Antibiotic efflux            | 1294  | 1196  | 1644  | 2458  | 1376  | 832   | 3456  | 2588  | 1234  | 1406  | 1366  | 1652  | 20502  |
| ARO:3003<br>962 | farB         | farB is the cytoplasmic transporter protein that is part of the farAB efflux pump. farB corresponds to 3 loci in <i>Pseudomonas aeruginosa</i> PAO1 and 3 loci in <i>Pseudomonas aeruginosa</i> LESB58. | major facilitator superfamily (MFS) antibiotic efflux pump | antibacterial free fatty acids   | Multidrug       | Antibiotic efflux            | 28    | 16    | 160   | 42    | 82    | 62    | 126   | 28    | 76    | 242   | 262   | 220   | 1344   |
| ARO:3003<br>964 | hp1181       | hp1181 is a translocase that is part of the MFS efflux pump family. It is found in <i>H. pylori</i> and has role in the active efflux of antibiotics.   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic;nitroimidazole antibiotic;tetracycline antibiotic | Multidrug       | Antibiotic efflux            | 590   | 1802  | 870   | 694   | 4656  | 842   | 878   | 1072  | 4086  | 1944  | 1846  | 2164  | 21444  |
| ARO:3003<br>967 | lfrA         | lfrA is involved in the active efflux of quinolones and is found in <i>Mycobacteroides abscessus</i> .  | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic   | Fluoroquinolone | Antibiotic efflux            | 92    | 30    | 60    | 94    | 84    | 68    | 288   | 98    | 162   | 852   | 1504  | 870   | 4202   |
| ARO:3003<br>971 | Erm(44)<br>v | Variant of Erm(44)v isolated from <i>Staphylococcus saprophyticus</i> , confers resistance to lincosamide and macrolide antibiotics but not streptogramins.   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide antibiotic;streptogramin antibiotic         | MLS             | Antibiotic target alteration | 128   | 12    | 14    | 14    | 2     | 36    | 90    | 22    | 0     | 10    | 0     | 4     | 332    |
| ARO:3003<br>980 | tetA(58)     | TetA(58) is a Tetracycline efflux pump described in <i>Paenibacillus</i> sp. LC231, a strain of <i>Paenibacillus</i> isolated from  | major facilitator superfamily (MFS)                        | tetracycline antibiotic  | Tetracycline    | Antibiotic efflux            | 18244 | 19722 | 19138 | 13676 | 16042 | 17726 | 18214 | 16114 | 17426 | 20182 | 21578 | 21610 | 219672 |

|                 |                                 |   |   |                          |               |                              |       |       |       |      |       |       |       |       |       |       |       |       |        |
|-----------------|---------------------------------|---|---|--------------------------|---------------|------------------------------|-------|-------|-------|------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| ARO:3003<br>981 | tetB(58)                        | Lechuguilla Cave, NM, USA. Described by Pawlowski et al. 2016. Tetracycline resistant TetB(58) efflux pump found in Paenibacillus sp. LC231, a strain of Paenibacillus isolated from Lechuguilla Cave, NM, USA. Described by Pawlowski et al. 2016. | antibiotic efflux pump                            | tetracycline antibiotic  | Tetracycline  | Antibiotic efflux            | 64    | 12    | 10    | 14   | 14    | 48    | 84    | 12    | 68    | 114   | 392   | 132   | 964    |
| ARO:3003<br>982 | ribosomal RNA methyltransferase | LlmA 23S RlmK 23S rRNA methyltransferase COG family. Detected in Paenibacillus sp. LC231, an isolated strain of Paenibacillus found in Lechuguilla Cave, NM, USA. Described by Pawlowski et al. 2016.   | Llm 23S ribosomal RNA methyltransferase           | lincosamide antibiotic   | MLS           | Antibiotic target alteration | 1812  | 3452  | 2710  | 1580 | 880   | 2340  | 1420  | 1642  | 1120  | 856   | 734   | 440   | 18986  |
| ARO:3003<br>983 | CatU                            | Chloramphenicol acetyltransferase conferring resistance to phenicol antibiotics detected in Paenibacillus sp. LC231, an isolated strain of Paenibacillus from Lechuguilla Cave, NM, USA. Described by Pawlowski et al. 2016.                        | chloramphenicol acetyltransferase (CAT)           | phenicol antibiotic      | Phenicol      | Antibiotic inactivation      | 4     | 10    | 12    | 2    | 8     | 8     | 16    | 14    | 14    | 10    | 10    | 4     | 112    |
| ARO:3003<br>984 | BahA                            | Bacitracin amidohydrolase found in Paenibacillus sp. LC231, an isolated strain of Paenibacillus from Lechuguilla Cave, NM, USA. Confers resistance by bacitracin inactivation through amidohydrolysis. Described by Pawlowski et al. 2016.          | Bah amidohydrolase                                | peptide antibiotic       | Peptide       | Antibiotic inactivation      | 146   | 14    | 0     | 0    | 0     | 36    | 0     | 0     | 0     | 40    | 74    | 64    | 374    |
| ARO:3003<br>986 | TaeA                            | Pleuromutilin (Tiamulin) ABC efflux pump found in Paenibacillus sp. LC231, a strain of Paenibacillus isolated from Lechuguilla Cave, NM, USA. Confers resistance to pleuromutilin antibiotics.  | ATP-binding cassette (ABC) antibiotic efflux pump | pleuromutilin antibiotic | Pleuromutilin | Antibiotic efflux            | 13330 | 12628 | 10672 | 9040 | 12758 | 10710 | 10828 | 10742 | 13048 | 17404 | 16768 | 21480 | 159408 |

|                 |             |   |                             |                           |                |                         |      |     |      |      |      |     |      |      |      |      |      |      |       |
|-----------------|-------------|---|-----------------------------|---------------------------|----------------|-------------------------|------|-----|------|------|------|-----|------|------|------|------|------|------|-------|
| ARO:3003<br>987 | VatI        | Described by Pawlowski et al. 2016.<br>Streptogramin A acetyltransferase found in Paenibacillus sp. LC231, isolated from Lechuguilla Cave, NM, USA. Confers resistance to streptogramin A antibiotics. Described by Pawlowski et al. 2016.  | n vat acetyltransferase     | streptogramin antibiotic  | MLS            | Antibiotic inactivation | 84   | 504 | 374  | 164  | 46   | 364 | 88   | 136  | 100  | 78   | 66   | 30   | 2034  |
| ARO:3003<br>988 | AAC(2')-IIb | AAC(2')-IIb is an intrinsic Kasugamycin 2' acetyltransferase protein found in Paenibacillus sp. LC231, a strain of Paenibacillus isolated from Lechuguilla Cave, NM, USA. Confers resistance to aminoglycoside antibiotics, including kasugamycin. Described by Pawlowski et al. 2016.  | AAC(2')                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 0    | 18  | 18   | 6    | 10   | 0   | 10   | 4    | 6    | 6    | 0    | 12   | 90    |
| ARO:3003<br>989 | AAC(6')-34  | AAC(6')-34 is an aminoglycoside 6'-phosphotransferase found in Paenibacillus sp. LC231, a strain of Paenibacillus from Lechuguilla Cave, NM, USA. Confers resistance to aminoglycoside antibiotics. Described by Pawlowski et al. 2016.   | AAC(6')                     | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 108  | 12  | 2    | 0    | 0    | 8   | 0    | 0    | 0    | 0    | 0    | 0    | 130   |
| ARO:3003<br>990 | vgbC        | VgbC is a streptogramin B-type lyase found in Paenibacillus sp. LC231, a strain of Paenibacillus isolated from Lechuguilla Cave, NM, USA. Confers resistance to streptogramin B-type antibiotics by linearization of the lactone ring on an ester bond, resulting in antibiotic inactivation. Described by Pawlowski et al. 2016. | streptogramin vgb lyase     | streptogramin antibiotic  | MLS            | Antibiotic inactivation | 0    | 0   | 10   | 0    | 6    | 0   | 0    | 0    | 0    | 16   | 18   | 12   | 62    |
| ARO:3003<br>992 | rphB        | rphB is a rifampin phosphotransferase protein found in Paenibacillus sp. LC231, a strain of Paenibacillus isolated from Lechuguilla Cave, NM, USA. Confers resistance to  | rifampin phosphotransferase | rifamycin antibiotic      | Rifamycin      | Antibiotic inactivation | 1558 | 564 | 1376 | 1154 | 1280 | 970 | 1914 | 1672 | 1004 | 3118 | 2788 | 4122 | 21520 |

|             |                               |   |   |                           |                |                         |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-------------|-------------------------------|---|---|---------------------------|----------------|-------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3003994 | cpaA                          | rifamycin antibiotics, specifically rifampin, through rifampin inactivation. Described by Pawlowski et al. 2016.<br>cpaA is a capreomycin acetyltransferase protein found in <i>Paenibacillus</i> sp. LC231, an isolated strain of <i>Paenibacillus</i> in Lechuguilla Cave, NM, USA. Confers resistance to capreomycin, an aminoglycoside antibiotic. Described by Pawlowski et al. 2016.<br>tetA(46) is a subunit of tetAB(46), a heterodimeric ABC transporter, that is required for conferring tetracycline resistance in <i>Streptococcus australis</i> isolated from the oral cavity. | cpa acetyltransferase                             | aminoglycoside antibiotic | Aminoglycoside | Antibiotic inactivation | 30   | 4    | 0    | 2    | 0    | 16   | 0    | 0    | 0    | 0    | 0    | 0    | 52    |
| ARO:3004032 | tetA(46)                      | tetB(46) is a subunit of tetAB(46), a heterodimeric ABC transporter, that is required for conferring tetracycline resistance in <i>Streptococcus australis</i> isolated from the oral cavity.   | ATP-binding cassette (ABC) antibiotic efflux pump | tetracycline antibiotic   | Tetracycline   | Antibiotic efflux       | 3206 | 2642 | 2496 | 1104 | 1026 | 4728 | 1284 | 1414 | 1190 | 3920 | 3624 | 5246 | 31880 |
| ARO:3004033 | tetB(46)                      | tetA(60) is a subunit of tetAB(60), an ABC transporter that confers resistance to tetracycline and tigercycline identified by screening a human saliva metagenomic library in <i>Escherichia coli</i> , which is required for resistance.   | ATP-binding cassette (ABC) antibiotic efflux pump | tetracycline antibiotic   | Tetracycline   | Antibiotic efflux       | 4040 | 3592 | 2846 | 1966 | 1524 | 4434 | 2720 | 2340 | 1510 | 2042 | 1910 | 2142 | 31066 |
| ARO:3004035 | tetA(60)                      | tetB(60) is a subunit of tetAB(60), an ABC transporter that confers resistance to tetracycline and tigercycline identified by screening a human saliva metagenomic library in <i>Escherichia coli</i> , which is required for resistance.   | ATP-binding cassette (ABC) antibiotic efflux pump | tetracycline antibiotic   | Tetracycline   | Antibiotic efflux       | 4364 | 3380 | 1794 | 3628 | 2738 | 4042 | 4334 | 3958 | 2472 | 4142 | 3422 | 4932 | 43206 |
| ARO:3004036 | tetB(60)                      | EmrE is a small multidrug transporter that functions as a homodimer and that couples the efflux of small polyaromatic   | small multidrug resistance (SMR)                  | aminoglycoside antibiotic | Multidrug      | Antibiotic efflux       | 1696 | 1970 | 1326 | 1248 | 546  | 2484 | 1254 | 1436 | 790  | 3416 | 2830 | 4724 | 23720 |
| ARO:3004038 | <i>Pseudomonas aeruginosa</i> |   |   |                           |                |                         | 64   | 10   | 2    | 0    | 0    | 80   | 14   | 0    | 6    | 114  | 144  | 98   | 532   |

