

Resource Summary Report

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Fungal Genome Initiative

RRID:SCR_003169

Type: Tool

Proper Citation

Fungal Genome Initiative (RRID:SCR_003169)

Resource Information

URL: <http://www.broad.mit.edu/annotation/fungi/fgi/>

Proper Citation: Fungal Genome Initiative (RRID:SCR_003169)

Description: Produces and analyzes sequence data from fungal organisms that are important to medicine, agriculture and industry. The FGI is a partnership between the Broad Institute and the wider fungal research community, with the selection of target genomes governed by a steering committee of fungal scientists. Organisms are selected for sequencing as part of a cohesive strategy that considers the value of data from each organism, given their role in basic research, health, agriculture and industry, as well as their value in comparative genomics.

Abbreviations: FGI

Resource Type: data or information resource, data set

Keywords: sequence, fungi, gene annotation, genome

Funding: NHGRI ;

NSF ;

NIAID ;

USDA

Availability: Free, Freely available

Resource Name: Fungal Genome Initiative

Resource ID: SCR_003169

Alternate IDs: nif-0000-30591

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T133323+0000

Ratings and Alerts

No rating or validation information has been found for Fungal Genome Initiative.

No alerts have been found for Fungal Genome Initiative.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Yao HY, et al. (2023) Arabidopsis Sec14 proteins (SFH5 and SFH7) mediate interorganelle transport of phosphatidic acid and regulate chloroplast development. *Proceedings of the National Academy of Sciences of the United States of America*, 120(6), e2221637120.

Cabral LM, et al. (2021) ABAP1 Plays a Role in the Differentiation of Male and Female Gametes in *Arabidopsis thaliana*. *Frontiers in plant science*, 12, 642758.

Goto-Yamada S, et al. (2019) Sucrose Starvation Induces Microautophagy in Plant Root Cells. *Frontiers in plant science*, 10, 1604.

Hehenberger E, et al. (2017) Novel Predators Reshape Holozoan Phylogeny and Reveal the Presence of a Two-Component Signaling System in the Ancestor of Animals. *Current biology : CB*, 27(13), 2043.

Li J, et al. (2017) Phylogenomic evolutionary surveys of subtilase superfamily genes in fungi. *Scientific reports*, 7, 45456.

Li J, et al. (2014) Independent expansion of zincin metalloproteinases in Onygenales fungi may be associated with their pathogenicity. *PloS one*, 9(2), e90225.

Kalleda N, et al. (2013) Targeting fungal genes by diced siRNAs: a rapid tool to decipher gene function in *Aspergillus nidulans*. *PloS one*, 8(10), e75443.

Lang GI, et al. (2011) Mutation rates across budding yeast chromosome VI are correlated with replication timing. *Genome biology and evolution*, 3, 799.

Bernhards Y, et al. (2011) The phocein homologue SmMOB3 is essential for vegetative cell fusion and sexual development in the filamentous ascomycete *Sordaria macrospora*. *Current genetics*, 57(2), 133.

Lombard L, et al. (2010) Species concepts in *Calonectria* (*Cylindrocladium*). *Studies in mycology*, 66, 1.

Elleuche S, et al. (2009) Beta-carbonic anhydrases play a role in fruiting body development and ascospore germination in the filamentous fungus *Sordaria macrospora*. PLoS one, 4(4), e5177.

Ma LJ, et al. (2009) Genomic analysis of the basal lineage fungus *Rhizopus oryzae* reveals a whole-genome duplication. PLoS genetics, 5(7), e1000549.

Arnaud MB, et al. (2007) Sequence resources at the *Candida* Genome Database. Nucleic acids research, 35(Database issue), D452.

Ronald J, et al. (2007) The evolution of gene expression QTL in *Saccharomyces cerevisiae*. PLoS one, 2(7), e678.

Thon MR, et al. (2006) The role of transposable element clusters in genome evolution and loss of synteny in the rice blast fungus *Magnaporthe oryzae*. Genome biology, 7(2), R16.

Idnurm A, et al. (2005) Light controls growth and development via a conserved pathway in the fungal kingdom. PLoS biology, 3(4), e95.

Gardner U, et al. (2005) CYGD: the Comprehensive Yeast Genome Database. Nucleic acids research, 33(Database issue), D364.

Ronald J, et al. (2005) Local regulatory variation in *Saccharomyces cerevisiae*. PLoS genetics, 1(2), e25.