Resource Summary Report

Generated by RRID on Apr 28, 2025

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, Acknowledgement required, Non-commercial, Commercial use requires permission

Resource Name: PHI-base

Resource ID: SCR_003331

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

Alternate URLs: https://bio.tools/phi-base

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

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250428T053030+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 178 mentions in open access literature.

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

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

Deng L, et al. (2024) Complete genome sequence analysis of Pestalotiopsis microspora, a fungal pathogen causing kiwifruit postharvest rots. BMC genomics, 25(1), 839.

Baranda P, et al. (2024) Whole-genome sequencing of marine water-derived Curvularia verruculosa KHW-7: a pioneering study. Frontiers in microbiology, 15, 1363879.

Wang L, et al. (2024) Prediction of protein interactions between pine and pine wood

nematode using deep learning and multi-dimensional feature fusion. Frontiers in plant science, 15, 1489116.

Lozano J, et al. (2024) Analyzing the safety of the parasiticide fungus Mucor circinelloides: first insights on its virulence profile and interactions with the avian gut microbial community. Microbiology spectrum, 12(5), e0407823.

Rozano L, et al. (2024) Template-Based Modelling of the Structure of Fungal Effector Proteins. Molecular biotechnology, 66(4), 784.

Guerrero-Egido G, et al. (2024) bacLIFE: a user-friendly computational workflow for genome analysis and prediction of lifestyle-associated genes in bacteria. Nature communications, 15(1), 2072.

Liu X, et al. (2024) Glyoxal oxidase-mediated detoxification of reactive carbonyl species contributes to virulence, stress tolerance, and development in a pathogenic fungus. PLoS pathogens, 20(7), e1012431.

Zhang Y, et al. (2024) Integrating multi-omics to unravel host-microbiome interactions in inflammatory bowel disease. Cell reports. Medicine, 5(9), 101738.

Yu J, et al. (2024) Contact-mediated algicidal mechanism of Vibrio coralliirubri ACE001 against the harmful alga Karenia mikimotoi. iScience, 27(11), 111254.

Zhang N, et al. (2024) Comparative Genomics and Pathogenicity Analysis of Three Fungal Isolates Causing Barnyard Grass Blast. Journal of fungi (Basel, Switzerland), 10(12).

Xu Y, et al. (2024) Whole-Genome Sequencing and Genome Annotation of Pathogenic Elsinoë batatas Causing Stem and Foliage Scab Disease in Sweet Potato. Journal of fungi (Basel, Switzerland), 10(12).

Zuo S, et al. (2024) FlgI Is a Sec-Dependent Effector of Candidatus Liberibacter asiaticus That Can Be Blocked by Small Molecules Identified Using a Yeast Screen. Plants (Basel, Switzerland), 13(2).

Zhou Y, et al. (2024) Pan-genome analysis of Streptococcus suis serotype 2 highlights genes associated with virulence and antibiotic resistance. Frontiers in microbiology, 15, 1362316.

Basenko EY, et al. (2024) What is new in FungiDB: a web-based bioinformatics platform for omics-scale data analysis for fungal and oomycete species. Genetics, 227(1).

Shi L, et al. (2024) Genomic characteristics of antimicrobial resistance and virulence factors of carbapenem-resistant Stutzerimonas nitrititolerans isolated from the clinical specimen. BMC microbiology, 24(1), 386.

Jiang F, et al. (2024) Metabolites of pathogenic microorganisms database (MPMdb) and its seed metabolite applications. Microbiology spectrum, 12(4), e0234223.

Ma T, et al. (2024) High-quality genome assembly and genetic transformation system of Lasiodiplodia theobromae strain LTTK16-3, a fungal pathogen of Chinese hickory. Microbiology spectrum, 12(3), e0331123.

Liang D, et al. (2024) The Comparative Genomics of Botryosphaeriaceae Suggests Gene Families of Botryosphaeria dothidea Related to Pathogenicity on Chinese Hickory Tree. Journal of fungi (Basel, Switzerland), 10(4).

Singh R, et al. (2024) Genetic and molecular landscapes of the generalist phytopathogen Botrytis cinerea. Molecular plant pathology, 25(1), e13404.