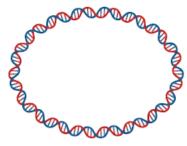
Genome Announcement: Proteus mirabilis

Accession# SRR23106352 (NCBI) INS0000478(INDA)

1. Genome Sequencing



BRIC-THSTI

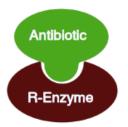
presenting the
whole genome
sequence of
Proteus mirabilis
isolated from the
cerebrospinal fluid
of an Indian patient.

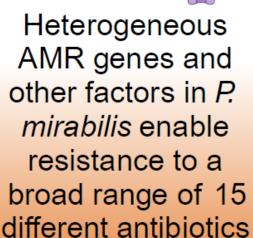
2. Analysis



Through this genomic analysis, we gain valuable insights into the specific virulence factors, treatment resistance mechanisms, and overall pathogenic potential.

3. Insights

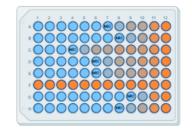




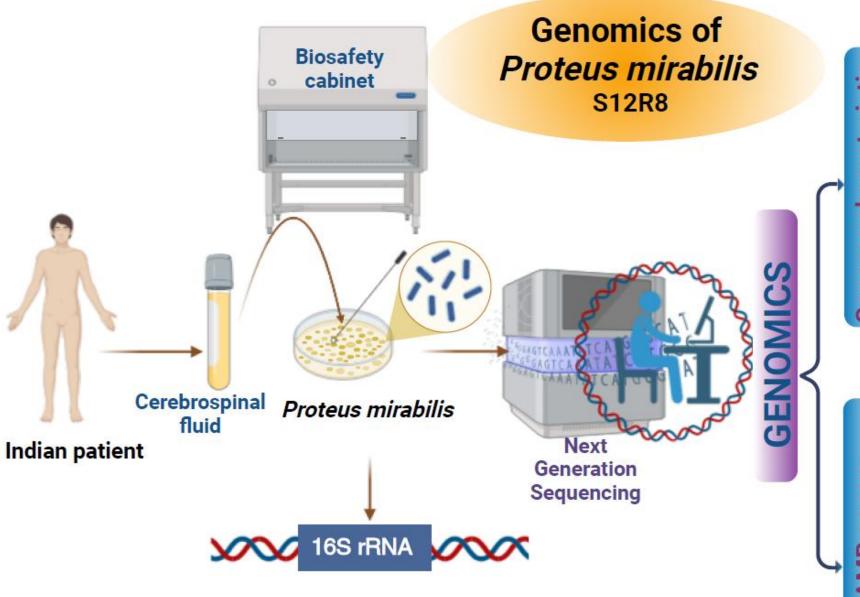
commonly used in

the clinical practice.

4. Translation



By understanding the genetic basis of antibiotic resistance, we can develop better molecular diagnostic tests and effective preventive measures to protect public health.



Genome characteristics

Genome size: 3.65 mb

GC percent: 39.8

CDS: 3487

Stable RNAs: 73

MGEs: Present

AMR genes

arnT, catA4, vanG, dfrA1, ant(2")-la, aac(6')-lb10, veb-6, qnrA1, Efflux pumps