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

Funding:

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: 20250428T053351+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 404 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Park EJ, et al. (2025) Characterization of Broad Spectrum Bacteriophage vB ESM-pEJ01 and Its Antimicrobial Efficacy Against Shiga Toxin-Producing Escherichia coli in Green Juice. Microorganisms, 13(1).

Liu B, et al. (2025) Targeted Next-Generation Sequencing in Pneumonia: Applications in the Detection of Responsible Pathogens, Antimicrobial Resistance, and Virulence. Infection and drug resistance, 18, 407.

Zhou S, et al. (2025) VFDB 2025: an integrated resource for exploring anti-virulence compounds. Nucleic acids research, 53(D1), D871.

Cipolla L, et al. (2025) Genomic epidemiology of invasive Group A Streptococcus infections in Argentina, 2023: high prevalence of emm1-global and detection of emm1 hypervirulent lineages. Microbiology spectrum, 13(1), e0131024.

Yakubovskij VI, et al. (2025) Phage vB_KlebPS_265 Active Against Resistant/MDR and Hypermucoid K2 Strains of Klebsiella pneumoniae. Viruses, 17(1).

Rungsirivanich P, et al. (2025) Functional genomic insights into Floricoccus penangensis ML061-4 isolated from leaf surface of Assam tea. Scientific reports, 15(1), 2951.

Huang Z, et al. (2024) Genomic insights into the evolution, pathogenicity, and extensively drug-resistance of emerging pathogens Kluyvera and Phytobacter. Frontiers in cellular and infection microbiology, 14, 1376289.

Avendaño-Herrera R, et al. (2024) Flavobacterium psychraquaticum sp. nov., isolated from water system of Atlantic salmon (Salmo salar) smolts cultured in Chile. International journal of systematic and evolutionary microbiology, 74(4).

Chen X, et al. (2024) Emergence and clonal expansion of Aeromonas hydrophila ST1172 that simultaneously produces MOX-13 and OXA-724. Antimicrobial resistance and infection control, 13(1), 28.

Huang Z, et al. (2024) Genome-wide expanding of genetic evolution and potential pathogenicity in Vibrio alginolyticus. Emerging microbes & infections, 13(1), 2350164.

Wang Z, et al. (2024) Effective binning of metagenomic contigs using contrastive multi-view representation learning. Nature communications, 15(1), 585.

Xiang Q, et al. (2024) Host genetic variation and specialized metabolites from wheat leaves enriches for phyllosphere Pseudomonas spp. with enriched antibiotic resistomes. The ISME journal, 18(1).

Shi Z, et al. (2024) Characterization of the novel broad-spectrum lytic phage Phage_Pae01 and its antibiofilm efficacy against Pseudomonas aeruginosa. Frontiers in microbiology, 15, 1386830.

Castelli M, et al. (2024) Host association and intracellularity evolved multiple times independently in the Rickettsiales. Nature communications, 15(1), 1093.

Chen J, et al. (2024) Genome-based model for differentiating between infection and carriage Staphylococcus aureus. Microbiology spectrum, 12(10), e0049324.

Chen WY, et al. (2024) Characterization of microbiome, resistome, mobilome, and virulome in anoxic and oxic wastewater treatment processes in Slovakia and Taiwan. Heliyon, 10(19), e38723.

Yang X, et al. (2024) Characterization of Escherichia coli strains producing Shiga Toxin 2f subtype from domestic Pigeon. Scientific reports, 14(1), 24481.

Zhang M, et al. (2024) Comprehensive pan-genome analysis of Mycobacterium marinum: insights into genomic diversity, evolution, and pathogenicity. Scientific reports, 14(1), 27723.

Yan W, et al. (2024) Antimicrobial resistance and genome characteristics of Salmonella enteritidis from Huzhou, China. PloS one, 19(6), e0304621.

Wu Q, et al. (2024) Characteristics and whole-genome analysis of a novel Pseudomonas syringae pv. tomato bacteriophage D6 isolated from a karst cave. Virus genes, 60(3), 295.