

Resource Summary Report

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VFDB - Virulence Factors of Bacterial Pathogens

RRID:SCR_007969

Type: Tool

Proper Citation

VFDB - Virulence Factors of Bacterial Pathogens (RRID:SCR_007969)

Resource Information

URL: <http://www.mgc.ac.cn/VFs/>

Proper Citation: VFDB - Virulence Factors of Bacterial Pathogens (RRID:SCR_007969)

Description: An integrated and comprehensive database of virulence factors for bacterial pathogens (also including Chlamydia and Mycoplasma). VFDB is a platform for further study of comparative pathogenomics. Major features include tabular comparison of pathogenomic composition in terms of virulence, multiple alignments and statistic analysis of homologous virulence genes, and graphical comparison of pathogenomic organization of VFs. Category: Genomics Databases (non-vertebrate) Subcategory: Prokaryotic genome databases

Abbreviations: VFDB

Synonyms: Virulence Factors of Bacterial Pathogens

Resource Type: database, data or information resource

Keywords: bio.tools, FASEB list

Resource Name: VFDB - Virulence Factors of Bacterial Pathogens

Resource ID: SCR_007969

Alternate IDs: nif-0000-03627, biotools:vfdb

Alternate URLs: <https://bio.tools/vfdb>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260725T191153+0000

Ratings and Alerts

No rating or validation information has been found for VFDB - Virulence Factors of Bacterial Pathogens.

No alerts have been found for VFDB - Virulence Factors of Bacterial Pathogens.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 483 mentions in open access literature.

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

Lysitsas M, et al. (2025) Companion Animals as Reservoirs of Multidrug Resistance-A Rare Case of an XDR, NDM-1-Producing *Pseudomonas aeruginosa* Strain of Feline Origin in Greece. *Veterinary sciences*, 12(6).

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. *GigaScience*, 14.

Sunmonu GT, et al. (2025) Genomic characterization of foodborne *Salmonella enterica* and *Escherichia coli* isolates from Saboba district and Bolgatanga Municipality Ghana. *PloS one*, 20(2), e0315583.

Jacobsen KL, et al. (2025) Temperature-dependent alterations in the proteome of the emergent fish pathogen *Edwardsiella piscicida*. *Journal of fish diseases*, 48(9), e14017.

Wei G, et al. (2025) Probiotic potential and safety properties of *Limosilactobacillus fermentum* A51 with high exopolysaccharide production. *Frontiers in microbiology*, 16, 1498352.

Yang C, et al. (2025) Genomic characteristics, virulence potential, antimicrobial resistance profiles, and phylogenetic insights into *Nocardia cyriacigeorgica*. *Annals of clinical microbiology and antimicrobials*, 24(1), 22.

Tsai Y-Y, et al. (2025) Whole-genome analysis of five *Escherichia coli* strains isolated from focal duodenal necrosis in laying hens reveals genetic similarities to the *E. coli* O25:H4 ST131 strain. *Microbiology spectrum*, 13(5), e0211024.

Ma R, et al. (2025) Prevalence, diversity, and parasitism of tailed prophages in *Vibrio harveyi*. *mSphere*, 10(9), e0022825.

Leite VLM, et al. (2025) Hidden diversity in *Enterococcus faecalis* revealed by CRISPR2 screening: eco-evolutionary insights into a novel subspecies. *Microbiology spectrum*, 13(10), e0142825.

Hu J, et al. (2025) Whole genome study and construction of SHERLOCK detection method for endemic strains of *Burkholderia pseudomallei* in Hainan based on third-

generation sequencing. *Microbiology spectrum*, 13(11), e0059225.

Ji X, et al. (2025) DnaK of *Parvimonas micra* extracellular vesicles interacts with the host fibroblasts BAG3-IKK- γ axis to accelerate TNF- α secretion in oral lichen planus. *Microbiome*, 13(1), 164.

Yuan J, et al. (2025) Whole genome sequencing analysis of a novel exopolysaccharide-producing *Bacillus velezensis* and its impact on the quality of soy sauce. *Food chemistry: X*, 28, 102585.

Yan Z, et al. (2025) Dietary microbiota-mediated shifts in gut microbial ecology and pathogen interactions in giant pandas (*Ailuropoda melanoleuca*). *Communications biology*, 8(1), 864.

Cui J, et al. (2025) High-alcohol-producing *Klebsiella pneumoniae* aggravates lung injury by affecting neutrophils and the airway epithelium. *Cell reports. Medicine*, 6(1), 101886.

Kuang S, et al. (2025) Prevalence and genetic characteristics of *Campylobacter jejuni* from laying-hens in Hubei Province, China. *BMC veterinary research*, 21(1), 84.

Yao F, et al. (2025) Unveiling the role of phages in shaping the periodontal microbial ecosystem. *mSystems*, 10(4), e0020125.

Song J, et al. (2025) Population structure, antibiotic resistance and molecular characteristics of *Streptococcus pneumoniae* causing invasive disease in Hubei, China. *Journal of medical microbiology*, 74(5).

Nesporova K, et al. (2025) Large-scale genomic analysis reveals the distribution and diversity of type VI secretion systems in *Escherichia coli*. *mSystems*, 10(7), e0010525.

Tu J, et al. (2025) Colanic acid-mediated phage resistance enhances virulence in high-risk global clone *Escherichia coli* ST410. *PLoS pathogens*, 21(12), e1013807.

Ghazawi A, et al. (2025) Comparative genomic study of blaKPC-2-carrying multidrug-resistant *Klebsiella pneumoniae* in the United Arab Emirates. *Scientific reports*, 15(1), 45259.