|             |                                 |   |  |   |                         |                      |                      |     |      |      |     |     |      |      |     |      |      |      |      |      |
|-------------|---------------------------------|---|--|---|-------------------------|----------------------|----------------------|-----|------|------|-----|-----|------|------|-----|------|------|------|------|------|
| ARO:3004039 | Escherichia coli<br>osa<br>emrE | ations from the cell with the import of protons down an electrochemical gradient.<br>Confers resistance to tetraphenylphosphonium, methyl viologen, gentamicin, kanamycin, and neomycin.<br>Member of the small MDR (multidrug resistance) family of transporters; in Escherichia coli this protein provides resistance against a number of positively charged compounds including ethidium bromide and erythromycin; proton-dependent secondary transporter which exchanges protons for compound translocation | antibiotic<br>efflux pump  | small<br>multidrug<br>resistance (SMR)<br>antibiotic<br>efflux pump   | macrolide<br>antibiotic | MLS                  | Antibiotic<br>efflux | 608 | 1200 | 64   | 232 | 238 | 656  | 272  | 226 | 162  | 286  | 216  | 352  | 4512 |
| ARO:3004041 | Klebsiella pneumoniae<br>acrA   | AcrA is a subunit of the AcrAB multidrug efflux system that in K. pneumoniae, which is encoded by the acrRAB operon.  | resistance-nodulation-cell division (RND)<br>antibiotic<br>efflux pump | cephalosporin; fluoroquinolone<br>antibiotic; glycolylc<br>ycline; penam; phenicol<br>antibiotic; rifamycin | Multidrug               | Antibiotic<br>efflux | 6                    | 0   | 4    | 4    | 2   | 0   | 12   | 0    | 18  | 90   | 132  | 162  | 430  |      |
| ARO:3004042 | Enterobacter cloacae<br>acrA    | AcrA is a subunit of the AcrAB-TolC multidrug efflux system that in E. cloacae.   | resistance-nodulation-cell division (RND)<br>antibiotic<br>efflux pump | cephalosporin; fluoroquinolone<br>antibiotic; glycolylc<br>ycline; penam; phenicol<br>antibiotic; rifamycin | Multidrug               | Antibiotic<br>efflux | 246                  | 272 | 354  | 184  | 122 | 168 | 156  | 190  | 82  | 1786 | 1166 | 2616 | 7342 |      |
| ARO:3004043 | Escherichia coli<br>acrA        | AcrA is a subunit of the AcrAB-TolC multidrug efflux system that in E. coli.  | resistance-nodulation-cell division (RND)<br>antibiotic<br>efflux pump | cephalosporin; fluoroquinolone<br>antibiotic; glycolylc<br>ycline; penam; phenicol<br>antibiotic; rifamycin | Multidrug               | Antibiotic<br>efflux | 530                  | 318 | 192  | 1094 | 428 | 112 | 1518 | 1312 | 394 | 350  | 604  | 466  | 7318 |      |



|             |                             |  |  |   |           |                         |      |      |      |      |      |      |      |      |      |      |      |       |       |
|-------------|-----------------------------|--|--|---|-----------|-------------------------|------|------|------|------|------|------|------|------|------|------|------|-------|-------|
| ARO:3004054 | Pseudomonas aeruginosa CpxR | CpxR is directly involved in activation of expression of RND efflux pump MexAB-OprM in P. aeruginosa. CpxR is required to enhance mexAB-oprM expression and drug resistance, in the absence of repressor MexR.           | resistance-nodulation-cell division (RND) antibiotic efflux pump | cin antibiotic;tetracycline antibiotic;triclosan aminocoumarin antibiotic;amino glycoside antibiotic;carbapenem;cephalosporin;cephamycin; diaminopyrimidine antibiotic;fluoroquinolone antibiotic;macrolide antibiotic;monobactam;penam;penem;peptide antibiotic;phenicol antibiotic;sulfonamide antibiotic;tetracycline antibiotic | Multidrug | Antibiotic efflux       | 2526 | 1176 | 2418 | 3336 | 5544 | 1628 | 4350 | 4504 | 5194 | 9872 | 9088 | 13550 | 63186 |
| ARO:3004063 | EdeQ                        | EdeQ is an N-acetyltransferase enzyme that confers high-level self-resistance to edeine in Brevibacillus brevis, a natural edeine producer. EdeQ converts active edeine to N-acetyledoine, which is ineffective in vivo. | Edeine acetyltransferase   | peptide antibiotic;polymyxine antibiotic  | Multidrug | Antibiotic inactivation | 4    | 14   | 10   | 0    | 16   | 22   | 0    | 2    | 14   | 4    | 14   | 8     | 108   |
| ARO:3004072 | OpmB                        | OpmB is an outer membrane efflux protein in Pseudomonas aeruginosa that shows functional cooperation with MuxABC, to form the efflux pump system MuxABC-OpmB.  | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminocoumarin antibiotic;macrolide antibiotic;monobactam;tetracycline antibiotic  | Multidrug | Antibiotic efflux       | 384  | 218  | 1530 | 792  | 5122 | 348  | 948  | 1434 | 4680 | 3086 | 3478 | 4244  | 26264 |
| ARO:3004073 | MuxA                        | MuxA is a membrane fusion protein component of the efflux pump system MuxABC-OpmB in Pseudomonas aeruginosa.   | resistance-nodulation-cell division (RND) antibiotic efflux pump | aminocoumarin antibiotic;macrolide antibiotic;monobactam;tetracycline antibiotic  | Multidrug | Antibiotic efflux       | 964  | 1442 | 2668 | 1710 | 4938 | 1256 | 1898 | 1896 | 5158 | 2488 | 2452 | 2654  | 29524 |
| ARO:3004074 | MuxB                        | MuxB is one of the two necessary RND components in   | resistance-nodulation-   | aminocoumarin antibiotic;macrol   | Multidrug | Antibiotic efflux       | 2096 | 2768 | 1836 | 1484 | 5594 | 1942 | 2292 | 2366 | 5300 | 4258 | 4650 | 5112  | 39698 |

|                 |              |   |   |  |                |                         |      |      |      |      |      |     |      |      |      |      |      |       |       |
|-----------------|--------------|---|---|--|----------------|-------------------------|------|------|------|------|------|-----|------|------|------|------|------|-------|-------|
| ARO:3004<br>075 | MuxC         | the Pseudomonas aeruginosa efflux pump system MuxABC-OpmB.<br><br>MuxC is one of the two necessary RND components of the MuxABC-OpmB efflux pumps system in Pseudomonas aeruginosa.<br><br>PmpM is a multidrug efflux pump belonging to the MATE family of Pseudomonas aeruginosa. PmpM is an H <sup>+</sup> drug antiporter and is the first reported case of an H <sup>+</sup> coupled efflux pump in the MATE family. PmpM confers resistance to fluoroquinolones, fradiomycin, benzalkonium chloride, chlorhexidine gluconate, ethidium bromide, tetraphenylphosphonium chloride (TPPCI), and rhodamine 6G. | cell division (RND) antibiotic;monobactam;tetracycline antibiotic efflux pump resistance-nodulation-cell division (RND) antibiotic;monobactam;tetracycline antibiotic efflux pump | ide antibiotic;monobactam;tetracycline antibiotic;aminocoumarin antibiotic;macrolide antibiotic;monobactam;tetracycline antibiotic | Multidrug      | Antibiotic efflux       | 1080 | 1136 | 1718 | 446  | 668  | 912 | 656  | 492  | 816  | 1772 | 1946 | 2368  | 14010 |
| ARO:3004<br>077 | PmpM         | PmpM confers resistance to fluoroquinolones, fradiomycin, benzalkonium chloride, chlorhexidine gluconate, ethidium bromide, tetraphenylphosphonium chloride (TPPCI), and rhodamine 6G.  | multidrug and toxic compound extrusion (MATE) transporter   | aminoglycoside antibiotic;benzalkonium chloride;fluoroquinolone antibiotic   | Multidrug      | Antibiotic efflux       | 340  | 284  | 674  | 350  | 1332 | 290 | 466  | 526  | 1436 | 3398 | 3094 | 4990  | 17180 |
| ARO:3004<br>085 | InuG         | InuG is a transposon-mediated nucleotidyltransferase found in Enterococcus faecalis on Tn6260.  | lincosamide nucleotidyltransferase (LNU)  | lincosamide antibiotic   | MLS            | Antibiotic inactivation | 176  | 266  | 118  | 64   | 118  | 162 | 140  | 104  | 94   | 1266 | 896  | 1300  | 4704  |
| ARO:3004<br>089 | ANT(3'')-IIa | ANT(3'')-IIa is a aminoglycoside nucleotidyltransferase identified in Acinetobacter spp. via horizontal gene transfer mechanisms.   | ANT(3'')  | aminoglycoside antibiotic  | Aminoglycoside | Antibiotic inactivation | 430  | 1242 | 772  | 1630 | 4442 | 346 | 2220 | 2214 | 4246 | 8080 | 6810 | 11412 | 43844 |
| ARO:3004<br>090 | ANT(3'')-IIb | ANT(3'')-IIb is a aminoglycoside nucleotidyltransferase identified in Acinetobacter spp. via horizontal gene transfer mechanisms.   | ANT(3'')  | aminoglycoside antibiotic  | Aminoglycoside | Antibiotic inactivation | 12   | 30   | 20   | 90   | 24   | 12  | 52   | 62   | 38   | 44   | 44   | 32    | 460   |
| ARO:3004<br>091 | ANT(3'')-IIc | ANT(3'')-IIc is a aminoglycoside nucleotidyltransferase identified in Acinetobacter spp. via horizontal gene transfer mechanisms.   | ANT(3'')  | aminoglycoside antibiotic  | Aminoglycoside | Antibiotic inactivation | 710  | 744  | 20   | 24   | 24   | 566 | 28   | 32   | 18   | 36   | 50   | 60    | 2312  |
| ARO:3004<br>094 | Erm(48)      | Erm(48) is a macrolide-lincosamide-streptogramin  | Erm 23S ribosomal   | lincosamide antibiotic;macrolide   | MLS            | Antibiotic target       | 156  | 174  | 70   | 12   | 104  | 134 | 36   | 22   | 122  | 0    | 12   | 6     | 848   |

