

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 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: database, data or information resource

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: 20260808T190355+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 239 mentions in open access literature.

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

Wang Q, et al. (2026) Revealing the early pathogenic mechanisms of *Agroatehlia rolfsii* in *Arachis hypogaea* through RNA-seq and identification of ArNIS1-like effectors. BMC plant biology, 26(1), 278.

Guo X, et al. (2026) Reactive oxygen species in the rhizosphere orchestrate the recruitment of beneficial bacteria. The EMBO journal, 45(4), 1245.

Wei C, et al. (2026) Large-scale genomic analysis of jumbo phages: coevolution, genome architecture, and host interaction mechanisms. Animal microbiome, 8(1).

Singh A, et al. (2026) Development of a multipurpose diagnostic marker using PCR, real-time PCR, and LAMP assays for rapid detection of *Rhizoctonia solani* in rice plants and soil. Frontiers in plant science, 17, 1724916.

Huang R, et al. (2026) Transcriptome Analysis Reveals Cross-Kingdom Virulence Factors in *Erwinia persicina* Cp2. Environmental microbiology reports, 18(2), e70322.

Sun W, et al. (2026) Comparative Genomics Reveals Host-Specific Adaptation of *Pyricularia oryzae* Strains Isolated from Rice and Barnyard Grass. Journal of fungi (Basel,

Switzerland), 12(2).

Wang R, et al. (2026) Characterization and therapeutic evaluation of a novel phage S18-3 targeting poultry-derived *Enterobacter hormaechei* infection in mice. *BMC veterinary research*, 22(1).

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.

Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.

Valadez-Cano C, et al. (2026) Phylogenomic and functional insights into *Staphylococcus shinii* from blueberry production environments: intra-species structure, probiotic traits and antimicrobial resistance. *Microbial genomics*, 12(2).

Hsu SY, et al. (2026) Genomic and metabolic uniformity across diverse observed ecological contexts suggest that interactions of *Pestalotiopsis formosana* and *P. neolitseae* are context-dependent. *IMA fungus*, 17, e192779.

Tahir MS, et al. (2026) Chromosome-level genome and transcriptome analysis of *Trichophyton verrucosum* reveals pathogenicity mechanisms and antifungal response. *Virulence*, 17(1), 2677294.

Zhen Z, et al. (2026) Genome-wide characteristics, antibiotic resistance, and pathogenicity analysis of *Streptococcus parasuis* strains isolated from diseased pigs. *BMC microbiology*, 26(1).

Han H, et al. (2026) Whole-genome analysis and fermentation-metabolite profiling of a cellulolytic *Arthrobacter* sp. FMD isolated from forest musk-deer faeces. *BMC microbiology*, 26(1), 43.

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.

Zheng X, et al. (2025) Complete genome assembly and functional characterization of *Brucella melitensis* strain IMHB1 from a clinical isolate in Inner Mongolia, China. *Frontiers in cellular and infection microbiology*, 15, 1653521.

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

Li J, et al. (2025) Identification, antifungal resistance, and genomic characterization of a single *Candida auris* isolate from urinary tract infection. *Frontiers in cellular and infection microbiology*, 15, 1641542.

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).

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.