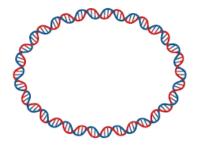
Genome Announcement: Klebsiella pneumoniae

Accession# SRR23106222(NCBI) INS0000458 (INDA)

1. Genome Sequencing



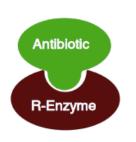
BRIC-THSTI has decoded the whole genome sequence of Klebsiella pneumoniae isolated from the pleural fluid of an Indian patient.

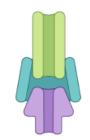
2. Analysis



In silico WGS
analysis of this
pathogen identified
factors contributing
to its pathogenicity,
AMR, and survival
under stress
conditions.

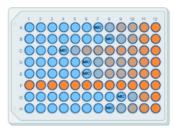
3. Insights





The genome of Klebsiella pneumoniae harbors multiple resistance genes against commonly used clinical antibiotics.

4. Translation



Exploring this genomic data is crucial for developing enhanced diagnostics to track the spread of AMR bacteria, ultimately supporting more effective clinical outcomes.

characteristic

Genome size: 5.49 mb

GC percent: 57.1

CDS: 5500

Stable RNAs: 83

Plasmid: Present

MR genes

fosA6, ompA, arnT, eptB, ompK37, SHV-1, vanG, MdtQ, QnrS1, OXA-232, rmtF, AAC(6')-lb, arr-2, mphA, Mrx, Efflux pumps