|             |                       |  |   |   |                 |   |      |     |     |      |      |     |      |      |      |      |      |      |       |
|-------------|-----------------------|--|---|---|-----------------|---|------|-----|-----|------|------|-----|------|------|------|------|------|------|-------|
|             |                       | resistance gene identified on resistance plasmid pJW2311.  | RNA methyltransferase   | ide antibiotic; streptomycin  | alteration      |   |      |     |     |      |      |     |      |      |      |      |      |      |       |
| ARO:3004099 | LpeA                  | LpeA is a subunit of the LpeAB efflux pump in <i>Legionella pneumophila</i> , which is homologous to AcrA in <i>E. coli</i> .  | resistance-nodulation-cell division (RND) antibiotic efflux pump  | macrolide antibiotic  | MLS             | Antibiotic efflux                               | 348  | 536 | 560 | 360  | 342  | 318 | 216  | 398  | 418  | 1782 | 1056 | 2464 | 8798  |
| ARO:3004100 | LpeB                  | LpeB is a subunit of the LpeAB efflux pump in <i>Legionella pneumophila</i> , which is homologous to AcrB in <i>E. coli</i> .  | resistance-nodulation-cell division (RND) antibiotic efflux pump  | macrolide antibiotic  | MLS             | Antibiotic efflux                               | 636  | 792 | 776 | 262  | 290  | 568 | 306  | 370  | 462  | 1090 | 826  | 924  | 7302  |
| ARO:3004103 | QepA2                 | QepA2 is a plasmid-mediated quinolone resistance pump found in an <i>Escherichia coli</i> isolate from France  | major facilitator superfamily (MFS) antibiotic efflux pump  | fluoroquinolone antibiotic  | Fluoroquinolone | Antibiotic efflux                               | 64   | 48  | 16  | 8    | 54   | 188 | 120  | 20   | 44   | 142  | 208  | 134  | 1046  |
| ARO:3004107 | Pseudoaeruginosa soxR | SoxR is a redox-sensitive transcriptional activator that induces expression of a small regulon that includes the RND efflux pump-encoding operon <i>mexGHJ-opmD</i> . SoxR was shown to be activated by pyocyanin. | ATP-binding cassette (ABC) antibiotic efflux pump; major facilitator superfamily (MFS) antibiotic efflux pump; resistance-nodulation-cell division (RND) antibiotic efflux pump | acridine dye; cephalosporins; fluoroquinolones; antibiotic; glycolycline; penam; phenicol; antibiotic; rifamycin; antibiotic; tetracycline; antibiotic; triclosan | Multidrug       | Antibiotic efflux; antibiotic target alteration | 342  | 200 | 166 | 634  | 354  | 110 | 920  | 950  | 396  | 472  | 532  | 514  | 5590  |
| ARO:3004113 | FosA7                 | <i>fosA7</i> is an enzyme that confers resistance to fosfomycin in <i>Escherichia coli</i> by breaking the epoxide ring of the molecule.   | fosfomycin thiol transferase  | fosfomycin  | Fosfomycin      | Antibiotic inactivation                         | 0    | 0   | 0   | 2    | 0    | 0   | 4    | 0    | 0    | 0    | 0    | 0    | 6     |
| ARO:3004122 | Klebsiella pneumoniae | <i>Klebsiella pneumoniae</i> outer membrane porin protein. Is preferentially detected in porin-deficient strains. Functional   | General Bacterial Porin with reduced  | carbapenem; cephalosporin; cephalosporin; monobactam  | Beta-lactam     | Reduced permeability to                         | 2060 | 972 | 554 | 4038 | 1830 | 242 | 6176 | 4754 | 1488 | 692  | 680  | 312  | 23798 |

|          |                                 |   |   |   |             |                                    |      |      |      |      |      |      |      |      |      |      |      |      |       |  |
|----------|---------------------------------|---|---|---|-------------|------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|--|
|          | niae                            | characterization of this new  | permeability  | am;penam;pene   | antibioti   |                                    |      |      |      |      |      |      |      |      |      |      |      |      |       |  |
|          | OmpK37                          | porin revealed a narrower pore than those of porins OmpK35 and OmpK36, which did not allow penetration by certain beta-lactams. Also, when a resistant strain expresses porin OmpK37 is less susceptible to cefotaxime and ceftazidime than when it is expressing either OmpK36 or OmpK35. Heterologous expression of Burkholderia pseudomallei | to beta-lactams   | m   | c           |                                    |      |      |      |      |      |      |      |      |      |      |      |      |       |  |
| ARO:3004 | Burkholderia pseudomallei Omp38 | Omp38 (BpsOmp38) in Omp-deficient E. coli host cells lowers their permeability and in consequence, their antimicrobial susceptibility to penicillin G, ceftazidime and imipenem.  | General Bacterial Porin with reduced permeability to beta-lactams | carbapenem;cephalosporin;ceftazidime;am;penam;pene                                      | Beta-lactam | Reduced permeability to antibiotic | 0    | 0    | 460  | 174  | 230  | 2    | 294  | 182  | 104  | 96   | 134  | 234  | 1910  |  |
| ARO:3004 | OprZ                            | OprZ is the outer membrane component of the AxyXY-OprZ efflux pump system in Achromobacter spp.   | resistance-nodulation-cell division (RND)                         | aminoglycoside antibiotic;cephalosporin;fluoroquinolone                                 | Multidrug   | Antibiotic efflux                  | 14   | 20   | 132  | 120  | 62   | 14   | 276  | 142  | 158  | 224  | 296  | 300  | 1758  |  |
| ARO:3004 | AxyX                            | AxyX is the inner membrane transporter of the AxyXY-OprZ efflux pump system in Achromobacter spp.   | antibiotic efflux pump resistance-nodulation-cell division (RND)  | antibiotic;macrolide antibiotic;aminoglycoside antibiotic;cephalosporin;fluoroquinolone | Multidrug   | Antibiotic efflux                  | 16   | 6    | 56   | 64   | 40   | 6    | 192  | 62   | 26   | 354  | 354  | 356  | 1532  |  |
| ARO:3004 | AxyY                            | AxyY is the periplasmic adaptor protein of the AxyXY-OprZ efflux pump system in Achromobacter spp.  | antibiotic efflux pump resistance-nodulation-cell division (RND)  | antibiotic;macrolide antibiotic;aminoglycoside antibiotic;cephalosporin;fluoroquinolone | Multidrug   | Antibiotic efflux                  | 44   | 28   | 186  | 134  | 74   | 100  | 298  | 154  | 118  | 380  | 296  | 252  | 2064  |  |
| ARO:3004 | cfrC                            | A cfr-like 23S rRNA methyltransferase shown to confer resistance to linezolid and phenicol antibiotics, including florfenicol and chloramphenicol, in Clostridium.  | Cfr 23S ribosomal RNA methyltransferase                           | phenicol antibiotic   | Phenicol    | Antibiotic target alteration       | 3026 | 3084 | 8298 | 4922 | 2408 | 2398 | 4146 | 5458 | 3192 | 3344 | 2898 | 3164 | 46338 |  |
| ARO:3004 | mecD                            | mecD is a PBP2a variant identified on a genomic resistance island in Micrococcus  | methicillin resistant PBP2  | carbapenem;cephalosporin;ceftazidime  | Beta-lactam | Antibiotic target                  | 1062 | 1804 | 836  | 962  | 3610 | 1182 | 908  | 1280 | 3164 | 1404 | 1376 | 1500 | 19088 |  |

|             |             |  |   |                                |                |                              |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-------------|-------------|--|---|--------------------------------|----------------|------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
|             |             | caseolyticus. MecD confers resistance to methicillin and other beta-lactam antibiotics through the production of an alternative low-affinity PBP. First described by Schwendener et al. 2017 and identified from canine and bovine sources.  |   | mycin;monobactam;penam         |                | replacement                  |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| ARO:3004191 | APH(2'')-If | Aminoglycoside 2''-phosphotransferase identified from the gram-negative pathogen Campylobacter jejuni. APH(2'')-If was shown to confer resistance to 4,6-disubstituted antibiotics kanamycin, tobramycin, dibekacin, gentamicin and sisomicin through antibiotic phosphorylation. Described by Toth et al. 2013. GOB-18 is a member of subclass B3 GOB family of beta-lactamases isolated from Elizabethkingia meningoseptica. | APH(2'')                                  | aminoglycoside antibiotic      | Aminoglycoside | Antibiotic inactivation      | 22  | 6   | 68  | 28  | 4   | 26  | 36  | 34  | 10  | 38  | 14  | 22  | 308  |  |
| ARO:3004213 | GOB-18      | GOB-18 is unlike other subclass B3 beta-lactamases as it is fully active against a broad range of beta-lactam substrates using a single Zn(II) ion in its active site. NPS-1 is a plasmid-encoded class D beta-lactamase identified from two Pseudomonas aeruginosa isolates in 1986.  | GOB beta-lactamase                        | carbapenem;cephalosporin;penam | Beta-lactam    | Antibiotic inactivation      | 14  | 96  | 44  | 22  | 14  | 38  | 16  | 34  | 16  | 170 | 182 | 190 | 836  |  |
| ARO:3004239 | NPS-1       |  | NPS beta-lactamase                        | cephalosporin;penam            | Beta-lactam    | Antibiotic inactivation      | 0   | 0   | 10  | 14  | 0   | 0   | 48  | 8   | 0   | 28  | 22  | 60  | 190  |  |
| ARO:3004253 | vanUG       | vanUG is a vanG variant found in the vanG gene cluster.  | glycopeptide resistance gene cluster;vanU | glycopeptide antibiotic        | Glycopeptide   | Antibiotic target alteration | 386 | 468 | 446 | 236 | 202 | 454 | 230 | 394 | 224 | 154 | 126 | 86  | 3406 |  |
| ARO:3004254 | vanVB       | vanVB is a vanV variant found in the vanB gene cluster. It is found in some but not all vanB operons in E. faecalis, suggesting the existence of varied gene compositions in vanB operons.   | glycopeptide resistance gene cluster;vanV | glycopeptide antibiotic        | Glycopeptide   | Antibiotic target alteration | 0   | 8   | 36  | 26  | 6   | 6   | 38  | 40  | 14  | 8   | 2   | 4   | 188  |  |

|                 |  |   |  |                       |             |                            |     |     |     |     |     |     |      |      |     |     |     |    |      |
|-----------------|--|---|--|-----------------------|-------------|----------------------------|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|----|------|
| ARO:3004<br>289 | Vibrio<br>cholerae<br>varG                         | varG is an Ambler class B metallo-beta-lactamase found on the antibiotic resistance var regulon in Vibrio cholerae, along with an antibiotic efflux pump varABCDEF. These genes are organized as a regulon under the control of VarR transcriptional activator. VarG was shown to have beta-lactamase activity against penicillins, carbapenems and cephalosporins in-vitro. Described by Lin HV et al. 2017. | subclass B1<br>Vibrio<br>cholerae<br>varG beta-lactamase | carbapenem            | Beta-lactam | Antibiotic<br>inactivation | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 2   | 14  | 0  | 16   |
| ARO:3004<br>290 | Escherichia coli<br>ampC beta-lactamase            | A class C ampC beta-lactamase (cephalosporinase) enzyme described in Escherichia coli shown clinically to confer resistance to penicillin-like and cephalosporin-class antibiotics.   | ampC-type<br>beta-lactamase                              | cephalosporin;penam   | Beta-lactam | Antibiotic<br>inactivation | 330 | 158 | 112 | 816 | 418 | 44  | 1272 | 1042 | 304 | 124 | 102 | 62 | 4784 |
| ARO:3004<br>291 | Rhodobacter<br>sphaeroides<br>ampC beta-lactamase  | A periplasmic cephalosporinase described in Rhodobacter sphaeroides shown to contribute to resistance of beta-lactam antibiotics.   | ampC-type<br>beta-lactamase                              | cephalosporin;penam   | Beta-lactam | Antibiotic<br>inactivation | 78  | 16  | 16  | 2   | 2   | 106 | 2    | 8    | 0   | 54  | 50  | 62 | 396  |
| ARO:3004<br>292 | Laribacter<br>hongkongensis<br>ampC beta-lactamase | A chromosome-encoded class C beta-lactamase described in the pathogen Laribacter hongkongensis, often associated with gastroenteritis. Laribacter ampC has been shown to confer resistance to non-carbapenem beta-lactamases, as described by Lau et al. 2005.  | ampC-type<br>beta-lactamase                              | cephalosporin;penam   | Beta-lactam | Antibiotic<br>inactivation | 0   | 0   | 0   | 0   | 0   | 0   | 4    | 0    | 0   | 4   | 16  | 4  | 28   |
| ARO:3004<br>294 | BUT-1  | A chromosome-encoded class C cephalosporinase and penicillinase from Buttiauxella spp. shown clinically to confer resistance to beta-lactam antibiotics. Described by Fihman et al. 2002.   | BUT beta-lactamase                                       | cephalosporin         | Beta-lactam | Antibiotic<br>inactivation | 0   | 4   | 20  | 14  | 0   | 0   | 6    | 16   | 0   | 70  | 114 | 96 | 340  |
| ARO:3004<br>325 | MCR-4.1  | MCR-4 is a plasmid-borne phosphoethanolamine transferase variant of MCR-1,  | MCR<br>phosphoeth  | peptide<br>antibiotic | Peptide     | Antibiotic<br>target       | 22  | 14  | 0   | 4   | 0   | 0   | 6    | 10   | 0   | 2   | 6   | 28 | 92   |

