**Antimicrobial Resistance Gene Analysis - Whole Genome Sequencing (WGS)**

**Specimen Information**

|  |  |
| --- | --- |
| WGS Analysis Date | : 2025-06-24 |
| DPH Lab ID | : AR\_0055 |
| Patient Name | : N/A |

**Organism Identification**

Escherichia coli

**Resistance Genes Detected**

|  |  |  |
| --- | --- | --- |
| Gene | AR Class | AR Subclass |
| aac(6')-Ib | AMINOGLYCOSIDE | AMIKACIN/KANAMYCIN/TOBRAMYCIN |
| rmtC | AMINOGLYCOSIDE | AMINOGLYCOSIDE |
| aac(3)-IIe | AMINOGLYCOSIDE | GENTAMICIN |
| aadA5 | AMINOGLYCOSIDE | STREPTOMYCIN |
| blaNDM-1 | BETA-LACTAM | CARBAPENEM |
| blaCMY-6 | BETA-LACTAM | CEPHALOSPORIN |
| blaOXA-1 | BETA-LACTAM | CEPHALOSPORIN |
| ble | BLEOMYCIN | BLEOMYCIN |
| mph(A) | MACROLIDE | AZITHROMYCIN/ERYTHROMYCIN/SPIRAMYCIN/TELITHROMYCIN |
| catB3 | PHENICOL | CHLORAMPHENICOL |
| sul1 | SULFONAMIDE | SULFONAMIDE |
| tet(A) | TETRACYCLINE | TETRACYCLINE |
| dfrA17 | TRIMETHOPRIM | TRIMETHOPRIM |

**Point Mutations**

|  |  |  |
| --- | --- | --- |
| Gene | AR Class | AR Subclass |
| ptsI\_V25I | FOSFOMYCIN | FOSFOMYCIN |
| uhpT\_E350Q | FOSFOMYCIN | FOSFOMYCIN |
| gyrA\_D87N | QUINOLONE | QUINOLONE |
| gyrA\_S83L | QUINOLONE | QUINOLONE |
| parC\_E84V | QUINOLONE | QUINOLONE |
| parC\_S80I | QUINOLONE | QUINOLONE |
| parE\_I529L | QUINOLONE | QUINOLONE |

**Other Possible Resistance Mechanisms**

|  |  |  |
| --- | --- | --- |
| Gene | AR Class | AR Subclass |
| blaEC | BETA-LACTAM | BETA-LACTAM |
| acrF | EFFLUX | EFFLUX |
| mdtM | EFFLUX | EFFLUX |

**Notes**

* Identifying a resistance marker or point mutation does not necessarily predict the therapeutic failure of antimicrobial agents. The gene or point mutation may be nonfunctional or expressed at clinically insignificant levels.
* The absence of a genetic marker or point mutation does not always indicate susceptibility.
* The presence of a genetic marker or mutation does not always correlate with phenotypic test results, and discordance between phenotypic and genotypic test results is possible.
* Discrepancies can occur due to the fact that the mechanism of resistance may be something other than what the genotypic test can identify, or expression may be inducible by environmental factors.
* Isolates with phenotypic susceptibility despite the presence of resistance markers may indicate the potential for resistance to emerge during therapy.
* Antimicrobial genes may be expressed but not enough/sufficient for an isolate to change the phenotypic interpretation of the clinical breakpoint.
* Whole Genome Sequencing antimicrobial susceptibility test results should be used in conjunction with other phenotypic test results, when applicable.

**Disclaimer**

This whole genome sequencing test method was developed, and its performance characteristics were determined by the Connecticut State Public Health Laboratory. This test has not been cleared or approved by the U.S. Food and Drug Administration.