Certificate of Analysis for NR-55230

Staphylococcus aureus, Strain AJUL16

Catalog No. NR-55230

Product Description:

Staphylococcus aureus (S. aureus), strain AJUL16 is deposited as a retapamulin-resistant strain derived from *S. aureus*, strain SH1000 through introduction of plasmid pSK5487M containing the gene *vga*(A) (encoding ABC-F-type ribosomal protection protein) and a chloramphenicol resistance gene *(cat)* for selection. NR-55230 was produced by resuspension of a lyophilized vial of deposited material in Tryptic Soy broth. Broth inoculum was added to Tryptic Soy broth containing 25 µg per mL chloramphenicol and grown for 1 day at 37°C in an aerobic atmosphere. The material from the initial growth was added to Tryptic Soy agar containing 25 µg per mL chloramphenicol 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: 70052853 **Manufacturing Date: 13MAY2022**

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TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-positive cocci	Gram-positive cocci
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Non-motile
Hemolysis	Report results	β-hemolytic
Catalase	Positive	Positive
VITEK® MS (MALDI-TOF)	*S. aureus*	*S. aureus* (99.9%)
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[1]	≥ 70% for species identification	*S. aureus* (99.5%)[2]
Next-Generation Sequencing (NGS) analysis for antimicrobial resistance genes[3]		
Retapamulin	Resistant	Inconclusive[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

[1] Relatedness 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.

[2] The whole genome of *S. aureus*, strain AJUL16 (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 AJUL16 was deposited as resistant to retapamulin. No antibiotic resistance data for this antibiotic for *S. aureus* is currently available. *In silico* analysis using the BV-BRC, ResFinder and Pathogenwatch genome analysis tools resulted in no data.

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