|             |         |   |                                     |                                     |             |                              |    |    |     |     |    |    |     |     |    |     |    |    |      |
|-------------|---------|---|-------------------------------------|-------------------------------------|-------------|------------------------------|----|----|-----|-----|----|----|-----|-----|----|-----|----|----|------|
|             |         | isolated from Salmonella enterica serovar Typhimurium of porcine origin in Italy, Spain and Belgium through 2013 and 2015-2016. MCR-4 confers resistance to collistin via addition of a phosphoethanolamine group to lipid A, reducing the negative charge of the cell membrane. Described by Carattoli et al. 2017.  | anolamine transferase               |                                     |             | alteration                   |    |    |     |     |    |    |     |     |    |     |    |    |      |
| ARO:3004332 | MCR-5.1 | MCR-5 is a transposon-associated phosphoethanolamine transferase gene, identified in Salmonella Paratyphi B dTa+ (d-tartrate fermenting Salmonella enterica subsp. enterica serovar Paratyphi B) isolates from food-producing animals. The isolates were collected between 2011 and 2013, and retrieved from the German National Reference Laboratory for Salmonella. MCR-5 confers resistance to collistin through the addition of a phosphoethanolamine group to lipid A, causing a reduction in negative charge of the cell membrane. Described by Borowiak et al, 2017. | MCR phosphoethanolamine transferase | peptide antibiotic                  | Peptide     | Antibiotic target alteration | 74 | 50 | 168 | 118 | 44 | 94 | 230 | 142 | 56 | 118 | 88 | 54 | 1236 |
| ARO:3004336 | PDC-73  | An AmpC-like beta-lactamase found in Pseudomonas aeruginosa.  | PDC beta-lactamase                  | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation      | 0  | 0  | 0   | 0   | 6  | 0  | 0   | 0   | 14 | 0   | 6  | 0  | 26   |
| ARO:3004337 | PDC-74  | An AmpC-like beta-lactamase found in Pseudomonas aeruginosa   | PDC beta-lactamase                  | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation      | 0  | 2  | 0   | 0   | 0  | 0  | 6   | 0   | 0  | 0   | 0  | 0  | 8    |
| ARO:3004338 | PDC-75  | An AmpC-like beta-lactamase found in Pseudomonas aeruginosa   | PDC beta-lactamase                  | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic inactivation      | 0  | 0  | 12  | 0   | 0  | 0  | 0   | 0   | 0  | 50  | 78 | 98 | 238  |
| ARO:3004353 | PDC-90  | An AmpC-like beta-lactamase found in Pseudomonas aeruginosa   | PDC beta-lactamase                  | carbapenem;cephalosporin;monobactam | Beta-lactam | Antibiotic                   | 0  | 0  | 2   | 0   | 0  | 2  | 2   | 0   | 0  | 0   | 0  | 0  | 6    |

|                 |                             |  |   |                                     |                 |                                      |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|-----------------------------|--|---|-------------------------------------|-----------------|--------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3004<br>354 | PDC-91                      | An AmpC-like beta-lactamase found in <i>Pseudomonas aeruginosa</i>   | PDC beta-lactamase  | carbapenem;cephalosporin;monobactam | Beta-lactam     | inactivation Antibiotic inactivation | 28   | 6    | 0    | 2    | 2    | 10   | 2    | 0    | 2    | 2    | 0    | 0    | 54    |
| ARO:3004<br>357 | catV                        | A chloramphenicol acetyltransferase identified in <i>Brevibacillus brevis</i> and shown to confer resistance to chloramphenicol antibiotics. Described by Pawlowski et al. 2017.   | chloramphenicol acetyltransferase (CAT)   | phenicol antibiotic                 | Phenicol        | Antibiotic inactivation              | 8    | 24   | 28   | 24   | 14   | 38   | 6    | 22   | 8    | 4    | 6    | 6    | 188   |
| ARO:3004<br>359 | ACI-1                       | A class A beta-lactamase described in <i>Acidaminococcus fermentans</i> . ACI-1 was the first description of a beta-lactamase enzyme in a gram-negative anaerobic cocci. Described by Galan et al 2000.  | ACI beta-lactamase  | cephalosporin;penam;penem           | Beta-lactam     | Antibiotic inactivation              | 160  | 216  | 312  | 146  | 288  | 184  | 206  | 154  | 332  | 48   | 24   | 14   | 2084  |
| ARO:3004<br>361 | sul4                        | sul4 is a dihydropteroate synthase gene and mobile sulfonamide resistance gene shown to confer resistance when expressed in <i>E. coli</i> . A plasmid-mediated quinolone efflux pump variant described in <i>Escherichia coli</i> . QepA4 confers resistance to quinolone and fluoroquinolone antibiotics by expulsion from the cell. Described by Manageiro et al. 2017. | sulfonamide resistant sul   | sulfonamide antibiotic              | Sulfonamide     | Antibiotic target replacement        | 3648 | 4156 | 3276 | 2952 | 4620 | 3356 | 3688 | 3308 | 4556 | 5894 | 6028 | 7688 | 53170 |
| ARO:3004<br>379 | QepA4                       |  | major facilitator superfamily (MFS) antibiotic efflux pump                        | fluoroquinolone antibiotic          | Fluoroquinolone | Antibiotic efflux                    | 12   | 32   | 14   | 36   | 6    | 26   | 94   | 42   | 10   | 1836 | 1098 | 2578 | 5784  |
| ARO:3004<br>441 | tet(59)                     | Tet(59) is a chromosome-encoded tetracycline efflux pump described from a Chinese pig manure sample.   | major facilitator superfamily (MFS) antibiotic efflux pump tetracycline-resistant | tetracycline antibiotic             | Tetracycline    | Antibiotic efflux                    | 0    | 34   | 510  | 260  | 2292 | 8    | 494  | 742  | 1910 | 1658 | 1562 | 2008 | 11478 |
| ARO:3004<br>442 | tet(W/N/W)                  | tet(W/N/W) is a mosaic tetracycline resistance gene and ribosomal protection protein.  | ribosomal protection protein  | tetracycline antibiotic             | Tetracycline    | Antibiotic target protection         | 1664 | 2478 | 2220 | 926  | 952  | 1976 | 946  | 1064 | 1176 | 628  | 414  | 258  | 14702 |
| ARO:3004<br>451 | <i>Agrobacterium fabrum</i> | A chloramphenicol resistance determinant described in the  | chloramphenicol   | phenicol antibiotic                 | Phenicol        | Antibiotic                           | 1862 | 710  | 1020 | 1944 | 966  | 922  | 2856 | 2302 | 1042 | 658  | 670  | 660  | 15612 |



|             |                                   |   |  |                     |          |                              |     |     |     |     |     |     |     |     |     |    |    |    |      |
|-------------|-----------------------------------|---|--|---------------------|----------|------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|------|
|             | chloramphenicol acetyltransferase | Gram-negative bacterium <i>Agrobacterium fabrum</i> .   | acetyltransferase (CAT)                                      |                     |          | inactivation                 |     |     |     |     |     |     |     |     |     |    |    |    |      |
| ARO:3004454 | chloramphenicol acetyltransferase | A chloramphenicol resistance determinant described in <i>Campylobacter coli</i> .   | chloramphenicol acetyltransferase (CAT)                      | phenicol antibiotic | Phenicol | Antibiotic inactivation      | 326 | 156 | 566 | 206 | 152 | 216 | 114 | 212 | 150 | 52 | 8  | 46 | 2204 |
| ARO:3004455 | chloramphenicol acetyltransferase | A chloramphenicol resistance determinant described in <i>Streptococcus suis</i> .   | chloramphenicol acetyltransferase (CAT)                      | phenicol antibiotic | Phenicol | Antibiotic inactivation      | 0   | 2   | 2   | 0   | 0   | 2   | 0   | 0   | 0   | 12 | 6  | 6  | 30   |
| ARO:3004457 | chloramphenicol acetyltransferase | A chloramphenicol resistance determinant described in <i>Staphylococcus intermedius</i>   | chloramphenicol acetyltransferase (CAT)                      | phenicol antibiotic | Phenicol | Antibiotic inactivation      | 0   | 2   | 38  | 0   | 60  | 0   | 0   | 0   | 52  | 70 | 78 | 92 | 392  |
| ARO:3004460 | chloramphenicol acetyltransferase | A chloramphenicol resistance determinant described in a <i>Vibrio anguillarum</i> plasmid sequence  | chloramphenicol acetyltransferase (CAT)                      | phenicol antibiotic | Phenicol | Antibiotic inactivation      | 4   | 6   | 6   | 4   | 42  | 20  | 6   | 10  | 36  | 0  | 0  | 0  | 134  |
| ARO:3004466 | ICR-Mc                            | A chromosomally-encoded colistin resistance phosphoethanolamine (PEtN) transferase of <i>Moraxella catarrhalis</i> . ICR-Mc is the protein that represents the closest known ortholog to the colistin resistance MCR-1 and MCR-2 PEtN transferases. | intrinsic colistin resistant phosphoethanolamine transferase | peptide antibiotic  | Peptide  | Antibiotic target alteration | 0   | 0   | 4   | 12  | 0   | 0   | 10  | 2   | 0   | 2  | 2  | 0  | 32   |

|                 |  |  |   |   |             |  |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|--|--|---|---|-------------|--|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3004<br>470 | poxTA  | PoxTA is an ABC-F subfamily ATP-binding cassette protein that confers resistance to tetracycline, -phenicol, and oxazolidinone via modification of the bacterial ribosome. The encoding gene was isolated from a methicillin-resistant <i>Staphylococcus aureus</i> strain.  | ABC-F ATP-binding cassette ribosomal protection protein   | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic | Multidrug   | Antibiotic target protection                               | 1892 | 1250 | 1296 | 598  | 390  | 2432 | 696  | 622  | 604  | 954  | 950  | 682  | 12366 |
| ARO:3004<br>476 | vmrR   | vmrR is an ABC-F ATPase ribosomal protection protein identified in <i>Bacillus subtilis</i> . Shown to confer resistance to lincomycin and streptogramin A virginiamycin. Described by Crowe-McAuliffe et al. 2018.  | ABC-F ATP-binding cassette ribosomal protection protein   | antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic   | Multidrug   | Antibiotic target protection                               | 3178 | 2660 | 1924 | 2678 | 4020 | 2624 | 3308 | 3448 | 4042 | 2080 | 2196 | 2336 | 34494 |
| ARO:3004<br>478 | OXA-665  | Beta-lactamase found in <i>Acinetobacter rudis</i> efficiently inactivating carbapenems and amoxicillin conferring resistance to cephalosporins  | OXA beta-lactamase  | cephalosporin;penam   | Beta-lactam | Antibiotic inactivation                                    | 0    | 0    | 12   | 0    | 18   | 0    | 0    | 0    | 0    | 6    | 0    | 14   | 50    |
| ARO:3004<br>480 | Bifidobacterium adolescentis mutants conferring resistance to rifampicin | Bifidobacterium are antibiotic resistant probiotics are prescribed to upkeep the population beneficial bacteria in the gut microbiome. However, horizontal gene transfer among gut microbes could create harmful antibiotic-resistant pathogenic bacteria, such as <i>Mycobacterium tuberculosis</i> . Lokesh et al. analyzed <i>Bifidobacterium antitubercular</i> drug resistance and mutations in rpoB. They found that <i>B. animalis</i> , <i>B. longum</i> and <i>B. adolescentis</i> showed | rifamycin-resistant beta-subunit of RNA polymerase (rpoB) | peptide antibiotic;rifamycin antibiotic   | Multidrug   | Antibiotic target alteration;antibiotic target replacement | 2214 | 2520 | 3516 | 1706 | 6384 | 2320 | 2270 | 3082 | 7512 | 3308 | 3310 | 2990 | 41132 |

