

Quality of Genome Assembly and Annotation:

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

Table 1: Assembly Details	
Contigs	36
GC Content	46.23
Contig L50	5
Genome length	4,189,249 bp
Contig N50	290,274

Table 2: Annotated Genome Features	
CDS	3,970
tRNA	55
Repeat Regions	7
rRNA	0

Subsystem Analysis

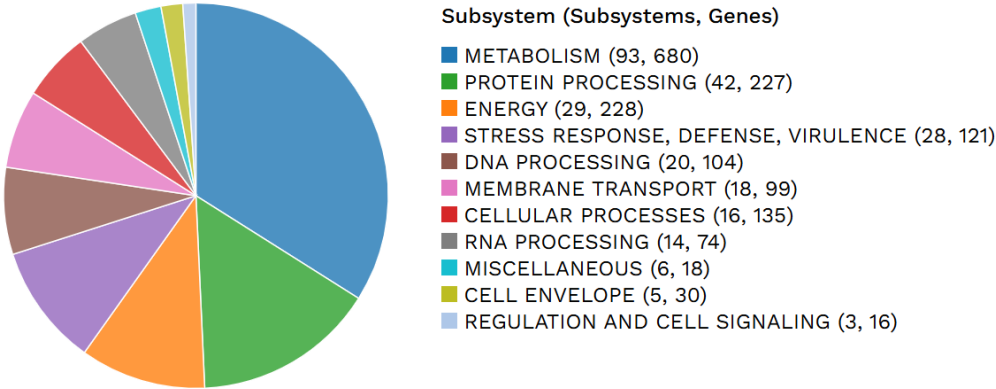


Table 3: Antimicrobial Resistance Genes	
AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	MexEF-OprN, TolC/OpmH
Regulator modulating expression of antibiotic resistance genes	OxyR
Antibiotic target replacement protein	fabV
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA

Genome Assembly

