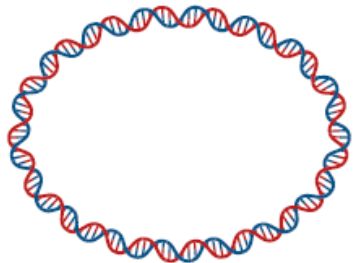


Genome Announcement: *Pseudomonas aeruginosa*

Accession# SRR23106254(NCBI)
INS0000469(INDA)

1. Genome Sequencing



BRIC-THSTI

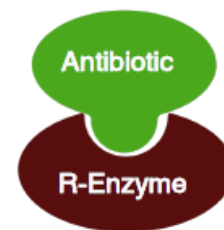
Presenting the Whole Genome Sequence of *Pseudomonas aeruginosa*: An Opportunistic Pathogen Isolated from Human Tissue

2. Analysis



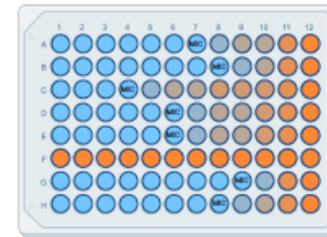
This genomic analysis reveals key insights into the resistance mechanisms, pathogenic traits, virulence factors, and metabolic capabilities of *P. aeruginosa*

3. Insights



AMR functions in *P. aeruginosa* are highly heterogeneous, linked with MGEs, with the potential to transfer resistance traits to other bacteria.

4. Translation



Genomic analysis is transforming our ability to track and combat antibiotic resistance, paving the way for improved prognostic outcomes and better overall health

Unraveling the *Pseudomonas aeruginosa* Genome: Understanding the Superbug That Threatens Our Health

Genomics of *Pseudomonas aeruginosa* SRR23106254

