

Resource Summary Report

Generated by [dkNET](#) on Aug 5, 2026

[resfinder](#)

RRID:SCR_024314

Type: Tool

Proper Citation

resfinder (RRID:SCR_024314)

Resource Information

URL: <https://bitbucket.org/genomicepidemiology/resfinder>

Proper Citation: resfinder (RRID:SCR_024314)

Description: Software tool identifies acquired antimicrobial resistance genes in total or partial sequenced isolates of bacteria. Used for identification of acquired antimicrobial resistance genes in whole-genome data.

Synonyms: ResFinder

Resource Type: data processing software, software application, software resource, data analysis software

Defining Citation: [PMID:22782487](#)

Keywords: acquired antimicrobial resistance genes identification, total or partial sequenced isolates, identification of acquired antimicrobial resistance genes, whole genome data,

Availability: Free, Available for download, Freely available,

Resource Name: resfinder

Resource ID: SCR_024314

Alternate URLs: <https://sources.debian.org/src/resfinder/>

License: Apache License, Version 2.0

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260805T044529+0000

Ratings and Alerts

No rating or validation information has been found for resfinder.

No alerts have been found for resfinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 832 mentions in open access literature.

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

Mahajan S, et al. (2026) Molecular insights into the antimicrobial and cardiometabolic functions of *Lactobacillus crispatus* isolated from the reproductive tract microbiota of Indian women. *Journal of biomedical science*, 33(1), 7.

Liang B, et al. (2026) Antimicrobial resistance and virulence analysis of *Escherichia coli* carried by black-faced spoonbill (*Platalea minor*) in Liaoning, China. *PloS one*, 21(1), e0339376.

Ansari F, et al. (2026) Characterisation of a Novel Jumbo Lytic *Aeromonas dhakensis* Bacteriophage P19 and Its Endolysin. *Microbial biotechnology*, 19(1), e70289.

Hu Y, et al. (2026) Novel KPC-2 variants and epidemic ST463 clones underlie ceftazidime/avibactam resistance in carbapenem-resistant *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(1), e0218725.

Bloomfield SJ, et al. (2025) Ecological insights into the microbiology of food using metagenomics and its potential surveillance applications. *Microbial genomics*, 11(1).

Chaichana N, et al. (2025) Genomic Characterization and Safety Evaluation of *Enterococcus lactis* RB10 Isolated from Goat Feces. *Antibiotics (Basel, Switzerland)*, 14(6).

Nishihama S, et al. (2025) Oral colonization of antimicrobial-resistant bacteria in home health care participants and their association with oral and systemic status. *Scientific reports*, 15(1), 5776.

Boralli CMDs, et al. (2025) Dissemination of IncQ1 Plasmids Harboring NTEKPC-IIId in a Brazilian Hospital. *Microorganisms*, 13(1).

Rebelo AR, et al. (2025) One day in Denmark: whole-genome sequence-based analysis of *Escherichia coli* isolates from clinical settings. *The Journal of antimicrobial chemotherapy*, 80(4), 1011.

Monte DFM, et al. (2025) Clonal spread of blaCTX-M-65 producing *Salmonella enterica* serovars detected in poultry retail meat in North Carolina, USA. *Scientific reports*, 15(1), 26520.

Boondech A, et al. (2025) Complete genome and comparative analysis of *Xanthomonas oryzae* pv. *oryzae* isolated from northern Thailand. *Access microbiology*, 7(6).

Lazarevic V, et al. (2025) Identification of causative agents of infective endocarditis by metagenomic next-generation sequencing of resected valves. *Frontiers in cellular and infection microbiology*, 15, 1532257.

Li J, et al. (2025) Genome-based assessment of antimicrobial resistance of *Escherichia coli* recovered from diseased swine in eastern China for a 12-year period. *mBio*, 16(5), e0065125.

Minotti C, et al. (2025) Interpreting whole-genome sequencing data during neonatal *Klebsiella oxytoca* complex outbreak management. *Antimicrobial resistance and infection control*, 14(1), 76.

Piispa M, et al. (2025) Detecting plasmid-mediated dissemination of bla KPC-3 and bla OXA-48-like genes in Enterobacterales across Finnish healthcare organizations using hybrid genome assembly. *Frontiers in microbiology*, 16, 1567913.

Wang Y, et al. (2025) Impact of *Pseudomonas aeruginosa* biofilm formation by different sequence types on treating lower limb vascular infections. *Current research in microbial sciences*, 8, 100379.

Li P, et al. (2025) Involvement of the bla CTX-M-3 gene in emergence of a peculiar resistance phenotype in *Klebsiella pneumoniae*. *Frontiers in cellular and infection microbiology*, 15, 1545157.

Dong N, et al. (2025) Genetic insights into *Shewanella* spp., progenitor of the bla OXA-48-like genes: a large-scale study. *Microbial genomics*, 11(6).

Wang X, et al. (2025) Molecular epidemiological analysis and research on resistance and virulence of carbapenem-resistant *Klebsiella pneumoniae* in a tertiary hospital from 2016 to 2023. *BMC microbiology*, 25(1), 217.

Fang Y, et al. (2025) Emergence of an XDR *Klebsiella pneumoniae* ST5491 strain co-harboring NDM-5, MCR-1.1, tmexCD1-toprJ1, and a novel plasmid carrying CTX-M-15. *Frontiers in microbiology*, 16, 1581851.