|             |          |   |                                     |                    |         |                              |   |    |    |    |   |    |    |    |   |   |    |   |    |
|-------------|----------|---|-------------------------------------|--------------------|---------|------------------------------|---|----|----|----|---|----|----|----|---|---|----|---|----|
|             |          | considerable resistance to pyrazinamide, isoniazid, and streptomycin, while B. adolescentis had mutations both in the rifampicin (RIF) pocket and in regions outside the pockets, and also showed considerable resistance to RIF. |                                     |                    |         |                              |   |    |    |    |   |    |    |    |   |   |    |   |    |
| ARO:3004500 | MCR-3.11 | An MCR-3 phosphoethanolamine transferase and polymyxin resistance gene variant differing by 2 amino acid substitutions, identified from an Escherichia coli isolate.  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 0 | 0  | 34 | 12 | 6 | 0  | 10 | 16 | 6 | 8 | 0  | 0 | 92 |
| ARO:3004501 | MCR-6.1  | An MCR-2 phosphoethanolamine transferase and polymyxin resistance gene variant identified in Moraxella isolated from pigs in the United Kingdom.  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 2 | 22 | 2  | 0  | 0 | 44 | 0  | 0  | 6 | 0 | 0  | 0 | 76 |
| ARO:3004502 | MCR-2.2  | An MCR-2 phosphoethanolamine transferase and polymyxin resistance gene variant identified in Moraxella isolated from pigs in Great Britain  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 0 | 0  | 0  | 2  | 0 | 0  | 2  | 0  | 0 | 0 | 0  | 0 | 4  |
| ARO:3004506 | MCR-1.10 | An MCR-1 phosphoethanolamine transferase and polymyxin (colistin) resistance gene variant identified from an Escherichia porcine isolate in Great Britain.  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 0 | 0  | 0  | 2  | 0 | 0  | 0  | 2  | 0 | 0 | 0  | 0 | 4  |
| ARO:3004508 | MCR-3.9  | An MCR-3 polymyxin (incl. colistin) resistance gene variant isolated from an Aeromonas isolate  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 0 | 8  | 0  | 6  | 0 | 10 | 12 | 0  | 0 | 0 | 0  | 0 | 36 |
| ARO:3004510 | MCR-3.7  | An MCR polymyxin (colistin) resistance gene variant identified in Aeromonas   | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 4 | 20 | 4  | 14 | 0 | 6  | 2  | 2  | 0 | 0 | 0  | 0 | 52 |
| ARO:3004514 | MCR-1.3  | An MCR-1 polymyxin resistance gene variant identified from a poultry Raoultella planticola isolate  | MCR phosphoethanolamine transferase | peptide antibiotic | Peptide | Antibiotic target alteration | 0 | 0  | 0  | 0  | 0 | 0  | 0  | 0  | 0 | 4 | 20 | 4 | 28 |

|                 |                |  |  |   |                   |                               |     |     |    |    |    |      |     |     |     |    |     |     |      |
|-----------------|----------------|--|--|---|-------------------|-------------------------------|-----|-----|----|----|----|------|-----|-----|-----|----|-----|-----|------|
| ARO:3004<br>516 | MCR-8.1        | A novel phosphoethanolamine transferase and mobile colistin resistance gene identified from carbapenem-resistant NDM-1-producing <i>Klebsiella pneumoniae</i> .  | MCR phosphoethanolamine transferase                          | peptide antibiotic                          | Peptide           | Antibiotic target alteration  | 146 | 110 | 74 | 26 | 8  | 94   | 94  | 58  | 18  | 18 | 42  | 70  | 758  |
| ARO:3004<br>517 | MCR-7.1        | A novel plasmid-mediated colistin-resistant phosphoethanolamine transferase identified from a poultry isolate of <i>Klebsiella pneumoniae</i> .  | MCR phosphoethanolamine transferase                          | peptide antibiotic                          | Peptide           | Antibiotic target alteration  | 26  | 64  | 8  | 68 | 0  | 74   | 104 | 90  | 14  | 30 | 46  | 62  | 586  |
| ARO:3004<br>539 | mphH           | A chromosomal macrolide 2'-phosphotransferase and resistance gene identified from a <i>Brachy bacterium faecium</i> cave isolate   | macrolide phosphotransferase (MPH)                           | macrolide antibiotic                        | MLS               | Antibiotic inactivation       | 0   | 0   | 0  | 0  | 26 | 0    | 0   | 0   | 30  | 16 | 52  | 100 | 224  |
| ARO:3004<br>543 | mphO           | A chromosomal macrolide phosphotransferase identified in <i>Brachy bacterium paraconglomeratum</i>   | macrolide phosphotransferase (MPH)                           | macrolide antibiotic                        | MLS               | Antibiotic inactivation       | 0   | 0   | 0  | 0  | 6  | 0    | 0   | 0   | 0   | 0  | 4   | 8   | 18   |
| ARO:3004<br>548 | dfrA9          | A dihydrofolate reductase and trimethoprim resistance gene identified from porcine isolates of <i>Escherichia coli</i>   | trimethoprim resistant dihydrofolate reductase dfr           | diaminopyrimidine antibiotic                | Diaminopyrimidine | Antibiotic target replacement | 2   | 8   | 6  | 30 | 8  | 12   | 58  | 102 | 8   | 50 | 26  | 124 | 434  |
| ARO:3004<br>551 | dfrA28         | A dihydrofolate reductase and trimethoprim resistance gene from <i>Aeromonas hydrophila</i>  | trimethoprim resistant dihydrofolate reductase dfr           | diaminopyrimidine antibiotic                | Diaminopyrimidine | Antibiotic target replacement | 0   | 4   | 2  | 0  | 2  | 0    | 6   | 2   | 4   | 10 | 14  | 36  | 80   |
| ARO:3004<br>568 | dfrA18         | A trimethoprim-resistant dihydrofolate reductase identified from <i>Vibrio cholerae</i>  | trimethoprim resistant dihydrofolate reductase dfr           | diaminopyrimidine antibiotic                | Diaminopyrimidine | Antibiotic target replacement | 28  | 16  | 48 | 4  | 2  | 48   | 6   | 2   | 12  | 2  | 10  | 24  | 202  |
| ARO:3004<br>569 | ICR-Mo         | A chromosomally-encoded colistin resistance phosphoethanolamine (PEtN) transferase of <i>Moraxella osloensis</i> . ICR-Mo represents the closest known ortholog to the colistin resistance MCR-1 and MCR-2 PEtN transferases | intrinsic colistin resistant phosphoethanolamine transferase | peptide antibiotic                          | Peptide           | Antibiotic target alteration  | 36  | 0   | 0  | 2  | 8  | 10   | 0   | 6   | 4   | 0  | 0   | 0   | 66   |
| ARO:3004<br>572 | Staphylococcus | MFS transporters are secondary active transporters with single-polypeptide chains containing   | major facilitator superfamily                                | aminoglycoside antibiotic;diaminopyrimidine | Multidrug         | Antibiotic efflux             | 600 | 242 | 78 | 8  | 98 | 1010 | 16  | 18  | 180 | 72 | 118 | 116 | 2556 |

|             |                              |   |  |   |                 |                   |      |     |     |      |      |      |      |      |      |      |      |      |       |  |  |
|-------------|------------------------------|---|--|---|-----------------|-------------------|------|-----|-----|------|------|------|------|------|------|------|------|------|-------|--|--|
|             | aureus LmrS                  | 400-600 amino acids that transport small solutes across the membrane by using electrochemical gradients. LmrS has 14 transmembrane helices and, when expressed in E. coli, is capable of extruding a variety of antibiotics including linezolid, trimethoprim, florfenicol, chloramphenicol, erythromycin, streptomycin, kanamycin, and fusidic acid  | (MFS) antibiotic efflux pump                               | antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic              |                 |                   |      |     |     |      |      |      |      |      |      |      |      |      |       |  |  |
| ARO:3004573 | Acinetobacter baumannii AbaF | Expression of abaF in E. coli resulted in increased resistance to fosfomycin.   | major facilitator superfamily (MFS) antibiotic efflux pump | fosfomycin  | Fosfomycin      | Antibiotic efflux | 2722 | 868 | 606 | 2954 | 1438 | 1718 | 4742 | 3266 | 1634 | 1740 | 2362 | 1690 | 25740 |  |  |
| ARO:3004574 | Acinetobacter baumannii AbaQ | AbaQ is an MFS transporter mainly involved in the extrusion of quinolone-type drugs in A. baumannii   | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic  | Fluoroquinolone | Antibiotic efflux | 1166 | 610 | 204 | 842  | 346  | 686  | 1100 | 814  | 348  | 156  | 140  | 106  | 6518  |  |  |
| ARO:3004577 | Acinetobacter baumannii AmvA | AmvA has 14 alpha-helical transmembrane segments, qualifying it as a member of the DHA2 transporter family of the major facilitator superfamily (MFS). When AmvA was expressed in E. coli, the cells had at least four-fold decreased susceptibility to erythromycin, acridine orange, acriflavine, deoxycholate and methyl viologen. AmvA from the AC0037 strain of A. baumannii was tested. | major facilitator superfamily (MFS) antibiotic efflux pump | acridine dye;macrolide antibiotic   | Multidrug       | Antibiotic efflux | 528  | 22  | 168 | 116  | 114  | 686  | 66   | 152  | 126  | 80   | 112  | 120  | 2290  |  |  |
| ARO:3004580 | Klebsiella pneumoniae KpnE   | KpnE subunit of KpnEF resembles EbrAB from E. coli. Mutation in KpnEF resulted in increased susceptibility to cefepime, ceftriaxone, colistin, erythromycin, rifampin, tetracycline, and streptomycin as well as enhanced sensitivity toward sodium dodecyl sulfate,  | major facilitator superfamily (MFS) antibiotic efflux pump | aminoglycoside antibiotic;cephalosporin;macrolide antibiotic;peptide antibiotic;rifamycin | Multidrug       | Antibiotic efflux | 238  | 58  | 56  | 320  | 128  | 10   | 556  | 374  | 86   | 440  | 458  | 666  | 3390  |  |  |

