SUPPORTING INFECTIOUS DISEASE RESEARCH

Escherichia coli K-12, Strain IM30B

Catalog No. NR-49807

Product Description:

Escherichia coli (*E. coli*) K-12, strain IM30B contains the *hsdM* (methylase) and *hsdS* (specificity) genes from *Staphylococcus aureus* MRSA252 clonal complex 30 (CC). This insertion mutant was produced in *E. coli* K-12, strain DC10B via recombination-mediated genetic engineering (recombineering). *E. coli* K-12, strain IM30B was deposited as resistant to streptomycin. NR-49807 was produced by the inoculation of BEI Resources seed lot 63849807 into Tryptic Soy broth containing 25 μ g/mL streptomycin and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar containing 25 μ g/mL streptomycin 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: 70056754

Manufacturing Date: 09NOV2022

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream (Figure 1)
Motility (wet mount)	Report results	Motile
VITEK [®] MS (MALDI-TOF)	Escherichia coli	Escherichia coli (99.9%)
Genotypic Analysis		
Sequencing of 16S ribosomal RNA gene	≥ 99% sequence identity to	99.7% sequence identity to
(~ 1480 base pairs)	<i>E. coli</i> , strain K-12	<i>E. coli</i> , strain K-12
	(GenBank: CP014225.1)	(GenBank: CP014225.1)
Analysis of <i>hsdMS</i> by PCR Assay ^{1,2}		
hsdM2 and hsdS2 (CC30)	~ 3400 base pair amplicon	~ 3400 base pair amplicon
hsdS1 (CC30)	~ 1800 base pair amplicon	~ 1800 base pair amplicon
Analysis of hsdMS by Sequence Analysis ^{1,2}		
<i>hsdM2</i> and <i>hsdS2</i> (~ 1650 base pairs)	Consistent with depositor sequence	Consistent with depositor sequence
hsdS1 (~ 880 base pairs)	Consistent with depositor sequence	Consistent with depositor sequence
Confirmation of Streptomycin Resistance	Growth	Growth
Purity		
7 days at 37°C in an aerobic atmosphere with and without 5% CO ₂ on Tryptic Soy agar with 5% defibrinated sheep blood	Consistent with expected colony morphology	Consistent with expected colony morphology
Viability	Growth	Growth

¹Performed on the previous lot of extracted material (NR-49807 lot 63849808).

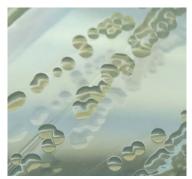
²PCR primers used for amplification were IM434 forward primer 5[']-ACTTTCTTTAAGGCTTAGAGTCAAGC-3['], IM435 reverse primer 5[']-TTTAACGCCACGTTCACTCTTTGC-3['], 179 forward primer 5[']-CGGCCATTTATACAGGAAAAGCCTA-3['] and 180 reverse primer 5[']-GTTACCTTCTATAGAGAGTGGTG-3[']. For additional information, refer to Monk, I., et al. "Complete Bypass of Restriction Systems for Major Staphylococcus aureus Lineages." <u>mBio</u> 26 (2015): e00308-15. PubMed: 26015493.

biei resources

Certificate of Analysis for NR-49807

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Figure 1: Colony Morphology



/Sonia Bjorum Brower/

Sonia Bjorum Brower

22 MAY 2023

Technical Manager or designee, ATCC Federal Solutions

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