

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: data or information resource, database

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: 20260905T133149+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 676 mentions in open access literature.

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

Huang Y, et al. (2026) Characterization of CRISPR-Cas systems in the Haemophilus genus CRISPR-Cas in Haemophilus spp. Genetics and molecular biology, 49(1), e20250166.

Long L, et al. (2026) Unveiling microbial risks in Chinese household dust: a comprehensive analysis from absolute abundance to virulence unit. Microbiome, 14(1).

Chen J, et al. (2026) Septic Shock Caused by Coinfection of Shewanella algae Bloodstream Infection and Epstein-Barr Virus: Clinical Characteristics and Genomic Analysis. MicrobiologyOpen, 15(1), e70221.

Wongsuk T, et al. (2026) Molecular insights into antimicrobial resistance and virulence in hospital-associated of vancomycin-resistant Enterococcus faecium isolates in a tertiary hospital in Bangkok Thailand. PloS one, 21(3), e0343967.

Anwer F, et al. (2026) Whole-Genome Sequencing of Multidrug-Resistant Acinetobacter baumannii Local Isolate and Molecular Dynamics Simulation Studies of a Modified KR-12 Analog Targeting AbaQ and BfmR. International journal of molecular sciences, 27(7).

Cao S, et al. (2026) Carbapenem-resistant enterobacterales in sterile body fluids: ten-year population genomics and clinical risk factors in a tertiary hospital, 2016-2025. Frontiers in cellular and infection microbiology, 16, 1821740.

Lu Q, et al. (2026) Genomic characterization of APEC phages and evaluation of the efficacy in reducing the loads of APEC O78 infections in chickens. Frontiers in microbiology, 17, 1670169.

Zhang Z, et al. (2026) Clonal and Plasmid-Mediated Dissemination of Multidrug-Resistant Salmonella Enteritidis in Chicken Production, Northeastern Thailand. Pathogens (Basel, Switzerland), 15(1).

Sapino R, et al. (2026) Development of Metagenomic Methods for Health Monitoring of Endangered Species Using Fecal Samples. Evolutionary applications, 19(2), e70199.

D??az JM, et al. (2026) Acquisition of toxin-encoding lysogenic bacteriophage elements enhances the virulence of pandemic *Streptococcus pyogenes* M1UK. *Infection and immunity*, 94(3), e0050325.

Liu L, et al. (2026) Phenotypic and genomic characterization of tigecycline-insensitive *Klebsiella pneumoniae* strains and validation of highly virulent MDR strains. *Microbiology spectrum*, 14(5), e0322825.

Wang K, et al. (2026) Multidrug-resistant mammary pathogenic *Escherichia coli* ST479 isolated from Holstein dairy cows in Jiangsu, China. *Frontiers in microbiology*, 17, 1737656.

Liu WZ, et al. (2026) Genomic insights into the broad-spectrum antifungal activity of a novel *Paenibacillus polymyxa* strain X-11. *BMC microbiology*, 26(1).

Su L, et al. (2026) Molecular epidemiological and genetic variability of *Salmonella* isolates from the tropical mountainous region of southern China (2017-2024). *Microbiology spectrum*, 14(4), e0267625.

Sonbol S, et al. (2026) The interplay of specialized metabolites, antibiotic resistance, and virulence in *Enterococcus faecium*: in silico analysis of bacterial genomes. *BMC genomics*, 27(1).

Cao X, et al. (2026) Identification and Genome Phylogenetic Analysis of Three *Brucella abortus* Strains From Sheep, Yak, and Cow in Qinghai, China. *Transboundary and emerging diseases*, 2026, 7831968.

Gong Y, et al. (2026) Prevalence, Characterization and Genetic Diversity of *Listeria monocytogenes* in Ready-to-Eat Raw Salmon (*Salmo salar*) and Trout (*Oncorhynchus mykiss*) Products. *Foods (Basel, Switzerland)*, 15(2).

Aldeia C, et al. (2026) A commercial bacteriophage cocktail failed to decolonize *Zophobas morio* larvae and promoted overgrowth of an OXA-48-producing *Salmonella enterica*. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 45(2), 363.

Deng B, et al. (2026) Type 2 diabetes mellitus wake-up call: fatal streptococcal toxic shock syndrome triggered by the M1(UK) *Streptococcus pyogenes* - a case report with genomic insights. *BMC infectious diseases*, 26(1).

Cui X, et al. (2026) Whole-genome sequencing identifies persistent transmission of a high-risk ST2 *Acinetobacter baumannii* clone in a Guangzhou Hospital. *Frontiers in microbiology*, 17, 1730485.