

Staphylococcus aureus, Strain AJUL22

Catalog No. NR-55236

Product Description:

Staphylococcus aureus (*S. aureus*), strain AJUL22 is deposited as a daptomycin-resistant spontaneous mutant of *S. aureus*, strain SH1000 resulting from a DNA mutation encoding amino acid substitution S₂₉₅L in the phosphatidylglycerol lysyltransferase (*mprF*) gene. NR-55236 was produced by resuspension of a lyophilized vial of deposited material in Tryptic Soy broth. Broth inoculum was added to Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. The material from the initial growth was added to Tryptic Soy agar with 5% defibrinated sheep blood kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70052865

Manufacturing Date: 25MAY2022

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TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis Cellular morphology Colony morphology Motility (wet mount) Hemolysis Catalase VITEK® MS (MALDI-TOF)	Gram-positive cocci Report results Report results Report results Positive <i>S. aureus</i>	Gram-positive cocci Circular, low convex, entire, smooth and cream (Figure 1) Non-motile β-hemolytic Positive <i>S. aureus</i> (99.9%)
Antibiotic Susceptibility Profile¹ Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar Daptomycin	Resistant	Resistant (2 µg per mL)
Genotypic Analysis Digital DNA-DNA hybridization (dDDH) ² Next-Generation Sequencing (NGS) analysis for antimicrobial resistance genes ⁴ Daptomycin	≥ 70% for species identification Resistant	<i>S. aureus</i> (99.4%) ³ Resistant
Purity (post-freeze) 7 days at 37°C in an aerobic atmosphere with and without 5% CO ₂ on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)	Growth	Growth

¹Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: Clinical & Laboratory Standards Institute (CLSI) M100-S28 (2018)

²Relatedness between bacterial strains has traditionally been determined using DDH. For additional information refer to Auch, A.F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." *Stand. Genomic Sci.* 2 (2010): 117-134. PubMed: 21304684.

³The whole genome of *S. aureus*, strain AJUL22 (contig total length approximately 2.66 megabase pairs) was sequenced using the Illumina® MiSeq® system.

⁴*In silico* analysis of NGS data for antimicrobial resistance genes was performed using the Bacterial and Viral Bioinformatics Resource Center, ResFinder and Pathogenwatch genome analysis tools.

Figure 1: Colony Morphology



/Sonia Bjorum Brower/
Sonia Bjorum Brower
Technical Manager or designee, ATCC Federal Solutions

30 JAN 2023

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