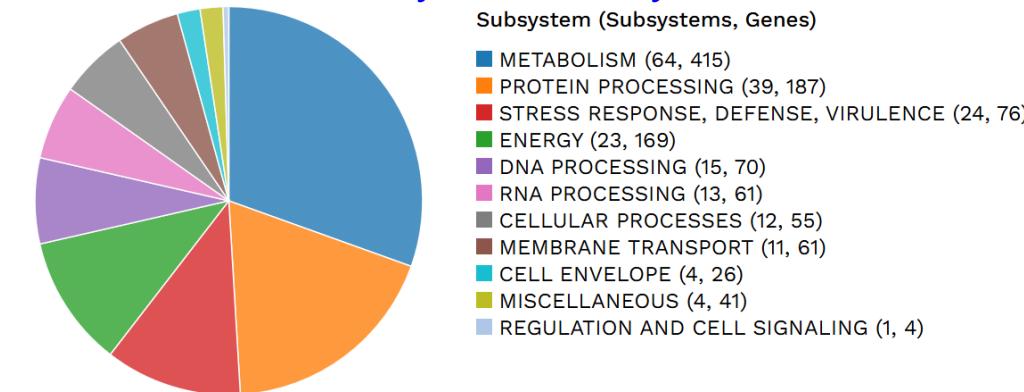


Quality of Genome Assembly and Annotation:Results from indigenously developed **BHARAT** analysis pipeline: (**Bacterial Hybrid genome Assembly and Rapid Annotation Toolset**)**Table 1: Assembly Details**

Contigs	121
GC Content	35.85
Contig L50	13
Genome length	4,573,526 bp
Contig N50	135,195

Table 2: Annotated Genome Features

CDS	4,428
tRNA	70
Repeat Regions	75
rRNA	2

Subsystem Analysis**Table 3: Antimicrobial Resistance Genes**

AMR Mechanism	Genes
Antibiotic target in susceptible species	Ddl, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, inhA, fabI, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Antibiotic inactivation enzyme	CIA family
Antibiotic activation enzyme	KatG
Gene conferring resistance via absence	gidB
Protein altering cell wall charge conferring antibiotic resistance	GdpD
Regulator modulating expression of antibiotic resistance genes	OxyR

Genome Assembly