

Resource Summary Report

Generated by T1D on Sep 5, 2026

VirulenceFinder

RRID:SCR_024371

Type: Tool

Proper Citation

VirulenceFinder (RRID:SCR_024371)

Resource Information

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

Proper Citation: VirulenceFinder (RRID:SCR_024371)

Description: Software tool for detection of E. coli virulence genes. Used to identify virulence genes in total or partial sequenced isolates of bacteria. E. coli, Enterococcus, S. aureus and Listeria are available for detection of E. coli virulence genes.

Synonyms: virulencefinder

Resource Type: software application, software resource

Defining Citation: [PMID:24574290](https://pubmed.ncbi.nlm.nih.gov/24574290/)

Keywords: detection of E. coli virulence genes,

Availability: Free, Available for download, Freely available,

Resource Name: VirulenceFinder

Resource ID: SCR_024371

Alternate IDs: OMICS_17862

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

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260904T000528+0000

Ratings and Alerts

No rating or validation information has been found for VirulenceFinder.

No alerts have been found for VirulenceFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 301 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Bao D, et al. (2026) Genomic characterization of extended-spectrum β -Lactamases (ESBLs)-producing *Escherichia coli* recovered from bloodstream infections in China. *BMC microbiology*, 26(1).

Wang Y, et al. (2026) Investigating the zoonotic origins of ESBL-producing *E. coli* in community-acquired urinary tract infections in Ecuador. *Microbiology spectrum*, 14(5), e0332525.

Erlina L, et al. (2026) Genomic Insights into Antimicrobial Resistance and Plasmid-Mediated Dissemination in *Escherichia coli* and *Klebsiella pneumoniae* from Pediatric Outpatients with Acute Diarrhea. *Antibiotics (Basel, Switzerland)*, 15(4).

Marín-Gordillo A, et al. (2026) Hybrid genome assembly and comprehensive genomic analysis of *Lactiplantibacillus pentosus* LP309 reveal its probiotic and technological potential. *BMC genomics*, 27(1).

P R, et al. (2026) Genomic analysis of ST117, 155, 1011, 167, 744, and 17391 in poultry-associated multidrug resistant *Escherichia coli* isolates from India. *Scientific reports*, 16(1).

van Duijkeren E, et al. (2026) Genomic comparison of methicillin-resistant *Staphylococcus aureus* CC398 isolates from livestock, meat and humans in the Netherlands. *Frontiers in microbiology*, 17, 1770695.

Hetsa BA, et al. (2026) Pathogenomics of multidrug-resistant *Escherichia coli* from bloodstream infections in South Africa. *BMC medical genomics*, 19(1).

Seo Y, et al. (2026) Genomic Insights into Ciprofloxacin-Resistant Enteropathogenic *Escherichia coli* ST752 in Republic of Korea: A One Health Perspective on Its Emergence and Transmission. *Antibiotics (Basel, Switzerland)*, 15(3).

Massacci FR, et al. (2026) Occurrence of oxazolidinone resistance genes in enterococci, staphylococci, and *Mammaliococcus sciuri* from swine slaughterhouse wastewater, Italy. *World journal of microbiology & biotechnology*, 42(5).

Pereira MF, et al. (2026) Genomics of Hospital-Associated Brazilian Multidrug-Resistant *Klebsiella pneumoniae*: Abundance of Resistance and Virulence Genes and Mosaicism of the blaKPC-2 Genetic Context Among Enterobacterales. *Current microbiology*, 83(8).

Zhang J, et al. (2026) Genomic insights into selected multidrug-resistant and ESBL-producing uropathogenic *Escherichia coli* isolates in central inner Mongolia. *Frontiers in microbiology*, 17, 1844989.

Habib I, et al. (2026) Genomic characterization and comparative analysis of multidrug-resistant *Salmonella* Indiana sequence type 17 carrying *mcr*-9.1 in retail eggs from the United Arab Emirates. *Frontiers in veterinary science*, 13, 1825641.

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.

Liao YT, et al. (2026) A new Epseptimavirus bacteriophage vB_SalS-SIY1lw as a potential antimicrobial alternative to multidrug-resistant *Salmonella* Infantis. *Scientific reports*, 16(1), 5376.

Kim DH, et al. (2026) Comparative Genomic and Epidemiologic Analysis of Methicillin-Resistant *Staphylococcus aureus* Isolates in Republic of Korea. *Antibiotics* (Basel, Switzerland), 15(3).

Szmolka A, et al. (2026) Antimicrobial resistance of *Escherichia coli* in Hungarian wild rats and characterization of a CTX-M-1 type ESBL plasmid. *Scientific reports*, 16(1).

van der Schalk TE, et al. (2026) Phenotypic convergence and collateral susceptibility development in *Pseudomonas aeruginosa* under antibiotic exposure in ICU patients. *npj antimicrobials and resistance*, 4(1).

Xi R, et al. (2026) Antimicrobial Resistance and Molecular Characteristics in Tigecycline-Resistant *Escherichia coli* Isolates from Broilers in Jinan City, China. *Microorganisms*, 14(6).

Nagaraja PK, et al. (2026) Genomic profiling of ESBL/AmpC-producing *Escherichia coli* from backyard poultry: resistome, virulome, plasmidome, and CRISPR-Cas insights. *Frontiers in microbiology*, 17, 1836952.

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).