|             |                            |  |  |   |              |                         |     |    |    |     |     |    |     |     |    |     |     |     |      |
|-------------|----------------------------|--|--|---|--------------|-------------------------|-----|----|----|-----|-----|----|-----|-----|----|-----|-----|-----|------|
| ARO:3004583 | Klebsiella pneumoniae KpnF | deoxycholate, dyes, benzalkonium chloride, chlorhexidine, and triclosan. KpnF subunit of KpnEF resembles EbrAB from E. coli. Mutation in KpnEF resulted in increased susceptibility to cefepime, ceftriaxone, colistin, erythromycin, rifampin, tetracycline, and streptomycin as well as enhanced sensitivity toward sodium dodecyl sulfate, deoxycholate, dyes, benzalkonium chloride, chlorhexidine, and triclosan. | major facilitator superfamily (MFS) antibiotic efflux pump | antibiotic;tetracycline antibiotic  | Multidrug    | Antibiotic efflux       | 134 | 36 | 48 | 324 | 106 | 8  | 460 | 336 | 84 | 58  | 92  | 40  | 1726 |
| ARO:3004586 | tet(51)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.   | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation | 0   | 6  | 48 | 0   | 104 | 0  | 50  | 0   | 30 | 172 | 176 | 320 | 906  |
| ARO:3004587 | tet(52)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.   | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation | 0   | 0  | 0  | 0   | 0   | 0  | 12  | 0   | 0  | 0   | 2   | 0   | 14   |
| ARO:3004588 | Klebsiella pneumoniae KpnG | KpnG consists of ~390 residues and resembles EmrA of E. coli. Disruption of the pump components KpnG-KpnH significantly decrease resistance to azithromycin, ceftazidime, ciprofloxacin, ertapenem, erythromycin, gentamicin, imipenem, ticarcillin, norfloxacin, polymyxin-B, piperacillin, spectinomycin, tobramycin, and streptomycin.  | major facilitator superfamily (MFS) antibiotic efflux pump | aminoglycoside antibiotic;carbapenem;cephalosporin;fluoroquinolone antibiotic;macrolide antibiotic;penam;penem;peptide antibiotic | Multidrug    | Antibiotic efflux       | 80  | 16 | 68 | 30  | 46  | 78 | 60  | 32  | 40 | 0   | 12  | 18  | 480  |
| ARO:3004589 | tet(53)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.   | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation | 0   | 2  | 14 | 74  | 4   | 0  | 28  | 60  | 2  | 0   | 0   | 0   | 184  |
| ARO:3004590 | tet(54)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.   | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation | 16  | 0  | 0  | 0   | 0   | 0  | 54  | 6   | 0  | 0   | 0   | 0   | 76   |
| ARO:3004591 | tet(55)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.   | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation | 14  | 6  | 20 | 10  | 34  | 12 | 50  | 42  | 60 | 242 | 488 | 358 | 1336 |

|             |                            |   |  |   |              |                              |    |    |    |    |    |    |    |    |    |    |     |    |     |
|-------------|----------------------------|---|--|---|--------------|------------------------------|----|----|----|----|----|----|----|----|----|----|-----|----|-----|
| ARO:3004592 | erm(32)                    | erm(32) is a rRNA methyltransferase. Encodes methyltransferases that modify 23S rRNA.   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide  | MLS          | Antibiotic target alteration | 34 | 38 | 14 | 4  | 28 | 46 | 18 | 4  | 16 | 24 | 32  | 32 | 290 |
| ARO:3004595 | erm(45)                    | Erm45 is an rRNA methylase that confers resistances to macrolide, lincosamide, and streptogramin B.   | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide  | MLS          | Antibiotic target alteration | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 6  | 0   | 0  | 6   |
| ARO:3004596 | erm(46)                    | erm(46) is transferable determinant that confers resistance to macrolides.  | Erm 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;macrolide  | MLS          | Antibiotic target alteration | 0  | 70 | 28 | 18 | 20 | 22 | 34 | 32 | 26 | 36 | 6   | 30 | 322 |
| ARO:3004597 | Klebsiella pneumoniae KpnH | KpnH consists of ~511 residues, resembles EmrB of E. coli, and is probably a translocase in the KpnGH-TolC efflux protein in K. pneumoniae. Disruption of the pump components KpnG-KpnH significantly decrease resistance to azithromycin, ceftazidime, ciprofloxacin, ertapenem, erythromycin, gentamicin, imipenem, ticarcillin, norfloxacin, polymyxin-B, piperacillin, spectinomycin, tobramycin, and streptomycin. | major facilitator superfamily (MFS) antibiotic efflux pump | aminoglycoside antibiotic;carbapenem;cephalosporin;fluoroquinolone antibiotic;macrolide antibiotic;penam;penem;peptide antibiotic | Multidrug    | Antibiotic efflux            | 0  | 4  | 0  | 16 | 0  | 0  | 58 | 10 | 0  | 6  | 18  | 24 | 136 |
| ARO:3004599 | clcD                       | clcD gene can provide resistance to representatives of five of the six antibiotic groups previously shown to be affected by Cfr. clcD was originally found in Clostridioides difficile and is cfr-like.   | Cfr 23S ribosomal RNA methyltransferase                    | lincosamide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic             | Multidrug    | Antibiotic target alteration | 66 | 32 | 52 | 10 | 12 | 30 | 28 | 24 | 14 | 76 | 102 | 30 | 476 |
| ARO:3004601 | LnuP                       | LnuP is a lincosamide nucleotidyltransferase major efflux facilitator   | lincosamide nucleotidyltransferase (LNU)                   | lincosamide antibiotic  | MLS          | Antibiotic inactivation      | 2  | 16 | 0  | 4  | 4  | 6  | 0  | 0  | 18 | 72 | 84  | 10 | 216 |
| ARO:3004603 | tet(56)                    | A tetracycline inactivating enzyme. A flavoenzyme capable of degrading tetracycline antibiotics.  | tetracycline inactivation enzyme                           | tetracycline antibiotic   | Tetracycline | Antibiotic inactivation      | 0  | 0  | 0  | 0  | 0  | 20 | 0  | 2  | 0  | 0  | 0   | 0  | 22  |

|                 |                      |   |   |                                  |                 |                              |      |      |      |      |      |      |      |      |      |      |      |      |       |
|-----------------|----------------------|---|---|----------------------------------|-----------------|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|-------|
| ARO:3004<br>606 | erm(40)              | erm(40) is an adenine RNA methylase and confers intrinsic resistance in Mycobacteria.   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS             | Antibiotic target alteration | 0    | 0    | 0    | 6    | 0    | 0    | 10   | 6    | 0    | 32   | 58   | 14   | 126   |
| ARO:3004<br>608 | EreD                 | erythromycin esterase protein   | macrolide esterase                      | macrolide antibiotic             | MLS             | Antibiotic inactivation      | 2    | 6    | 134  | 84   | 100  | 10   | 98   | 226  | 84   | 1098 | 750  | 1274 | 3866  |
| ARO:3004<br>611 | ampC1 beta-lactamase | Escherichia coli An ampC-like beta-lactamase identified from Escherichia coli.  | ampC-type beta-lactamase                | cephalosporin;penam              | Beta-lactam     | Antibiotic inactivation      | 1184 | 864  | 1218 | 956  | 642  | 650  | 1244 | 1156 | 670  | 590  | 520  | 490  | 10184 |
| ARO:3004<br>612 | ampH beta-lactamase  | Escherichia coli AmpH is a class C ampC-like beta-lactamase and penicillin-binding protein identified in Escherichia coli.                | ampC-type beta-lactamase                | cephalosporin;penam              | Beta-lactam     | Antibiotic inactivation      | 660  | 454  | 376  | 1192 | 466  | 360  | 1614 | 1364 | 462  | 362  | 338  | 264  | 7912  |
| ARO:3004<br>623 | AAC(3)-IId           | AAC(3)-IId is a plasmid-encoded aminoglycoside acetyltransferase in E. coli   | AAC(3)                                  | aminoglycoside antibiotic        | Aminoglycoside  | Antibiotic inactivation      | 234  | 1126 | 46   | 456  | 430  | 358  | 534  | 492  | 332  | 264  | 224  | 344  | 4840  |
| ARO:3004<br>624 | QnrS11               | QnrS11 is a plasmid-mediated quinolone resistance protein.  | quinolone resistance protein (qnr)      | fluoroquinolone antibiotic       | Fluoroquinolone | Antibiotic target protection | 206  | 2    | 0    | 4    | 0    | 44   | 2    | 6    | 0    | 0    | 0    | 0    | 264   |
| ARO:3004<br>626 | Erm(49)              | Erm(49) is an rRNA methylase gene   | Erm 23S ribosomal RNA methyltransferase | lincosamide antibiotic;macrolide | MLS             | Antibiotic target alteration | 278  | 362  | 350  | 260  | 98   | 408  | 212  | 188  | 108  | 178  | 110  | 122  | 2674  |
| ARO:3004<br>629 | AAC(6')-Im           | AAC(6')-Im is an aminoglycoside acetyltransferase encoded by plasmids in E. coli, and E. faecium  | AAC(6')                                 | aminoglycoside antibiotic        | Aminoglycoside  | Antibiotic inactivation      | 22   | 36   | 96   | 94   | 56   | 114  | 72   | 90   | 76   | 6    | 4    | 8    | 674   |
| ARO:3004<br>636 | qnrE1                | qnrE1 is a member of the qnrE family of plasmid-borne (fluoro)quinolone-resistance genes, with chromosomal origins from Enterobacter spp. | quinolone resistance protein (qnr)      | fluoroquinolone antibiotic       | Fluoroquinolone | Antibiotic target protection | 0    | 0    | 0    | 2    | 2    | 0    | 2    | 14   | 0    | 22   | 18   | 18   | 78    |
| ARO:3004<br>639 | Corynebacterium      | tetAB genes of the Corynebacterium striatum R-plasmid which encode an ABC transporter and confer  | major facilitator superfamily (MFS)     | penam;tetracycline antibiotic    | Multidrug       | Antibiotic efflux            | 2074 | 1838 | 1490 | 1790 | 1016 | 2048 | 2446 | 2060 | 1310 | 2154 | 2860 | 2150 | 23236 |



