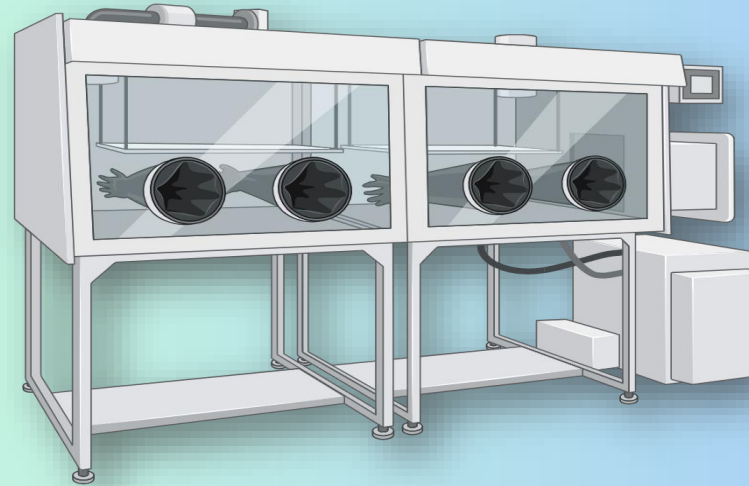
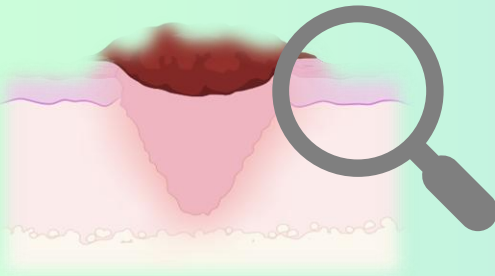




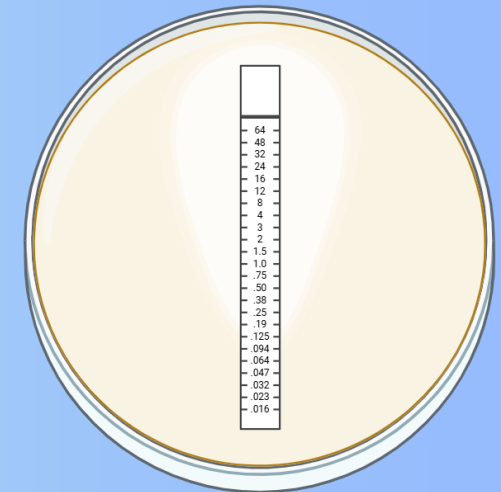
## *Klebsiella pneumoniae* (NIBMG\_HMR\_27)

A Major Human Pathogen of Wound and Systematic Infection

Genome Sequencing will help in formulating Prompt Diagnosis and Effective Treatment options



Isolated from Diabetic Foot Ulcers



Multi Drug Resistant Pathogen  
Invade Host Immunity

***Klebsiella pneumoniae* (NIBMG\_HMR\_27)**      **Genome Accession Number:** [INS0009754](#)

**Quality of Genome Assembly and Annotation:**

Results from indigenously developed **BHARAT** analysis pipeline: (**B**acterial **H**ybrid genome **A**ssembly and **R**apid **A**nnotation **T**oolset)

Table 1: Assembly Details

|               |              |
|---------------|--------------|
| Contigs       | 87           |
| GC Content    | 57.16        |
| Contig L50    | 5            |
| Genome length | 5,541,106 bp |
| Contig N50    | 361,227      |

Table 2: Annotated Genome Features

|                |       |
|----------------|-------|
| CDS            | 5,506 |
| tRNA           | 76    |
| rRNA           | 3     |
| Repeat Regions | 0     |

Subsystem Analysis

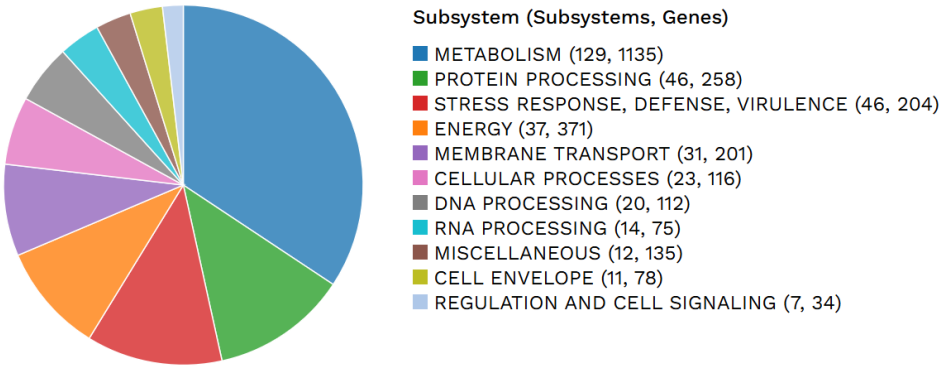


Table 3: Predicted Antimicrobial Resistance Phenotypes

|             |                                                                                                                        |
|-------------|------------------------------------------------------------------------------------------------------------------------|
| Resistant   | Amikacin, Aztreonam, Cefepime, Ciprofloxacin, Trimethoprim/Sulfamethoxazole                                            |
| Susceptible | Cefoxitin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Piperacillin/Tazobactam, Tetracycline, Tobramycin |

Table 4: Antimicrobial Resistance Genes

| AMR Mechanism                                 | Genes                                                                                                                       |
|-----------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| Antibiotic inactivation enzyme                | AAC(6')-Ib/AAC(6')-II, CatB family, CTX-M family, FONA/SFO family, Mph(A) family, NDM family, SHV family                    |
| Antibiotic target in susceptible species      | Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, inhA, fabI, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p      |
| Efflux pump conferring antibiotic resistance  | AcrAB-TolC, AcrAD-TolC, AcrEF-TolC , AcrZ, EmrAB-TolC, EmrD, MacA, MacB, MdfA/Cmr, MdtABC-TolC, MdtL, MdtM, SugE, TolC/OpmH |
| Protein modulating permeability to antibiotic | OccD6/OprQ, OprB                                                                                                            |

Genome Assembly

