

Resource Summary Report

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Abricate

RRID:SCR_021093

Type: Tool

Proper Citation

Abricate (RRID:SCR_021093)

Resource Information

URL: <https://github.com/tseemann/abricate>

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Description: Software tool for mass screening of contigs for antimicrobial and virulence genes. Mass screening of contigs for antimicrobial resistance or virulence genes. It comes bundled with multiple databases: NCBI, CARD, ARG-ANNOT, Resfinder, MEGARES, EcOH, PlasmidFinder, Ecoli_VF and VFDB.

Synonyms: ABRicate

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

Keywords: contigs mass screening, antimicrobial genes, virulence genes, antimicrobial genes contigs, virulence genes contigs, FASEB list

Availability: Free, Available for download, Freely available

Resource Name: Abricate

Resource ID: SCR_021093

License: GNU General Public License v2.0

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260919T195448+0000

Ratings and Alerts

No rating or validation information has been found for Abricate.

No alerts have been found for Abricate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1355 mentions in open access literature.

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

Wang X-Y, et al. (2026) Genomic epidemiology and plasmid characterization of antimicrobial resistance and virulence in cattle *Escherichia coli* from China. *Microbiology spectrum*, 14(1), e0325625.

Zhang J, et al. (2026) Clonal dissemination of ST19 *Salmonella* Typhimurium within a Chinese poultry breeding pyramid and One-Health implications. *Poultry science*, 105(1), 106097.

Fu B, et al. (2026) Genomic characterization of *Neisseria meningitidis* from urethritis in a sentinel surveillance hospital, China. *BMC microbiology*, 26(1), 79.

Boncompagni SR, et al. (2026) NDM-63: a novel NDM metallo- β -lactamase variant in the L3 loop, from a *Klebsiella pneumoniae* clinical isolate. *Antimicrobial agents and chemotherapy*, 70(2), e0128625.

Zeng Y, et al. (2026) The prevalence and molecular epidemiology of *Clostridioides difficile* in hospital-based pediatric populations in China. *Emerging microbes & infections*, 15(1), 2602319.

Frentzel H, et al. (2026) Complete genome of a cereulide-producing *Bacillus mobilis* strain. *Microbiology resource announcements*, 15(1), e0078225.

Ozawa M, et al. (2026) Characterization of *Lactococcus* isolated from diseased yellowtail in Japan using whole-genome sequencing. *The Journal of veterinary medical science*, 88(2), 305.

Ishibashi M, et al. (2026) Isolation of *Clostridioides difficile* from the atmospheric fine particulate matter. *BMC microbiology*, 26(1).

Boateng W, et al. (2026) Predominance of antimicrobial resistance genes and high-risk clones among Gram negatives from clinical sources in Accra-Ghana. *PloS one*, 21(4), e0344837.

Souza SSR, et al. (2026) Diversity and evolution of leukotoxin operons in *Staphylococcus aureus*. *mSystems*, 11(5), e0173525.

Zhou M, et al. (2026) Genomic Insights Into Carbapenem-Resistant *Klebsiella pneumoniae* in Pediatric Bloodstream Infections in Zhejiang, China (2019-2024). *Journal of clinical laboratory analysis*, 40(10), e70232.

Shin JH, et al. (2026) Comparison of hybrid-and mono-pathotype *Escherichia coli* isolates from South Korea based on whole genome analysis and cytotoxicity assay. *Journal of biomedical science*, 33(1).

Bah SY, et al. (2026) Molecular analysis of Lancefield group C/G streptococci causing human infections in Sheffield, UK. *Microbial genomics*, 12(5).

Shen H, et al. (2026) Co-occurrence of the tigecycline resistance gene cluster *tmexCD3-toprJ1* and verona integron-encoded metallo- β -lactamase (VIM) in a human-derived *Pseudomonas sediminis* isolate. *Microbiology spectrum*, 14(6), e0349125.

Tomás Fornés D, et al. (2026) Efficacy of Environmental Sampling Devices for *Listeria monocytogenes* Detection in a Ready-to-Eat Production Facility. *Foods (Basel, Switzerland)*, 15(8).

Lei D, et al. (2026) Clade-specific adaptation and global spread of *Staphylococcus aureus* ST188 with emergence of a multidrug-resistant MRSA sublineage. *mSystems*, 11(1), e0084825.

Morgado SM, et al. (2026) Tracking a misclassified pathogen: genomic and epidemiological features of *Vibrio paracholerae*. *Microbial genomics*, 12(1).

Mohamed FA, et al. (2026) Emergence of OXA-48-like Carbapenemase-Producing *Escherichia coli* in Baranya County, Hungary. *Antibiotics (Basel, Switzerland)*, 15(1).

Zhou W, et al. (2026) Emergence and genomic adaptation of the globally disseminated ST2250 lineage within the *Staphylococcus aureus* complex. *Antimicrobial agents and chemotherapy*, 70(3), e0162825.

Wang Y, et al. (2026) A Genomic Catalog of Migratory Microbiomes from Wild Birds across China's Habitats. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(26), e74581.