

Accession number	Organism name	Culture type	Pathogenicity	Genome Size	No. of Genes	Pathogenic genes	Importance
<u>INS0005653</u>	Staphylococcus aureus (OG15)	Aerobic, Gram +ve, Coagulase positive	Highly pathogenic	2.8 million bp	2,670	Resistance to beta-lactams, aminoglycosides and tetracyclines, virulence factors such as multidrug efflux pumps and enterotoxins	Its genome will provide invaluable insights for improving healthcare strategies, particularly in combating infections and understanding resistance mechanisms

Genome sequencing of highly pathogenic *Staphylococcus aureus* could lead to effective treatment options



Quality of Genome Assembly and Annotation:

Staphylococcus aureus (OG15) Draft genome accession number: INS0005653

Table 1. Assembly Details		Table 2. Annotated Genome Features		
Contigs	26	CDS	2,670	
GC Content	32.70	tRNA	57	
Plasmids	0	PDNA	2	
Contig L50	2		5	
Genome Length	2,799,804 bp	Partial CDS	0	
Contig N50	538,821			