

Resource Summary Report

Generated by [ASWG](#) on Aug 26, 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 analysis software, data processing software, software application, software resource

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: 20260821T194253+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 969 mentions in open access literature.

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

Tang B, et al. (2026) Acquired antimicrobial resistance genes in Bordetella Species: a global genomic analysis. The Journal of antimicrobial chemotherapy, 81(1).

Qin S, et al. (2026) Global emergence, evolution and international dissemination of the ST145 Klebsiella oxytoca lineage. npj antimicrobials and resistance, 4(1).

Cao M, et al. (2026) Synergistic antibacterial activity and mechanism of arginine combined with florfenicol against Escherichia coli. Virulence, 17(1), 2666994.

Lee J, et al. (2026) Probiogenomic and Functional Profiling of the Novel Human Gut-Derived Probiotic Strain Lactococcus lactis SNU-H10 with Multifunctional Traits. Journal of microbiology and biotechnology, 36, e2601069.

Sornsene P, et al. (2026) Probiotic Potential, Genomic Characterization, and In Silico Insights of Five Lactiplantibacillus plantarum Strains Isolated from Fermented Cacao Beans Against Multidrug-Resistant Pseudomonas aeruginosa. Antibiotics (Basel, Switzerland), 15(4).

Pirollo M, et al. (2026) Cross-species and cross-border spread of aph(3')-II-mediated neomycin resistance in Escherichia coli from animals: a genomic perspective. The Journal of antimicrobial chemotherapy, 81(5).

Bahri S, et al. (2026) Spread of Multidrug-Resistant Enterobacterales Strains Isolated From the Hospital Environment and Clinical Specimens Within ICUs in Tunisia. Cureus, 18(1), e102231.

Declerck C, et al. (2026) Spread of extended-spectrum β -lactamase-producing Enterobacterales (ESBL-E) in the community living spaces of patients identified as ESBL-E carriers: impact of the housing density in an African context. Tropical medicine and health, 54(1).

Zhu Y, et al. (2026) Emergence of Carbapenem-Resistant Hypervirulent ST111 K63 Klebsiella pneumoniae in China. Polish journal of microbiology, 75(1), 96.

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.

Zhang R, et al. (2026) Genomic characterization of a virulent multidrug-resistant *Salmonella enterica* serovar Enteritidis strain isolated from meat rabbits (*Oryctolagus cuniculus*) in China. BMC microbiology, 26(1), 116.

Awad MM, et al. (2026) Comparative genomic analysis of RNA-binding proteins across some drug resistant and sensitive *Staphylococcus aureus*. Applied microbiology and biotechnology, 110(1).

Soto E, et al. (2026) Diagnosis of Weissellosis in Cultured Rainbow Trout in Costa Rica Further Evidence Emergence of *Weissella tructae* as Important Pathogen of Salmonids in Latin America. Transboundary and emerging diseases, 2026(1), e4690289.

Weng R, et al. (2026) Heterogeneous multicopy of blaCTX-M variants on the same plasmid enhances evolutionary adaptability in clinical *Klebsiella pneumoniae*. Nature communications, 17(1).

Wang Q, et al. (2026) Novel ST3871 *Escherichia coli* exhibits diverse transmission modes, carrying the tet(X4) resistance gene. Microbiology spectrum, 14(3), e0052125.

Hashim EA, et al. (2026) Global threats in local wards: Dissemination of high-risk clones resistant to last-generation cephalosporins and carbapenems in Iraqi hospitals. IJID regions, 18, 100852.

Chukamnerd A, et al. (2026) Genomic Epidemiology of Carbapenem-Resistant *Acinetobacter baumannii* Isolated from Patients Admitted to Intensive Care Units in Network Hospitals in Southern Thailand. Antibiotics (Basel, Switzerland), 15(2).

Boripun R, et al. (2026) Whole-Genome Sequence Analysis of Colistin-Resistant, mcr-Harboring *Escherichia coli* Isolated from a Swine Slaughterhouse in Thailand. Antibiotics (Basel, Switzerland), 15(2).

Yu D, et al. (2026) Exosome-like Nanovesicles from *Hordeum vulgare* L. Fermented with *Lactiplantibacillus plantarum* BMSE-HMP251 Ameliorate LPS-Induced Inflammation in HT-29 and RAW 264.7 Cells. Molecules (Basel, Switzerland), 31(4).

Legese MH, et al. (2026) High magnitude of carbapenemase-producing *Acinetobacter baumannii* in sepsis patients at Ethiopian referral hospitals: a whole genome analysis. Scientific reports, 16(1).