

Staphylococcus aureus, Strain AJUL25

Catalog No. NR-55239

Product Description:

Staphylococcus aureus (*S. aureus*), strain AJUL25 is deposited as a sulfamethoxazole-resistant spontaneous mutant of *S. aureus*, strain SH1000 containing two common resistance mutations, F₁₇L and E₂₀₈K, in the dihydropteroate synthase (*dhps*) gene created by Φ80-mediated transduction of this locus from *S. aureus*, strain Newman in which these mutations occur naturally. NR-55239 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 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: 70052871

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, convex, entire, smooth and cream-to-yellow Non-motile β-hemolytic Positive <i>S. aureus</i> (99.9%)
Genotypic Analysis Digital DNA-DNA hybridization (dDDH) ¹ Next-Generation Sequencing (NGS) analysis for antimicrobial resistance genes ³ Sulfamethoxazole	≥ 70% for species identification Resistant	<i>S. aureus</i> (99.4%) ² Sensitive ⁴
Purity (post-freeze) 8 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

¹Relatedness 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.

²The whole genome of *S. aureus*, strain AJUL25 (contig total length approximately 2.66 megabase pairs) was sequenced using the Illumina® MiSeq® system.

³*In silico* analysis of NGS data for antimicrobial resistance genes was performed using the Bacterial and Viral Bioinformatics Resource Center (BV-BRC), ResFinder and Pathogenwatch genome analysis tools.

⁴*S. aureus*, strain AJUL25 was deposited as resistant to sulfamethoxazole. *In silico* analysis determined the predicted phenotype of this antibiotic as sensitive (ResFinder). No data for this antibiotic is available in the BV-BRC or Pathogenwatch.

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