|                 |                                       |  |   |   |  |  |      |      |     |     |     |     |     |     |     |     |     |      |      |  |
|-----------------|---------------------------------------|--|---|---|--|--|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|--|
|                 | striatum<br>tetA                      | tetracycline, oxytetracycline,<br>and oxalic resistance  | antibiotic<br>efflux pump<br>trimethopri<br>m resistant<br>dihydrofolat<br>e reductase<br>dfr |   |  |  |      |      |     |     |     |     |     |     |     |     |     |      |      |  |
| ARO:3004<br>642 | dfrA3b                                | A dihydrofolate reductase that<br>confers resistance to<br>trimethoprim  | diaminopyrimidi<br>ne antibiotic  | Diaminopy<br>rimidine   | Antibioti<br>c target<br>replace<br>ment | 0  | 4    | 0    | 0   | 0   | 6   | 0   | 0   | 0   | 2   | 6   | 0   | 18   |      |  |
| ARO:3004<br>643 | Erm(K)                                | 23S rRNA (adenine(2058)-N(6))-<br>methyltransferase Erm(K)<br>[Bacillus halodurans]  | Erm 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase  | lincosamide<br>antibiotic;macrol<br>ide<br>gramin antibiotic      | MLS                                      | 408                                      | 1028 | 458  | 374 | 250 | 570 | 414 | 394 | 296 | 106 | 136 | 70  | 4504 |      |  |
| ARO:3004<br>644 | dfrA6<br>from<br>Proteus<br>mirabilis | dfrA6 is a dihydrofolate<br>reductase that confers<br>resistance to trimethoprim.  | trimethopri<br>m resistant<br>dihydrofolat<br>e reductase<br>dfr                              | diaminopyrimidi<br>ne antibiotic                                  | Diaminopy<br>rimidine                    | Antibioti<br>c target<br>replace<br>ment | 2    | 0    | 10  | 2   | 60  | 2   | 2   | 0   | 30  | 152 | 144 | 300  | 704  |  |
| ARO:3004<br>645 | dfrI                                  | dfrI is a dihydrofolate reductase<br>that is resistant to<br>trimethoprim.   | trimethopri<br>m resistant<br>dihydrofolat<br>e reductase<br>dfr                              | diaminopyrimidi<br>ne antibiotic                                  | Diaminopy<br>rimidine                    | Antibioti<br>c target<br>replace<br>ment | 28   | 202  | 522 | 122 | 98  | 100 | 64  | 104 | 124 | 88  | 122 | 138  | 1712 |  |
| ARO:3004<br>648 | AQU-3                                 | AQU-3 is a chromosomally-<br>encoded AQU class C beta-<br>lactamase and cephalosporinase<br>from   | AQU beta-<br>lactamase  | cephalosporin   | Beta-<br>lactam                          | Antibioti<br>c<br>inactivat<br>ion       | 0    | 0    | 0   | 26  | 0   | 0   | 66  | 18  | 0   | 14  | 2   | 2    | 128  |  |
| ARO:3004<br>649 | cfr(B)                                | cfr(B) has been observed in<br>mobile genetic elements in E.<br>faecium and Clostridioides<br>difficile and confers resistance<br>to linezolid, clindamycin,<br>erythromycin, chloramphenicol,<br>and retapamulin. | Cfr 23S<br>ribosomal<br>RNA<br>methyltransf<br>erase  | lincosamide<br>antibiotic;oxazoli<br>dione<br>phenicol antibiotic | Multidrug                                | Antibioti<br>c target<br>alteratio<br>n  | 666  | 1006 | 854 | 416 | 404 | 816 | 410 | 444 | 398 | 432 | 358 | 310  | 6514 |  |
| ARO:3004<br>650 | tetU                                  | Tetracycline-resistant<br>determinant encoded on the<br>plasmid pKQ10 in Enterococcus<br>faecium   | major<br>facilitator<br>superfamily<br>(MFS)<br>antibiotic<br>efflux pump                     | tetracycline<br>antibiotic  | Tetracyclin<br>e                         | Antibioti<br>c efflux                    | 26   | 4    | 8   | 0   | 102 | 56  | 0   | 0   | 96  | 2   | 0   | 0    | 294  |  |
| ARO:3004<br>651 | lin                                   | Listeria monocytogenes EGD-e<br>lin gene for lincomycin<br>resistance ABC-F type ribosomal<br>protection protein, complete<br>CDS.   | lincosamide<br>nucleotidyltr<br>ansferase<br>(LNU)  | lincosamide<br>antibiotic   | MLS                                      | Antibioti<br>c<br>inactivat<br>ion       | 66   | 236  | 164 | 128 | 104 | 186 | 114 | 168 | 190 | 274 | 262 | 294  | 2186 |  |
| ARO:3004<br>652 | Erm(O)-<br>Irm                        | ErmO (gene Irm) lincomycin<br>resistance methylase<br>[Streptomyces lividans].   | Erm 23S<br>ribosomal<br>RNA   | lincosamide<br>antibiotic;macrol<br>ide                           | MLS                                      | Antibioti<br>c target                    | 0    | 0    | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 2   | 24   | 26   |  |

|             |   |   |  |  |              |                              |     |     |     |     |      |    |     |      |      |      |      |      |       |
|-------------|---|---|--|--|--------------|------------------------------|-----|-----|-----|-----|------|----|-----|------|------|------|------|------|-------|
|             |   |   |  | methyltransferase; streptomycin antibiotic |              | alteration                   |     |     |     |     |      |    |     |      |      |      |      |      |       |
| ARO:3004656 | catII from <i>Escherichia coli</i> K-12 | catII is a chloramphenicol acetyltransferase. This particular catII is found in <i>E. coli</i> K-12. Confers resistance to chloramphenicol.   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic                        | Phenicol     | Antibiotic inactivation      | 0   | 82  | 16  | 0   | 2    | 16 | 4   | 4    | 2    | 0    | 0    | 0    | 126   |
| ARO:3004657 | catA4                                   | catA4 is a chloramphenicol acetyltransferase that confers resistance to chloramphenicol.  | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic                        | Phenicol     | Antibiotic inactivation      | 6   | 4   | 10  | 32  | 14   | 8  | 12  | 12   | 2    | 2    | 4    | 4    | 110   |
| ARO:3004658 | catA8                                   | catA8 is a chloramphenicol acetyltransferase that confers resistance to chloramphenicol.  | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic                        | Phenicol     | Antibiotic inactivation      | 0   | 0   | 0   | 2   | 0    | 0  | 4   | 2    | 0    | 22   | 10   | 16   | 56    |
| ARO:3004659 | Mef(En2)                                | NBU2-encoded resistance gene. An MefE homolog in <i>Bacteroides</i> species. Macrolide efflux MFS transporter   | major facilitator superfamily (MFS) antibiotic efflux pump | macrolide antibiotic                       | MLS          | Antibiotic efflux            | 100 | 60  | 232 | 30  | 20   | 76 | 40  | 54   | 44   | 36   | 20   | 12   | 724   |
| ARO:3004660 | catB11                                  | catB11 is a chloramphenicol acetyltransferase that confers resistance to chloramphenicol.   | chloramphenicol acetyltransferase (CAT)                    | phenicol antibiotic                        | Phenicol     | Antibiotic inactivation      | 6   | 102 | 556 | 404 | 3120 | 28 | 594 | 1156 | 2976 | 1736 | 1940 | 2120 | 14738 |
| ARO:3004662 | MCR-3.3                                 | MCR-3.3 is a colistin resistance gene variant in the chromosome of an <i>Aeromonas veronii</i> . Conferred polymyxin resistance in both <i>E. coli</i> and <i>Aeromonas salmonicida</i> | MCR phosphoethanolamine transferase                        | peptide antibiotic                         | Peptide      | Antibiotic target alteration | 0   | 2   | 0   | 2   | 0    | 10 | 6   | 0    | 0    | 2    | 12   | 0    | 34    |
| ARO:3004663 | FusF                                    | A fusidic acid resistance determinant in <i>Staphylococcus cohnii</i> . FusD-like   | fusidic acid inactivation enzyme                           | fusidic acid                               | Fusidic acid | Antibiotic inactivation      | 2   | 2   | 0   | 2   | 0    | 28 | 0   | 2    | 0    | 0    | 0    | 0    | 36    |
| ARO:3004665 | cmlA8                                   | cmlA8 is a plasmid that confers resistance to chloramphenicol.  | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic                        | Phenicol     | Antibiotic efflux            | 0   | 0   | 0   | 4   | 0    | 0  | 18  | 20   | 0    | 14   | 16   | 56   | 128   |
| ARO:3004666 | pexA                                    | pexA is a florfenicol and chloramphenicol resistance gene discovered in Alaskan soil.   | major facilitator superfamily (MFS) antibiotic efflux pump | phenicol antibiotic                        | Phenicol     | Antibiotic efflux            | 0   | 0   | 6   | 0   | 0    | 0  | 0   | 0    | 0    | 26   | 34   | 8    | 74    |

|                 |                               |  |  |                            |                 |                              |     |      |     |    |     |     |     |    |     |      |      |      |      |
|-----------------|-------------------------------|--|--|----------------------------|-----------------|------------------------------|-----|------|-----|----|-----|-----|-----|----|-----|------|------|------|------|
| ARO:3004<br>667 | Staphylococcus aureus<br>norA | NorA gene cloned from Staphylococcus aureus conferred relatively high resistance to hydrophilic quinolones such as norfloxacin, enoxacin, ofloxacin, and ciprofloxacin in S. aureus and Escherichia coli. Had low or no resistance at all to hydrophobic ones such as nalidixic acid, oxolinic acid, and sparfloxacin in S. aureus and Escherichia coli. Expression of cloned aphA15 gene in Escherichia coli reduced the susceptibility to kanamycin and neomycin, as well as to amikacin, netilmicin, and streptomycin | major facilitator superfamily (MFS) antibiotic efflux pump | fluoroquinolone antibiotic | Fluoroquinolone | Antibiotic efflux            | 182 | 16   | 34  | 2  | 196 | 162 | 8   | 2  | 160 | 296  | 268  | 474  | 1800 |
| ARO:3004<br>675 | aphA15                        | APH(3')-VIIIa is an aminoglycoside phosphoryltransferase that acts on the 3-OH target of aminoglycosides found in Streptomyces rimosus. Small mobilizable plasmid pALWED1.8 containing a novel variant of the streptomycin/spectinomycin resistance gene   | APH(3')  | aminoglycoside antibiotic  | Aminoglycoside  | Antibiotic inactivation      | 0   | 0    | 0   | 0  | 0   | 0   | 2   | 4  | 6   | 70   | 94   | 88   | 264  |
| ARO:3004<br>680 | APH(3')-VIIIa                 | a novel Tn4551 streptomycin-resistance gene that was phenotypically silent in wild-type Bacteroides; expression could be activated by a trans-acting chromosomal mutation  | APH(3')  | aminoglycoside antibiotic  | Aminoglycoside  | Antibiotic inactivation      | 0   | 0    | 0   | 0  | 0   | 0   | 0   | 0  | 0   | 4    | 18   | 0    | 22   |
| ARO:3004<br>682 | aadA27                        | A mobilized and plasmid-mediated colistin resistance gene and phosphoethanolamine transferase identified from a Salmonella enterica isolate  | ANT(3'')   | aminoglycoside antibiotic  | Aminoglycoside  | Antibiotic inactivation      | 162 | 1832 | 4   | 34 | 26  | 410 | 22  | 54 | 38  | 62   | 58   | 84   | 2786 |
| ARO:3004<br>683 | aadS                          | A plasmid-mediated MCR-3.1 variant   | ANT(6)   | aminoglycoside antibiotic  | Aminoglycoside  | Antibiotic inactivation      | 22  | 50   | 244 | 32 | 120 | 70  | 176 | 52 | 106 | 1230 | 1178 | 1348 | 4628 |
| ARO:3004<br>684 | MCR-9.1                       | A plasmid-mediated MCR-3.1 variant   | MCR phosphoethanolamine transferase                        | peptide antibiotic         | Peptide         | Antibiotic target alteration | 128 | 98   | 32  | 86 | 18  | 84  | 80  | 66 | 48  | 318  | 150  | 228  | 1336 |
| ARO:3004<br>691 | MCR-3.4                       | aadA10 is a aminoglycoside nucleotidyltransferase gene   | MCR phosphoethanolamine transferase                        | peptide antibiotic         | Peptide         | Antibiotic target alteration | 26  | 160  | 50  | 0  | 12  | 70  | 2   | 0  | 28  | 0    | 0    | 0    | 348  |
| ARO:3004<br>692 | aadA10                        |  | ANT(3'')   | aminoglycoside antibiotic  | Aminoglycoside  | Antibiotic                   | 0   | 0    | 22  | 36 | 18  | 0   | 6   | 42 | 20  | 132  | 218  | 224  | 718  |

