

# Escherichia coli, Strain H263

Catalog No. NR-15829

## Product Description:

*Escherichia coli* (*E. coli*), strain H263 was isolated in 2001 from a human feces sample collected in Canberra, Australian Capital Territory, Australia. NR-15829 was produced by inoculation of the deposited material into Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum 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: 70003319

Manufacturing Date: 24MAR2017

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| TEST                                                                                                                                                                                                                                                                                                                                                                        | SPECIFICATIONS                                                                                                       | RESULTS                                                                                                                                                                                                                                                                                                                                               |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Phenotypic Analysis</b><br>Cellular morphology<br>Colony morphology<br><br>Motility<br>VITEK® MS (MALDI-TOF)                                                                                                                                                                                                                                                             | Gram-negative rods<br>Report results<br><br>Report results<br><i>E. coli</i>                                         | Gram-negative rods<br>Circular, convex, entire, smooth and cream (Figure 1)<br>Motile<br><i>E. coli</i> (99.9%)                                                                                                                                                                                                                                       |
| <b>Genotypic Analysis</b><br>Digital DNA-DNA hybridization (dDDH) <sup>1</sup><br><br>Whole-Genome Sequencing (WGS) analysis<br>Virulence gene prediction <sup>4</sup><br><br>Antimicrobial resistance (AMR) gene prediction <sup>5</sup><br><br>Serotype prediction by gene analysis <sup>6</sup><br><i>fliC</i><br>Multi-Locus Sequence Type (MLST) analysis <sup>7</sup> | ≥ 70% for species identification<br><br>Report results<br><br>Report results<br><br>Report results<br>Report results | <i>E. coli</i> (97.1%) <sup>2,3</sup><br><i>Shigella sonnei</i> (74.0%)<br><i>Shigella flexneri</i> (73.8%)<br><i>Shigella boydii</i> (73.7%)<br><i>Shigella dysenteriae</i> (72.2%)<br><br>Virulence genes present:<br><i>gad</i> , <i>ireA</i> , <i>lss</i> , <i>senB</i><br>No acquired AMR genes or point mutations identified<br><br>H7<br>ST-95 |
| <b>Purity (post-freeze)</b><br>7 days at 37°C in an aerobic atmosphere with and without 5% CO <sub>2</sub> on Tryptic Soy agar                                                                                                                                                                                                                                              | Growth consistent with expected colony morphology                                                                    | Growth consistent with expected colony morphology                                                                                                                                                                                                                                                                                                     |
| <b>Viability (post-freeze)</b>                                                                                                                                                                                                                                                                                                                                              | Growth                                                                                                               | Growth                                                                                                                                                                                                                                                                                                                                                |

<sup>1</sup>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.

<sup>2</sup>Reclassification of *Shigella sonnei*, *Shigella boydii*, *Shigella flexneri* and *Shigella dysenteriae* as subspecies of *E. coli* (*E. coli* subsp. *shigella* subsp. nov.) has been proposed [Dif, G., et al. "In-Depth Genome-Based Analysis of *Shigella* spp. and *Escherichia* spp.: Resolving Ambiguities and Unveiling Phylogenetic Relationships." *Curr. Microbiol.* 82 (2025): 170. PubMed: 40045049].

<sup>3</sup>The whole genome of *E. coli*, strain H263 (Total Contig Length ~ 5.1 megabase pairs) was sequenced using the Illumina® MiSeq™ platform and was analyzed and assembled using CLC Genomics Workbench software.

<sup>4</sup>*In silico* analysis of WGS data for virulence-associated genes was performed using the [Center for Genomic Epidemiology \(CGE\)](#) VirulenceFinder 1.5 genome analysis tool. [Joensen, K. G., et al. "Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic *Escherichia coli*." *J. Clin. Microbiol.* 52 (2014): 1501-1510. PubMed: 24574290.]

<sup>5</sup>*In silico* analysis of WGS data for identification of genes or known point mutations associated with antimicrobial resistance was performed using the [Center for Genomic Epidemiology \(CGE\)](#) ResFinder 3.0 genome analysis tool. [Zankari, E., et al. "Identification of Acquired Antimicrobial Resistance Genes." *J. Antimicrob. Chemother.* 67 (2012): 2640-2644. PubMed: 22782487.]

<sup>6</sup>*In silico* analysis of WGS data for serotype prediction based on flagellin and O-antigen processing system genes was performed using the [Center for Genomic Epidemiology \(CGE\)](#) SerotypeFinder 1.1 genome analysis tool. [Joensen, K. G., et al. "Rapid and Easy *in silico* Serotyping of *Escherichia coli* Isolates by Use of Whole-Genome Sequencing Data." *J. Clin. Microbiol.* 53 (2015): 2410-2426. PubMed: 25972421.]

<sup>7</sup>*In silico* analysis of WGS data for Multi-Locus Sequence Type (MLST) analysis was performed using the [Center for Genomic Epidemiology \(CGE\)](#) MLST web service. [Larsen, M. V., et al. "Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria." *J. Clin. Microbiol.* 50 (2012): 1355-1361. PubMed: 22238442.]

**Figure 1: Colony Morphology**



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