

Resource Summary Report

Generated by T1D on Jul 31, 2026

PHI-base

RRID:SCR_003331

Type: Tool

Proper Citation

PHI-base (RRID:SCR_003331)

Resource Information

URL: <http://www.phi-base.org/>

Proper Citation: PHI-base (RRID:SCR_003331)

Description: Database that catalogs experimentally verified pathogenicity, virulence and effector genes from fungal, Oomycete and bacterial pathogens, which infect animal, plant, fungal and insect hosts. It is an invaluable resource in the discovery of genes in medically and agronomically important pathogens, which may be potential targets for chemical intervention. In collaboration with the FRAC team, it also includes antifungal compounds and their target genes. Each entry is curated by domain experts and is supported by strong experimental evidence (gene disruption experiments, STM etc), as well as literature references in which the original experiments are described. Each gene is presented with its nucleotide and deduced amino acid sequence, as well as a detailed description of the predicted protein's function during the host infection process. To facilitate data interoperability, genes have been annotated using controlled vocabularies and links to external sources (Gene Ontology terms, EC Numbers, NCBI taxonomy, EMBL, PubMed and FRAC).

Abbreviations: PHI-base

Synonyms: Pathogen Host Interaction base, Pathogen Host Interaction, Pathogen Host Interaction-Base

Resource Type: data or information resource, database

Defining Citation: [PMID:17942425](#), [PMID:17153929](#), [PMID:16381911](#)

Keywords: gene expression, pathogenic bacteria, virulence, infection, target site, gene, pathogen-host interaction, interaction, phenotype, pathogen, disease, host, anti-infective, nucleotide sequence, amino acid sequence, bio.tools, FASEB list

Funding: BBSRC BB/1000488/1

Availability: Free, Freely available

Resource Name: PHI-base

Resource ID: SCR_003331

Alternate IDs: nif-0000-03276, r3d100011301, biotools:phi-base

Alternate URLs: <https://bio.tools/phi-base>, <https://doi.org/10.17616/R35D1V>

Old URLs: <http://www4.rothamsted.bbsrc.ac.uk/phibase/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260729T044041+0000

Ratings and Alerts

No rating or validation information has been found for PHI-base.

No alerts have been found for PHI-base.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 198 mentions in open access literature.

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

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Auzane A, et al. (2025) A Novel Pathosystem With the Model Plant *Arabidopsis thaliana* for Defining the Molecular Basis of *Taphrina* Infections. *Environmental microbiology reports*, 17(3), e70118.

Feng S, et al. (2025) Fungal virulence factors datasets for inflammatory bowel disease-specific antifungal drug discovery. *Scientific data*, 12(1), 1796.

Adhikari TB, et al. (2025) Genomic insights and comparative analysis of *Colletotrichum* species associated with anthracnose fruit rot and crown rot of strawberry in North Carolina. *Frontiers in microbiology*, 16, 1515894.

Miguel CB, et al. (2025) Adaptative Divergence of *Cryptococcus neoformans*: Phenetic and Metabolomic Profiles Reveal Distinct Pathways of Virulence and Resistance in Clinical vs. Environmental Isolates. *Journal of fungi (Basel, Switzerland)*, 11(3).

Qiu M, et al. (2025) Screening, Identification, and Whole-Genome Sequencing of Ferulic Acid Esterase-Producing Lactic Acid Bacteria from Sheep Rumen. *Microorganisms*, 13(6).

Han C, et al. (2025) Machine learning based on pangenome-wide association studies reveals the impact of host source on the zoonotic potential of closely related bacterial pathogens. *Communications biology*, 8(1), 1253.

Song L, et al. (2025) Biological and Genomic Insights into *Fusarium acuminatum* Causing Needle Blight in *Pinus tabulaeformis*. *Journal of fungi (Basel, Switzerland)*, 11(9).

Kharte S, et al. (2025) Whole genome sequencing and functional annotation of *Fusarium oxysporum* f. sp. *lentis* to unravel virulence and secondary metabolite biosynthesis gene clusters. *Frontiers in genetics*, 16, 1585510.

Urban M, et al. (2025) PHI-base - the multi-species pathogen-host interaction database in 2025. *Nucleic acids research*, 53(D1), D826.

Gu T, et al. (2025) *Faucicola mancuniensis* isolated from human respiratory tract and its genomic characteristics. *BMC microbiology*, 25(1), 587.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi (Basel, Switzerland)*, 11(3).

Wang Y, et al. (2025) Whole-genome sequencing and comparative genomic analysis of *Irpeex lacteus* isolated from the female reproductive tract. *Microbial genomics*, 11(6).

Yue X, et al. (2025) Loss of Pathogenicity and Evidence of Horizontal Gene Transfer in *Colletotrichum gloeosporioides* From a Medicinal Plant. *Molecular plant pathology*, 26(6), e70098.

Xia L, et al. (2025) Genomic features, antimicrobial resistance and pathogenicity assessment of *Escherichia coli* serotype O177:H51 strain JS01 isolated from a diseased chicken. *BMC microbiology*, 25(1), 194.

Xu S, et al. (2025) Chromosome-level genome assembly of *Fusarium tricinctum*, a fungal pathogen associated with root rot in alfalfa. *Scientific data*, 12(1), 1676.

Paudel R, et al. (2025) Genome assembly and comparative analysis of *Alternaria Linariae* reveal novel genes associated with host colonization and virulence. *BMC genomics*, 26(1), 638.

Zhao Y, et al. (2025) Global soil antibiotic resistance genes are associated with increasing risk and connectivity to human resistome. *Nature communications*, 16(1), 7141.

Su F, et al. (2025) Integrating multi-omics data to reveal the host-microbiota interactome in inflammatory bowel disease. *Gut microbes*, 17(1), 2476570.

Wang L, et al. (2025) Metagenomic analysis reveals distinct patterns of gut microbiota features with diversified functions in *C. difficile* infection (CDI), asymptomatic carriage and non-CDI diarrhea. *Gut microbes*, 17(1), 2505269.