|             |                              |   |   |  |              |                              |     |      |     |      |      |     |      |      |      |      |      |      |       |
|-------------|------------------------------|---|---|--|--------------|------------------------------|-----|------|-----|------|------|-----|------|------|------|------|------|------|-------|
| ARO:3004693 | MCR-3.12                     | encoded by plasmids in <i>P. aeruginosa</i> .<br>A plasmid-mediated phosphoethanolamine transferase and MCR-3 variant conferring resistance to colistin antibiotics.    | MCR phosphoethanolamine transferase                     | peptide antibiotic   | Peptide      | Antibiotic target alteration | 0   | 42   | 0   | 4    | 0    | 2   | 2    | 10   | 0    | 0    | 0    | 0    | 60    |
| ARO:3004694 | MCR-4.2                      | A plasmid-mediated MCR-4 variant which confers resistance to colistin antibiotics.  | MCR phosphoethanolamine transferase                     | peptide antibiotic   | Peptide      | Antibiotic target alteration | 230 | 18   | 44  | 2    | 12   | 182 | 4    | 4    | 40   | 2    | 6    | 0    | 544   |
| ARO:3004695 | MCR-4.3                      | A plasmid-mediated MCR-4 variant and colistin resistance gene from clinical Enterobacteriaceae  | MCR phosphoethanolamine transferase                     | peptide antibiotic   | Peptide      | Antibiotic target alteration | 2   | 2    | 0   | 0    | 2    | 10  | 6    | 4    | 4    | 2    | 0    | 0    | 32    |
| ARO:3004696 | MCR-4.4                      | A plasmid-mediated MCR-4 variant and colistin resistance gene   | MCR phosphoethanolamine transferase                     | peptide antibiotic   | Peptide      | Antibiotic target alteration | 434 | 202  | 114 | 1168 | 558  | 58  | 1552 | 1234 | 418  | 118  | 170  | 38   | 6064  |
| ARO:3004698 | MCR-5.2                      | A plasmid-mediated MCR-5 variant from <i>Escherichia coli</i> which confers resistance to colistin antibiotics.   | MCR phosphoethanolamine transferase                     | peptide antibiotic   | Peptide      | Antibiotic target alteration | 448 | 456  | 202 | 1164 | 532  | 178 | 1516 | 1280 | 480  | 1474 | 974  | 2058 | 10762 |
| ARO:3004699 | sta                          | Streptothricin acetyltransferase gene (STAT gene) that confers streptothricin resistance on <i>Escherichia coli</i> and <i>Bacillus subtilis</i> .                      | streptothricin acetyltransferase (SAT)                  | nucleoside antibiotic  | Nucleoside   | Antibiotic inactivation      | 0   | 0    | 4   | 36   | 0    | 4   | 14   | 20   | 0    | 48   | 128  | 62   | 316   |
| ARO:3004715 | vga(E) Staphylococcus cohnii | vga(E) gene variant that confers resistance to pleuromutilins, lincosamides and streptogramins. A antibiotics in staphylococci  | ABC-F ATP-binding cassette ribosomal protection protein | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic | Multidrug    | Antibiotic target protection | 84  | 158  | 128 | 80   | 32   | 144 | 78   | 76   | 36   | 132  | 158  | 90   | 1196  |
| ARO:3004719 | Tet(X3)                      | A tetracycline resistance gene located on an approximately 300-kb plasmid, designated p47AB. It inactivates all tetracyclines, including tigecycline, eravacycline, and | tetracycline inactivation enzyme                        | glycylcycline;tetracycline antibiotic  | Tetracycline | Antibiotic inactivation      | 474 | 1026 | 970 | 1126 | 6586 | 622 | 1056 | 1868 | 5994 | 2600 | 2400 | 3166 | 27888 |

|                 |         |   |   |  |              |                              |     |      |      |     |      |      |     |     |      |      |     |      |       |
|-----------------|---------|---|---|--|--------------|------------------------------|-----|------|------|-----|------|------|-----|-----|------|------|-----|------|-------|
| ARO:3004<br>720 | Tet(X4) | omadacycline.Adjacent to insertion sequence ISVsa3 on the conjugative plasmid. A tetracycline resistance gene located on an approximately 180-kb plasmid, designated p47EC. It inactivates all tetracyclines, including tigecycline, eravacycline, and omadacycline.Adjacent to insertion sequence ISVsa3 on the conjugative plasmid.   | tetracycline inactivation enzyme                        | glycylcycline;tetracycline antibiotic  | Tetracycline | Antibiotic inactivation      | 92  | 100  | 276  | 224 | 1012 | 106  | 204 | 616 | 1088 | 902  | 806 | 1012 | 6438  |
| ARO:3004<br>730 | tva(A)  | A pleuromutilin resistance gene encoding a predicted ABC-F transporter. The presence of inhibitory or sub-inhibitory concentrations of tiamulin showed that tva(A) confers reduced pleuromutilin susceptibility that does not lead to clinical resistance but facilitates the development of higher-level resistance via mutations in genes encoding ribosome-associated functions. | ABC-F ATP-binding cassette ribosomal protection protein | lincosamide antibiotic;macrolide antibiotic;oxazolidinone antibiotic;phenicol antibiotic;pleuromutilin antibiotic;streptogramin antibiotic;tetracycline antibiotic | Multidrug    | Antibiotic target protection | 984 | 1814 | 1170 | 696 | 482  | 1154 | 664 | 724 | 690  | 1100 | 886 | 994  | 11358 |
| ARO:3004<br>747 | BAT-1   | BAT-1 is a class D beta-lactamase found in <i>Bacillus atrophaeus</i> .   | BAT Beta-lactamase                                      | cephalosporin  | Beta-lactam  | Antibiotic inactivation      | 2   | 0    | 90   | 14  | 124  | 2    | 10  | 38  | 98   | 0    | 0   | 0    | 378   |
| ARO:3004<br>749 | BCL-1   | BCL-1 is a class A beta-lactamase found in <i>Bacillus clausii</i> .  | BCL Beta-lactamase                                      | penam  | Beta-lactam  | Antibiotic inactivation      | 20  | 0    | 0    | 0   | 0    | 30   | 0   | 0   | 0    | 0    | 0   | 0    | 50    |
| ARO:3004<br>755 | BIL-1   | BIL-1 is a plasmid-borne beta-lactamase that is also a class C beta-lactamase.  | BIL Beta-lactamase                                      | cephalosporin  | Beta-lactam  | Antibiotic inactivation      | 0   | 0    | 0    | 0   | 0    | 0    | 0   | 0   | 2    | 248  | 136 | 344  | 730   |
| ARO:3004<br>757 | BKC-1   | BKC-1 is a beta-lactamase conferring resistance to carbapenem and is found in <i>Brazilian Klebsiella</i> .   | BKC Beta-lactamase                                      | carbapenem   | Beta-lactam  | Antibiotic inactivation      | 0   | 0    | 14   | 12  | 12   | 6    | 56  | 24  | 30   | 30   | 16  | 4    | 204   |
| ARO:3004<br>761 | BRO-1   | BRO-1 is a class A beta-lactamase found in <i>M.catarrhalis</i> .   | BRO Beta-lactamase                                      | penam  | Beta-lactam  | Antibiotic inactivation      | 2   | 2    | 82   | 12  | 16   | 22   | 14  | 8   | 10   | 16   | 22  | 2    | 208   |

|                 |        |  |                    |                                |             |                         |     |     |    |     |     |    |      |     |     |     |     |      |      |
|-----------------|--------|--|--------------------|--------------------------------|-------------|-------------------------|-----|-----|----|-----|-----|----|------|-----|-----|-----|-----|------|------|
| ARO:3004<br>764 | CBP-1  | CBP-1 is a class A beta-lactamase gene found in <i>C. botulinum</i> .                      | CBP beta-lactamase | penam                          | Beta-lactam | Antibiotic inactivation | 8   | 26  | 24 | 0   | 2   | 6  | 6    | 2   | 2   | 2   | 0   | 0    | 78   |
| ARO:3004<br>780 | DES-1  | DES-1 is a class A beta-lactamase gene found in <i>Desulfovibrio desulfuricans</i> .       | DES beta-lactamase | penam                          | Beta-lactam | Antibiotic inactivation | 0   | 0   | 0  | 0   | 0   | 0  | 6    | 0   | 0   | 0   | 0   | 0    | 6    |
| ARO:3004<br>802 | GOB-10 | GOB-10 is a class B beta-lactamase gene found in <i>Chryseobacterium meningosepticum</i> . | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 16  | 16 | 64  | 6   | 8  | 14   | 44  | 4   | 4   | 6   | 0    | 182  |
| ARO:3004<br>803 | GOB-11 | GOB-11 is a class B beta-lactamase gene found in <i>Chryseobacterium meningosepticum</i> . | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 2   | 4   | 2  | 0   | 8   | 2  | 2    | 0   | 2   | 26  | 58  | 48   | 154  |
| ARO:3004<br>804 | GOB-12 | GOB-12 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .   | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 0   | 2  | 18  | 0   | 4  | 2    | 10  | 2   | 0   | 0   | 0    | 38   |
| ARO:3004<br>805 | GOB-13 | GOB-13 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .   | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 332 | 144 | 66 | 666 | 304 | 32 | 1092 | 786 | 222 | 106 | 90  | 46   | 3886 |
| ARO:3004<br>807 | GOB-15 | GOB-15 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .   | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 2   | 0   | 0  | 0   | 2   | 0  | 0    | 0   | 2   | 16  | 22  | 18   | 62   |
| ARO:3004<br>808 | GOB-16 | GOB-16 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .   | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 18  | 50  | 30 | 44  | 32  | 48 | 56   | 86  | 44  | 66  | 94  | 62   | 630  |
| ARO:3004<br>810 | GOB-3  | GOB-3 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .    | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 20  | 16  | 40 | 2   | 0   | 24 | 8    | 12  | 4   | 0   | 4   | 0    | 130  |
| ARO:3004<br>812 | GOB-5  | GOB-5 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .    | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 0   | 32  | 0  | 0   | 0   | 4  | 2    | 6   | 0   | 0   | 0   | 0    | 44   |
| ARO:3004<br>813 | GOB-6  | GOB-6 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .    | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 54  | 4   | 2  | 50  | 0   | 44 | 24   | 30  | 0   | 680 | 692 | 1210 | 2790 |
| ARO:3004<br>816 | GOB-9  | GOB-9 is a class B beta-lactamase gene found in <i>Elizabethkingia meningoseptica</i> .    | GOB beta-lactamase | carbapenem;cephalosporin;penam | Beta-lactam | Antibiotic inactivation | 6   | 42  | 20 | 0   | 4   | 0  | 8    | 4   | 4   | 112 | 102 | 134  | 436  |

|                 |        |  |                    |  |             |                                    |    |    |    |    |    |    |    |    |    |    |    |     |     |
|-----------------|--------|--|--------------------|--|-------------|------------------------------------|----|----|----|----|----|----|----|----|----|----|----|-----|-----|
|                 |        |  |                    |  |             | inactivat<br>ion                   |    |    |    |    |    |    |    |    |    |    |    |     |     |
| ARO:3004<br>826 | LAP-2  | LAP-2 is an Ambler Class A beta-lactamase gene conferring resistance to quinolones.  | LAP beta-lactamase | aminoglycoside<br>antibiotic;fluoro<br>quinolone<br>antibiotic;rifamy<br>cin<br>antibiotic;tetracy<br>cline antibiotic | Multidrug   | Antibioti<br>c<br>inactivat<br>ion | 18 | 52 | 0  | 12 | 0  | 10 | 36 | 12 | 0  | 2  | 14 | 4   | 160 |
| ARO:3004<br>856 | SCO-1  | Narrow-spectrum beta-lactamase isolated from several Acinetobacter spp. isolates from Argentina, as well as E. Coli. Hydrolyzes penicillins at a high level and cephalosporins and carbapenems at a very low level | SCO beta-lactamase | cephalosporin;pe<br>nam;penem  | Beta-lactam | Antibioti<br>c<br>inactivat<br>ion | 0  | 0  | 6  | 0  | 0  | 0  | 0  | 0  | 0  | 6  | 10 | 14  | 36  |
| ARO:3004<br>870 | NDM-27 | A class B New Delhi metallo-beta-lactamase and NDM-1 variant   | NDM beta-lactamase | carbapenem;cep<br>halosporin;cepha<br>mycin;penam  | Beta-lactam | Antibioti<br>c<br>inactivat<br>ion | 0  | 0  | 34 | 0  | 36 | 0  | 0  | 0  | 24 | 68 | 64 | 148 | 374 |