

**Escherichia coli K-12, Strain IM93B**

**Catalog No. NR-49808**

**Product Description:**

*Escherichia coli* (*E. coli*) K-12, strain IM93B contains the *hsdM* (methylase) and *hsdS* (specificity) genes from *Staphylococcus aureus* JKD6159 sequence type 93 (ST93). This insertion mutant was produced in *E. coli* K-12, strain DC10B ( $\Delta dcm$ ). *E. coli* K-12, strain IM93B was deposited as resistant to streptomycin. NR-49808 was produced by inoculation of BEI Resources seed lot 63849810 into Tryptic Soy broth containing 25 µg/mL streptomycin and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar containing 25 µg/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: 70065133**

**Manufacturing Date: 15DEC2023**

TEST	SPECIFICATIONS	RESULTS
<b>Phenotypic Analysis</b> Cellular morphology Colony morphology  Motility (wet mount) VITEK® MS (MALDI-TOF)	Gram-negative rods Report results  Report results <i>Escherichia coli</i>	Gram-negative rods Circular, convex, entire, smooth and cream (Figure 1) Motile <i>Escherichia coli</i> (99.9%)
<b>Genotypic Analysis</b> Sequencing of 16S ribosomal RNA gene (~ 1470 base pairs)	≥ 99% sequence identity to <i>E. coli</i> K-12 strain (GenBank: CP014225.1)	99.9% sequence identity to <i>E. coli</i> K-12 strain (GenBank: CP014225.1) <sup>1</sup>
<b>Analysis of <i>hsdMS</i> by PCR Assay<sup>2,3</sup></b> <i>hsdM2</i> , <i>hsdS2</i> and <i>hsdS1</i> (ST93) <i>hsdM3</i> and <i>hsdS3</i> (ST93)	~ 3200 base pair amplicon ~ 4600 base pair amplicon	~ 3200 base pair amplicon ~ 4600 base pair amplicon
<b>Analysis of <i>hsdMS</i> by Sequence Analysis<sup>2,3</sup></b> <i>hsdM2</i> , <i>hsdS2</i> and <i>hsdS1</i> (~ 740 base pairs) <i>hsdM3</i> and <i>hsdS3</i> (~ 1010 base pairs)	Consistent with depositor sequence Consistent with depositor sequence	Consistent with depositor sequence Consistent with depositor sequence
<b>Confirmation of Streptomycin Resistance</b>	Growth	Growth
<b>Purity</b> 7 days at 37°C in an aerobic atmosphere with 5% CO <sub>2</sub> on Tryptic Soy agar with 5% defibrinated sheep blood	Consistent with expected colony morphology	Consistent with expected colony morphology
<b>Viability</b>	Growth	Growth

<sup>1</sup>Also consistent with *Shigella* and other *Escherichia* species

<sup>2</sup>Performed on BEI Resources seed lot NRS-49808 lot 63849810

<sup>3</sup>PCR primers used for amplification were IM434 forward primer 5'-ACTTCTTTAAGGCTTAGAGTCAAGC-3', IM435 reverse primer 5'-TTTAACGCCACGTTCACTCTTTGC-3', 179 forward primer 5'-CGGCCATTTATACAGGAAAAGCCTA-3' and 180 reverse primer 5'-GTTACCTTCTCTATAGAGAGTGGTG-3'. For additional information, refer to Monk, I., et al. "Complete Bypass of Restriction Systems for Major *Staphylococcus aureus* Lineages." *mBio* 6 (2015): e00308-15. PubMed: 26015493.

Figure 1: Colony Morphology



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