

# Resource Summary Report

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## CARD

RRID:SCR\_016602

Type: Tool

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### Proper Citation

CARD (RRID:SCR\_016602)

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### Resource Information

**URL:** <https://card.niaid.nih.gov>

**Proper Citation:** CARD (RRID:SCR\_016602)

**Description:** Web application for integrated analysis and interactive visualization of RNA interference (RNAi) screening data.

**Abbreviations:** CARD

**Synonyms:** CARD, Comprehensive Analysis of RNAi-screen Data

**Resource Type:** data or information resource, web application, database, software resource, data analysis service, production service resource, service resource, analysis service resource

**Defining Citation:** [PMID:26902267](#)

**Keywords:** integrated, analysis, interactive, visualization, RNA, interference, screening, data, bio.tools

**Funding:** Australian Cancer Research Foundation ;  
Victorian Department of Industry ;  
Innovation and Regional Development ;  
Australian Government's Education Investment Fund ;  
Australasian Genomics Technologies Association ;  
Brockhoff Foundation ;  
Peter MacCallum Cancer Centre Foundation

**Availability:** Free, Freely available

**Resource Name:** CARD

**Resource ID:** SCR\_016602

**Alternate IDs:** biotools:CARD

**Alternate URLs:** <https://bio.tools/CARD>

**Record Creation Time:** 20220129T080331+0000

**Record Last Update:** 20260806T054637+0000

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## Ratings and Alerts

No rating or validation information has been found for CARD.

No alerts have been found for CARD.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 20 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

Tristancho-Baró A, et al. (2025) Genomic Characterization of Carbapenemase-Producing Enterobacteriaceae from Clinical and Epidemiological Human Samples. *Antibiotics* (Basel, Switzerland), 14(1).

Zhao M, et al. (2024) Whole genome sequence data of ZEN-degrading strain *Levilactobacillus brevis* PYN10\_6\_2 isolated from *Tenebrio molitor* larval feces. *Data in brief*, 57, 110911.

Maggi F, et al. (2024) Pangenome analysis of *Paenibacillus polymyxa* strains reveals the existence of multiple and functionally distinct *Paenibacillus* species. *Applied and environmental microbiology*, 90(11), e0174024.

Patangia DV, et al. (2024) Influence of age, socioeconomic status, and location on the infant gut resistome across populations. *Gut microbes*, 16(1), 2297837.

Hefetz I, et al. (2024) Rapid Phenotypic Antibiotic Susceptibility Profiling of Clinical *Escherichia coli* and *Klebsiella pneumoniae* Blood Cultures. *Antibiotics* (Basel, Switzerland), 13(3).

Xu Y, et al. (2024) A widespread single amino acid mutation in AcrA reduces tigecycline susceptibility in *Klebsiella pneumoniae*. *Microbiology spectrum*, 12(1), e0203023.

Yan M, et al. (2024) Viruses contribute to microbial diversification in the rumen ecosystem and are associated with certain animal production traits. *Microbiome*, 12(1), 82.

Alioto TS, et al. (2023) Development of a novel streamlined workflow (AACRE) and database (inCREDBle) for genomic analysis of carbapenem-resistant Enterobacterales. *Microbial genomics*, 9(11).

Simpson AC, et al. (2023) Phylogenomics, phenotypic, and functional traits of five novel (Earth-derived) bacterial species isolated from the International Space Station and their prevalence in metagenomes. *Scientific reports*, 13(1), 19207.

Fostervold A, et al. (2022) A nationwide genomic study of clinical *Klebsiella pneumoniae* in Norway 2001-15: introduction and spread of ESBLs facilitated by clonal groups CG15 and CG307. *The Journal of antimicrobial chemotherapy*, 77(3), 665.

Ji X, et al. (2022) The effect of carbon-based copper nanocomposites on *Microcystis aeruginosa* and the movability of antibiotic resistance genes in urban water. *Chemosphere*, 286(Pt 3), 131744.

Prieto Riquelme MV, et al. (2022) Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. *Environmental science & technology*, 56(21), 14982.

Whittle E, et al. (2022) Optimizing Nanopore Sequencing for Rapid Detection of Microbial Species and Antimicrobial Resistance in Patients at Risk of Surgical Site Infections. *mSphere*, 7(1), e0096421.

Hennart M, et al. (2022) A Dual Barcoding Approach to Bacterial Strain Nomenclature: Genomic Taxonomy of *Klebsiella pneumoniae* Strains. *Molecular biology and evolution*, 39(7).

Králová S, et al. (2021) *Flavobacterium flabelliforme* sp. nov. and *Flavobacterium geliluteum* sp. nov., Two Multidrug-Resistant Psychrotrophic Species Isolated From Antarctica. *Frontiers in microbiology*, 12, 729977.

Aradanas M, et al. (2021) Serotypes, Virulence-Associated Factors, and Antimicrobial Resistance of *Streptococcus suis* Isolates Recovered From Sick and Healthy Pigs Determined by Whole-Genome Sequencing. *Frontiers in veterinary science*, 8, 742345.

Mahfouz N, et al. (2020) Large-scale assessment of antimicrobial resistance marker databases for genetic phenotype prediction: a systematic review. *The Journal of antimicrobial chemotherapy*, 75(11), 3099.

Constantinides B, et al. (2020) Genomic surveillance of *Escherichia coli* and *Klebsiella* spp. in hospital sink drains and patients. *Microbial genomics*, 6(7).

Kariuki S, et al. (2020) High relatedness of invasive multi-drug resistant non-typhoidal *Salmonella* genotypes among patients and asymptomatic carriers in endemic informal settlements in Kenya. *PLoS neglected tropical diseases*, 14(8), e0008440.

Sanderson H, et al. (2020) Comparative genomics of multidrug-resistant *Enterococcus* spp. isolated from wastewater treatment plants. *BMC microbiology*, 20(1), 20.