Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 8, 2025

CARD

RRID:SCR_023995
Type: Tool

Proper Citation

CARD (RRID:SCR_023995)

Resource Information

URL: https://card.mcmaster.ca/

Proper Citation: CARD (RRID:SCR_023995)

Description: Comprehensive antibiotic resistance database. Bioinformatic database of resistance genes, their products and associated phenotypes.

Synonyms: card-rgi, Comprehensive Antibiotic Resistance Database, The Comprehensive Antibiotic Resistance Database

Resource Type: data or information resource, database

Defining Citation: PMID:31665441

Keywords: Antibiotic resistance data, resistance genes and associated phenotypes, resistance genes, phenotypes,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CARD

Resource ID: SCR_023995

Old URLs: https://sources.debian.org/src/card-rgi/

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Record Creation Time: 20230824T050211+0000

Record Last Update: 20250404T061624+0000

Ratings and Alerts

No rating or validation information has been found for CARD.

No alerts have been found for CARD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 133 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Yum SJ, et al. (2025) Antibiotic Resistance Genes and Microbiota in Brassica oleracea var. acephala Cultivated in South Korea: Potential for Resistance Transmission. Journal of agricultural and food chemistry, 73(3), 2156.

Wan S, et al. (2025) Biological Characteristics and Whole-Genome Analysis of a Porcine E. coli Phage. Veterinary sciences, 12(1).

Rózsa Á, et al. (2025) Bacteriophage Treatment Induces Phenotype Switching and Alters Antibiotic Resistance of ESBL Escherichia coli. Antibiotics (Basel, Switzerland), 14(1).

Liu B, et al. (2025) Targeted Next-Generation Sequencing in Pneumonia: Applications in the Detection of Responsible Pathogens, Antimicrobial Resistance, and Virulence. Infection and drug resistance, 18, 407.

Brodíková K, et al. (2025) Clonal Complex 398 Methicillin-Resistant Staphylococcus aureus Producing Panton-Valentine Leukocidin, Czech Republic, 2023. Emerging infectious diseases, 31(1), 174.

Lian S, et al. (2025) Genomic insights on cgMLST markers, drug resistance, and urease cluster of Proteus mirabilis strains. Microbiology spectrum, 13(1), e0099224.

Rungsirivanich P, et al. (2025) Functional genomic insights into Floricoccus penangensis ML061-4 isolated from leaf surface of Assam tea. Scientific reports, 15(1), 2951.

Wu W, et al. (2025) Antimicrobial resistance, virulence gene profiles, and molecular epidemiology of enterococcal isolates from patients with urinary tract infections in Shanghai, China. Microbiology spectrum, 13(1), e0121724.

Wang L, et al. (2024) Fecal PCR survey and genome analysis of Lawsonia intracellularis in China. Frontiers in veterinary science, 11, 1324768.

Liu XL, et al. (2024) Detecting and characterizing new endofungal bacteria in new hosts: Pandoraea sputorum and Mycetohabitans endofungorum in Rhizopus arrhizus. Frontiers in microbiology, 15, 1346252.

Gargano V, et al. (2024) Scolopax rusticola Carrying Enterobacterales Harboring Antibiotic Resistance Genes. Antibiotics (Basel, Switzerland), 13(3).

Xia X, et al. (2024) Genomic Epidemiology of Clostridioides difficile ST81 in Multiple Hospitals in China. Infection and drug resistance, 17, 5535.

Branck T, et al. (2024) Comprehensive profile of the companion animal gut microbiome integrating reference-based and reference-free methods. The ISME journal, 18(1).

Lu W, et al. (2024) fosA11, a novel chromosomal-encoded fosfomycin resistance gene identified in Providencia rettgeri. Microbiology spectrum, 12(2), e0254223.

Yan W, et al. (2024) Antimicrobial resistance and genome characteristics of Salmonella enteritidis from Huzhou, China. PloS one, 19(6), e0304621.

Dahdouh E, et al. (2024) Characterizing carbapenemase-producing Escherichia coli isolates from Spain: high genetic heterogeneity and wide geographical spread. Frontiers in cellular and infection microbiology, 14, 1390966.

Zhao F, et al. (2024) Influence of helicobacter pylori on composition and function of gastric microbiota in patients with chronic non-atrophic gastritis. Heliyon, 10(10), e31472.

Mukhopadhyay S, et al. (2024) Comparative Genomics and Characterization of Shigella flexneri Isolated from Urban Wastewater. Microbes and environments, 39(2).

Li J, et al. (2024) Molecular characterization of extensively drug-resistant hypervirulent Pseudomonas aeruginosa isolates in China. Annals of clinical microbiology and antimicrobials, 23(1), 13.

Feng J, et al. (2024) Genetic epidemiology and plasmid-mediated transmission of mcr-1 by Escherichia coli ST155 from wastewater of long-term care facilities. Microbiology spectrum, 12(3), e0370723.