

Resource Summary Report

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FungiDB

RRID:SCR_006013

Type: Tool

Proper Citation

FungiDB (RRID:SCR_006013)

Resource Information

URL: <http://fungidb.org/fungidb/>

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Description: FungiDB is a database for functional and evolutionary comparison of fungal genomes. FungiDB is a functional genomic resource for pan-fungal genomes that was developed in partnership with the Eukaryotic Pathogen Bioinformatic resource center (<http://EuPathDB.org>). FungiDB uses the same infrastructure and user interface as EuPathDB, which allows for sophisticated and integrated searches to be performed using an intuitive graphical system. The current release of FungiDB contains genome sequence and annotation from 18 species spanning several fungal classes, including the Ascomycota classes, Eurotiomycetes, Sordariomycetes, Saccharomycetes and the Basidiomycota orders, Pucciniomycetes and Tremellomycetes, and the basal "Zygomycete" lineage Mucormycotina. Additionally, FungiDB contains cell cycle microarray data, hyphal growth RNA-sequence data and yeast two hybrid interaction data. The underlying genomic sequence and annotation combined with functional data, additional data from the FungiDB standard analysis pipeline and the ability to leverage orthology provides a powerful resource for in silico experimentation.

Abbreviations: FungiDB

Synonyms: FungiDB - Fungi Genomics Resources

Resource Type: data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:22064857](https://pubmed.ncbi.nlm.nih.gov/22064857/)

Keywords: genomics, functional genomics, genome, microarray, genome sequence, annotation, rna sequence, orthology, FASEB list

Funding: Burroughs Wellcome Fund ;
Alfred P. Sloan Foundation

Availability: Much of the data in FungiDB is provided by independent researchers. Please cite them if you use their data.

Resource Name: FungiDB

Resource ID: SCR_006013

Alternate IDs: nlx_151401, r3d100011906

Alternate URLs: <https://doi.org/10.17616/R35K9M>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260801T042620+0000

Ratings and Alerts

No rating or validation information has been found for FungiDB.

No alerts have been found for FungiDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 250 mentions in open access literature.

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

Zhang H, et al. (2026) Oxidoreductase gene fabG contributes to fungal development, cell wall integrity, and virulence in *Aspergillus fumigatus*. *Microbiology spectrum*, 14(1), e0209225.

Moon H, et al. (2025) Integrative glycomic analysis reveals the crucial role of protein glycosylation in fungal pathogenesis. *PLoS pathogens*, 21(7), e1013325.

Wang X, et al. (2025) MoMtg1 Acts as a Novel Transcriptional Repressor of MoSwi6 During Appressorium-Mediated Penetration in the Rice Blast Fungus. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 12(43), e09002.

Li Y, et al. (2025) Identification of a protective antigen reveals the trade-off between iron acquisition and antigen exposure in a global fungal pathogen. *Proceedings of the National Academy of Sciences of the United States of America*, 122(7), e2420898122.

Yadav V, et al. (2025) Calcineurin controls the cytokinesis machinery during thermal stress in *Cryptococcus deneoformans*. *Proceedings of the National Academy of Sciences of the United States of America*, 122(21), e2503751122.

Billmyre RB, et al. (2025) Landscape of essential growth and fluconazole-resistance genes in the human fungal pathogen *Cryptococcus neoformans*. *PLoS biology*, 23(5), e3003184.

Stuckey PV, et al. (2025) The Vacuolar Protein 8 (Vac8) Homolog in *Cryptococcus neoformans* Impacts Stress Responses and Virulence Traits Through Conserved and Unique Roles. *Journal of fungi (Basel, Switzerland)*, 11(12).

Yadav V, et al. (2025) Calcineurin controls the cytokinesis machinery during thermal stress in *Cryptococcus deneoformans*. *bioRxiv : the preprint server for biology*.

Kovacs F, et al. (2025) A comprehensive analysis of the effect of quorum-sensing molecule 3-oxo-C12-homoserine lactone on *Candida auris* and *Candida albicans*. *Biofilm*, 9, 100259.

Henry M, et al. (2025) Manganese-modulated proteome and phosphoproteome dataset in the opportunistic yeast *Candida albicans*. *Data in brief*, 61, 111862.

Puerner C, et al. (2025) Transcriptional and metabolic modeling analyses of developing *Aspergillus fumigatus* biofilms reveal metabolic shifts required for biofilm maturation. *mSphere*, 10(12), e0075225.

Tang W, et al. (2025) The Signal Peptidase MoSpc2 Orchestrates Fungal Development, Protein Secretion and Pathogenicity in *Magnaporthe oryzae*. *Rice (New York, N.Y.)*, 18(1), 105.

Bastakis E, et al. (2025) Molecular circuit between *Aspergillus nidulans* transcription factors MsnA and VelB to coordinate fungal stress and developmental responses. *PLoS genetics*, 21(7), e1011578.

Acevedo KL, et al. (2025) Population Genomics of *Aspergillus sojae* is Shaped by the Food Environment. *Genome biology and evolution*, 17(4).

Lohmar JM, et al. (2025) The putative forkhead transcription factor FhpA is necessary for development, aflatoxin production, and stress response in *Aspergillus flavus*. *PloS one*, 20(3), e0315766.

Yu P, et al. (2025) PWWP domain-containing protein Crf4-3 specifically modulates fungal azole susceptibility by regulating sterol C-14 demethylase ERG11. *mSphere*, 10(1), e0070324.

Silva HGS, et al. (2025) Integrating tRNA gene epigenomics and expression with codon usage unravels an intricate connection with translational dynamics in *Trypanosoma cruzi*. *mBio*, 16(9), e0162225.

Welsh LRJ, et al. (2025) Oomycetes manipulate plant innate immunity through galacturonide oxidases. *Nature communications*, 16(1), 9093.

Antoniacci ACC, et al. (2025) Rme1: Unveiling a Novel Repressor in the Cellulolytic Pathway of *Trichoderma reesei*. *Journal of fungi (Basel, Switzerland)*, 11(9).

Huang J, et al. (2025) First Report of *Cystobasidium slooffiae* in Human Wounds from China: Molecular Identification and Clinical Insights. *Infection and drug resistance*, 18,

5877.