

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

Defining Citation: [PMID: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: 20260821T193750+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 278 mentions in open access literature.

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

Zhou X, et al. (2026) Recurrent mutations in the stress regulator Cap1 reveal a trade-off between azole resistance and oxidative stress response in *Candida albicans*. *PLoS biology*, 24(2), e3003631.

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.

Phan-Canh T, et al. (2026) *Candida auris* skin tropism and antifungal resistance are mediated by carbonic anhydrase Nce103. *Nature microbiology*, 11(2), 461.

Dai T, et al. (2026) FcLRR1 Regulates Hyphal Growth and Plant Infection in *Fusarium circinatum*. *Journal of fungi (Basel, Switzerland)*, 12(4).

Vierling MM, et al. (2026) ARS2, a Cofactor of CBC, Promotes Meiotic Silencing by Unpaired DNA. *Epigenomes*, 10(1).

Sy VT, et al. (2026) An Hsp70 Chaperone Is Involved in Meiotic Silencing by Unpaired DNA. *Epigenomes*, 10(1).

- Rapala JR, et al. (2026) Deep homology and design of proteasome chaperone proteins in *Candidozyma auris*. *Nature communications*, 17(1).
- Rahnama M, et al. (2026) Protocol for conditional gene expression in *Magnaporthe oryzae* via fungal nitrate reductase promoter replacement. *STAR protocols*, 7(1), 104334.
- Antonieli EP, et al. (2026) Overexpression of *msnA* reprograms metabolism to enhance recombinant protein secretion across *Aspergillus* species. *Microbial cell factories*, 25(1).
- Krishnan P, et al. (2026) An integrative ultrastructural and transcriptomic analysis of host-pathogen interactions with human brain microvascular endothelial cells during cryptococcal infection: a preliminary study. *Frontiers in cellular and infection microbiology*, 16, 1735570.
- Zhao H, et al. (2026) RT-qPCR-Based Estimation of *Phytophthora infestans* Sporangia Using the MFS Transporter Gene *PITG_13011*. *Journal of fungi* (Basel, Switzerland), 12(5).
- Akhtari G, et al. (2026) Rhythmicity of TOR (Target of Rapamycin) Activity Supports Circadian Function in *Neurospora crassa*. *Journal of biological rhythms*, 41(2), 259.
- Souza TN, et al. (2026) Effects of human immunoglobulins on *Cryptococcus neoformans* morphology and proteome. *mBio*, 17(3), e0382725.
- Morihara N, et al. (2026) Functional Annotation Workflow for Fungal Transcriptomes. *Journal of fungi* (Basel, Switzerland), 12(2).
- Kovács F, et al. (2026) Synergistic activity of caspofungin and posaconazole against *Candida* (*Candidozyma*) *auris* biofilms based on phenotypic, transcriptomic, and in vivo insights. *Microbiology spectrum*, 14(4), e0268625.
- Louvet M, et al. (2026) Role of the transcription factor *Wor2* in biofilm formation of *Candidozyma auris*. *mSphere*, 11(5), e0005726.
- Christensen KE, et al. (2026) Signatures of Innovation and Selection in the Extremotolerant Yeast *Kluyveromyces marxianus*. *Genome biology and evolution*, 18(3).
- Mohamed ET, et al. (2026) Antifungal efficacy of linoleic-acid-rich *Cucurbita pepo* L. seed oil revealed by GC-MS profiling of lipids and bioactive markers, ergosterol depletion, and network pharmacology. *BMC microbiology*, 26(1).
- Ma Q, et al. (2026) The Oligosaccharyltransferase Catalytic Subunit *PsSTT3B* Is Required for Asexual Development and Pathogenicity in *Phytophthora sojae*. *Journal of fungi* (Basel, Switzerland), 12(4).
- Zhang X, et al. (2026) Ovoid cell is an inducible small-sized morphotype that enhances proliferation and antifungal drug tolerance in the human fungal pathogen *Cryptococcus neoformans*. *PLoS pathogens*, 22(6), e1014302.