

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 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](#)

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: 20260727T040825+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 262 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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.

Kaktcham PM, et al. (2025) Genomic insights into the beneficial potential of *Bifidobacterium* and *Enterococcus* strains isolated from Cameroonian infants. *Microbial genomics*, 11(2).

Pitton M, et al. (2025) Targeting Chronic Biofilm Infections With Patient-derived Phages: An In Vitro and Ex Vivo Proof-of-concept Study in Patients With Left Ventricular Assist Devices. *Open forum infectious diseases*, 12(4), ofaf158.

du Toit SA, et al. (2025) Profiling *Listeria monocytogenes* in Hummus, Fresh Produce, and Food Processing Environments in the Western Cape, South Africa. *MicrobiologyOpen*, 14(5), e70060.

Banerjee S, et al. (2025) *Foliimonas ilicis* gen. nov., sp. nov., a carbon monoxide-oxidizing bacterium belonging to a novel genus of the family Phyllobacteriaceae isolated from leaves of *Ilex aquifolium*. *International journal of systematic and evolutionary microbiology*, 75(11).

Van Haute MJ, et al. (2025) Comparative genomic and phenotypic analysis of potential beneficial properties of *Bifidobacterium adolescentis*. *mSphere*, 10(11), e0067325.

Liao YT, et al. (2025) A Tequintavirus bacteriophage SIA3lw isolated from sewage water with antimicrobial potential against antibiotic-resistant *Salmonella* *Infantis*. *BMC microbiology*, 25(1), 806.

Saeju P, et al. (2025) Enhanced efficiency of virulent and temperate phage combination mediated through bacterial membrane vesicles. *Journal of virology*, 99(12), e0094125.

Aldaz N, et al. (2025) In Silico Detection of Virulence Genes in Whole-Genome Sequences of Extra-Intestinal Pathogenic *Escherichia coli* (ExPEC) Documented in Countries of the Andean Community. *Current issues in molecular biology*, 47(3).

Oh JY, et al. (2025) Whole genome sequencing analysis of enteropathogenic *Escherichia coli* from human and companion animals in Korea. *Journal of veterinary science*, 26(1), e1.

Chaudhary DK, et al. (2025) *Microbacterium chionoecetis* sp. nov. and *Agrococcus chionoecetis* sp. nov.: Novel Gut Bacteria from Red Snow Crab. *Journal of microbiology and biotechnology*, 35, e2412044.

Vela AI, et al. (2025) Antibiotic Resistance to Critically Important Antimicrobials and Virulence Genes in *Enterococcus faecalis* Strains Isolated from Eurasian Griffon Vultures (*Gyps fulvus*) and Their Association with Mobile Genetic Elements. *Veterinary sciences*, 12(11).

Ordaz AFC, et al. (2025) Unveiling the Genomic Landscape of *Escherichia coli* O1:K1:H7 ST59 in Non-complicated Urinary Infections from Colombia Through Whole-Genome Sequencing. *Current microbiology*, 82(11), 505.

Shirzad-Aski H, et al. (2025) Isolation, characterization, and genomic analysis of three novel Herelleviridae family lytic bacteriophages against uropathogenic isolates of *Staphylococcus saprophyticus*. *Virology journal*, 22(1), 87.

Maeda A, et al. (2025) Prevalence, antimicrobial susceptibility, and virulence profiles of fluoroquinolone-resistant *Escherichia coli* isolated from companion animals in Sapporo, Japan. *The Journal of veterinary medical science*, 87(11), 1249.

McDougall FK, et al. (2025) Novel strains of typical enteropathogenic *Escherichia coli* (tEPEC) in Pteropus bats, including the first report of a phylogroup G tEPEC. *Microbial genomics*, 11(8).

Emgård J, et al. (2025) Distinct MAIT cell phenotypes associated with sepsis clinical outcome in emergency department patients. *Clinical & translational immunology*, 14(3), e70028.

Aoki K, et al. (2025) Tracking Antimicrobial Resistant Organisms Timely: a workflow validation study for successive core-genome SNP-based nosocomial transmission analysis. *JAC-antimicrobial resistance*, 7(3), dlaf069.

Kiiru S, et al. (2025) Molecular characterization of multidrug-resistant *E. coli* recovered from diarrheagenic children under 5 years from Mukuru Informal Settlement, Nairobi, Kenya, based on whole-genome sequencing analysis. *Microbiology spectrum*, 13(6), e0142024.