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

**Specimen Information**

|  |  |
| --- | --- |
| WGS Analysis Date: | 2025-01-06 |
| DPH Lab ID: | AR55 |
| Patient Name: |  |

**Predicted Organism**

|  |  |
| --- | --- |
| Escherichia coli | 99.72% |

**Resistance Genes**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | AR Subclass/Mechanism | Coverage(%) | Identity(%) |
| aac(6')-Ib | AMIKACIN/KANAMYCIN/TOBRAMYCIN | 100.0 | 100.0 |
| rmtC | AMINOGLYCOSIDE | 100.0 | 100.0 |
| mph(A) | AZITHROMYCIN/ERYTHROMYCIN/SPIRAMYCIN/TELITHROMYCIN | 100.0 | 100.0 |
| blaEC | BETA-LACTAM | 88.59 | 99.1 |
| ble | BLEOMYCIN | 100.0 | 100.0 |
| blaNDM-1 | CARBAPENEM | 100.0 | 100.0 |
| blaCMY-6 | CEPHALOSPORIN | 100.0 | 100.0 |
| blaOXA-1 | CEPHALOSPORIN | 100.0 | 100.0 |
| catB3 | CHLORAMPHENICOL | 70.0 | 100.0 |
| acrF | EFFLUX | 100.0 | 99.52 |
| mdtM | EFFLUX | 99.76 | 97.31 |
| aac(3)-IIe | GENTAMICIN | 100.0 | 100.0 |
| aadA5 | STREPTOMYCIN | 100.0 | 100.0 |
| sul1 | SULFONAMIDE | 100.0 | 100.0 |
| tet(A) | TETRACYCLINE | 100.0 | 100.0 |
| dfrA17 | TRIMETHOPRIM | 100.0 | 100.0 |

**Point Mutations**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | AR Subclass/Mechanism | Coverage(%) | Identity(%) |
| glpT\_E448K | FOSFOMYCIN | 100.0 | 99.78 |
| ptsI\_V25I | FOSFOMYCIN | 100.0 | 99.65 |
| uhpT\_E350Q | FOSFOMYCIN | 100.0 | 99.78 |
| gyrA\_D87N | QUINOLONE | 99.66 | 98.86 |
| gyrA\_S83L | QUINOLONE | 99.66 | 98.86 |
| parC\_E84V | QUINOLONE | 100.0 | 99.2 |
| parC\_S80I | QUINOLONE | 100.0 | 99.2 |
| parE\_I529L | QUINOLONE | 100.0 | 99.52 |

**Notes**

* Coverage(%) refers to the percentage of the sequenced gene length compared to the reference resistance gene.
* Identity(%) refers to the similarity between the identified and the reference genes.

**Disclaimer**

This whole genome sequencing (WGS) test result was developed and its performance characteristics determined by the State Public Health Laboratory. This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA).  
  
Detection Limitations: Identifying a resistance marker does not necessarily predict therapeutic failure of antimicrobial agents. The gene may be nonfunctional or expressed at clinically insignificant levels.  
  
False Negatives: The absence of a genetic marker does not always indicate susceptibility. Technical issues such as inhibition or the emergence of genetic variants can interfere with detection.  
  
Genotypic vs. Phenotypic Correlation: 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.  
  
Interpretation: WGS antimicrobial susceptibility test results should be used in conjunction with other phenotypic test results, when applicable.