# Resource Summary Report

Generated by NIF on Apr 18, 2025

# 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 set, data or information resource

**Keywords:** sequence, fungi, gene annotation, genome

**Funding:** NHGRI ;
NSF ;
NIAID ;
USDA

**Resource Name:** Fungal Genome Initiative

**Resource ID:** SCR_003169

**Alternate IDs:** nif-0000-30591

**Record Creation Time:** 20220129T080217+0000

**Record Last Update:** 20250411T054836+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 NIF.

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.

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

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.

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.

Güldener 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.