



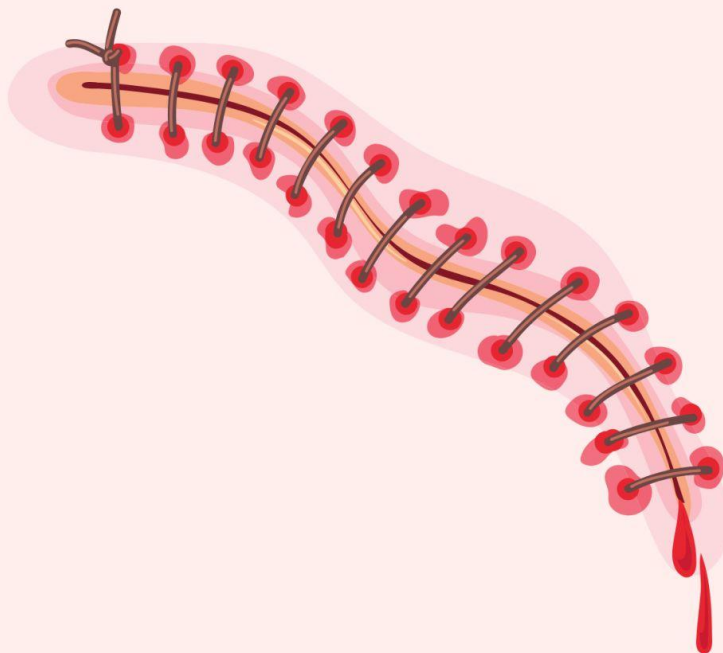
Government of India
Ministry of Science & Technology
Department of Biotechnology



One Day One Genome

Luteimonas sp.

The microbe expands our understanding
of microbial diversity in chronic wounds



Luteimonas sp.

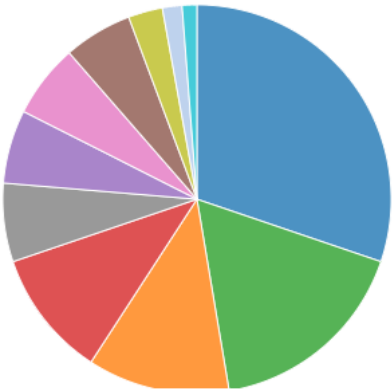
Genome Accession Number: INS0025521

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	34
GC Content	69.40
Contig L50	5
Genome length	3,181,466 bp
Contig N50	265,442

Table 2: Annotated Genome Features	
CDS	2,949
tRNA	49
rRNA	3



Subsystem Analysis

- Subsystem (Subsystems, Genes)
- METABOLISM (74, 398)
 - PROTEIN PROCESSING (42, 222)
 - ENERGY (29, 228)
 - STRESS RESPONSE, DEFENSE, VIRULENCE (26, 103)
 - DNA PROCESSING (16, 69)
 - MEMBRANE TRANSPORT (15, 94)
 - RNA PROCESSING (15, 69)
 - CELLULAR PROCESSES (14, 89)
 - CELL ENVELOPE (7, 35)
 - MISCELLANEOUS (4, 9)
 - REGULATION AND CELL SIGNALING (3, 10)

Table 3: Antimicrobial Resistance Genes	
AMR Mechanism	Genes
Antibiotic target replacement protein	fabV
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
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Gene conferring resistance via absence	gidB
Efflux pump conferring antibiotic resistance	MacA, TolC/OpmH
Regulator modulating expression of antibiotic resistance genes	OxyR

Genome Assembly

