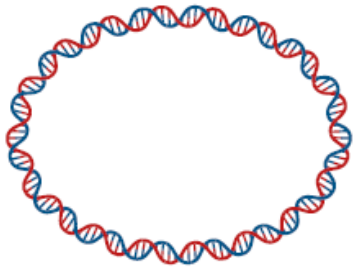
Genome Announcement: *Escherichia coli*

Accession# SRR23106403(NCBI)
INS0000450 (INDA)

1. Genome Sequencing

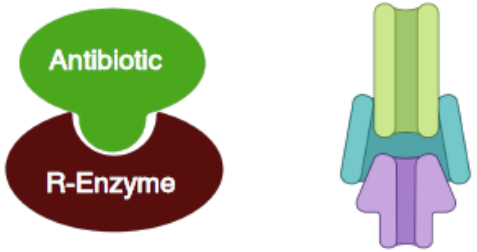


BRIC-THSTI presenting the whole genome sequence of *Escherichia coli* isolated from the urine of a patient with a urinary tract infection.

2. Analysis

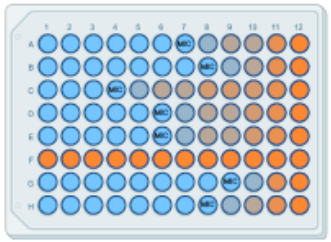
This genomic analysis highlights the functional factors that contribute to AMR, pathogenicity, and survival under stress conditions.

3. Insights



Genes contributing to AMR in *E. coli* are highly heterogeneous, associated with mobile genetic elements, and can be transferred to other bacteria via HGT.

4. Translation

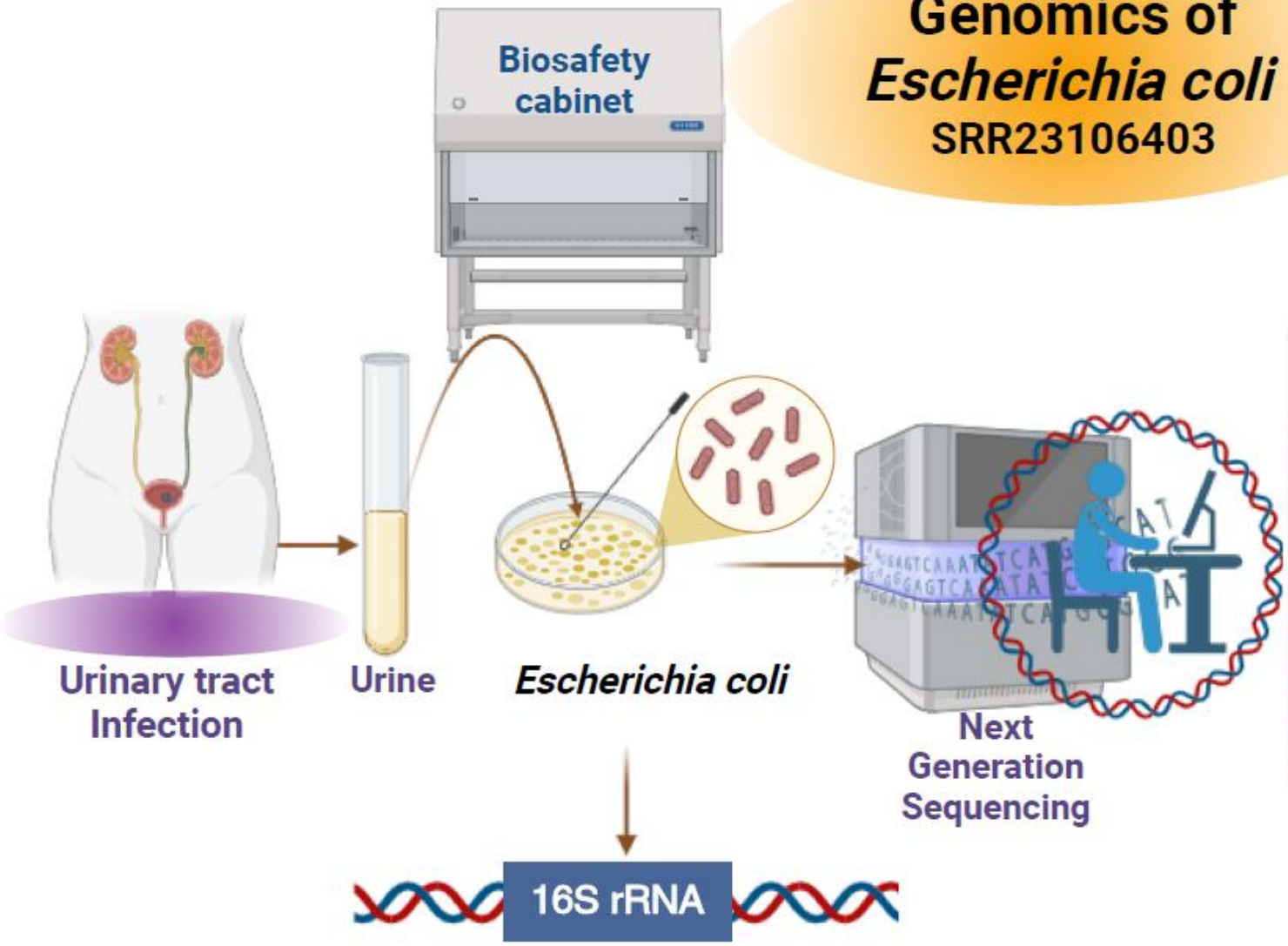


Exploring this genomic information aids in developing better diagnostics and new drugs for improved clinical outcomes.

MDR *Escherichia coli*: Unveiling its Molecular Weapons

Genomics of *Escherichia coli*

SRR23106403



GENOMICS

Genome characteristics

- Genome size: 4.97 mb
- GC percent: 50.7
- CDS: 5011
- Stable RNAs: 81
- Plasmid: Present

AMR genes

arnT, pmrF, vanG, eptA, bacA, EC-15, CMY-42, NDM-5, BRP(MBL), ermB, CTXM-15, aadA2, dfrA12, aadA5, dfrA17, sul1, OXA-140, Efflux pumps