

Resource Summary Report

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MycoCosm

RRID:SCR_005312

Type: Tool

Proper Citation

MycoCosm (RRID:SCR_005312)

Resource Information

URL: <http://genome.jgi.doe.gov/programs/fungi/index.jsf>

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Description: Fungal genomics database and interactive analytical tools that integrates all fungal genomes for diverse fungi that are important for energy and environment, the focus of the JGI Fungal program. It integrates genomics data from the DOE JGI and its users and promotes user community participation in data submission, annotation and analysis. Over 100 newly sequenced and annotated fungal genomes from JGI and elsewhere are available to the public through MycoCosm, and new annotated genomes are being added to this resource upon completion of annotation. MycoCosm offers web-based genome analysis tools for fungal biologists to "navigate" through sequenced genomes and explore them in the context of "genome-centric" and "comparative views".

Abbreviations: MycoCosm

Synonyms: MycoCosm - the fungal genomics resource

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

Defining Citation: [PMID:24297253](#), [PMID:22110030](#)

Keywords: gene, genome, geneome map, jgi, fungus, genomics, energy, environment, annotation, FASEB list

Funding: DOE

Availability: Public, Acknowledgement requested, The community can contribute to this resource

Resource Name: MycoCosm

Resource ID: SCR_005312

Alternate IDs: OMICS_01657, nlx_144366, r3d100011751

Alternate URLs: <https://doi.org/10.17616/R3QQ0J>

Old URLs: <http://jgi.doe.gov/fungi>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260808T190233+0000

Ratings and Alerts

No rating or validation information has been found for MycoCosm.

No alerts have been found for MycoCosm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 254 mentions in open access literature.

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

LeBlanc CJ, et al. (2026) Evolutionary turnover of key amino acids explains conservation of function without conservation of sequence in transcriptional activation domains. PLoS genetics, 22(3), e1012069.

Vitale S, et al. (2026) Mating-Type Loci Modulate Pathogenicity and Non-Sexual Development Through Autocrine Pheromone Signalling in the Asexual Fungus Fusarium oxysporum. Molecular plant pathology, 27(3), e70248.

El Mahboubi K, et al. (2026) Plant-fungi interactions in Marchantia polymorpha are associated with horizontal gene transfer and terpene metabolism. Proceedings of the National Academy of Sciences of the United States of America, 123(6), e2532723123.

Zhou Y, et al. (2026) Mechanism and evolutionary divergence of a novel oxidized polyvinyl alcohol hydrolase in Stenotrophomonas rhizophila QL-P4. Scientific reports, 16(1), 6411.

Laurent-Webb L, et al. (2026) Endophytic and ectomycorrhizal, an overlooked dual ecological niche? Insights from natural environments and Russula species. The New phytologist, 250(6), 3946.

Steindorff AS, et al. (2026) Phenogenomics reveals the ecology and evolution of Trichoderma fungi for sustainable agriculture. Nature microbiology, 11(3), 815.

Guerreiro MA, et al. (2026) Genomic and physiological signatures of adaptation in pathogenic fungi. *Nature communications*, 17(1), 748.

Spanner RE, et al. (2026) Allelic variation of Avr genes in highly virulent strains explains severe wheat stem rust epidemics. *Nature communications*, 17(1).

Padilla-Garfias F, et al. (2026) Mechanisms of the marine yeast *Debaryomyces hansenii* for protection against reactive oxygen species produced during benzo(a)pyrene biotransformation. *Applied and environmental microbiology*, 92(2), e0231425.

Marin-Carvajal S, et al. (2026) Whole-genome sequencing, phenotypic characterization, and antifungal susceptibility profiles of three *Aspergillus hortae* clinical isolates from Colombia. *PloS one*, 21(2), e0342479.

Gacesa R, et al. (2026) Proteomic profiling of a *Sporobolomyces* yeast reveals global responses to UV-B-induced oxidative stress. *PloS one*, 21(2), e0333568.

Dauphin B, et al. (2026) Chromosome-scale Genome Assembly of the Most Abundant Ectomycorrhizal Fungus *Cenococcum Geophilum* Reveals Massive TE Expansion and RIP Defense Mechanism. *Genome biology and evolution*, 18(2).

Cendoya E, et al. (2026) Members of the *Fusarium fujikuroi* Species Complex Isolated from Asymptomatic Wetland Grasses in Argentina Include Previously Described Species Pathogenic on Cereal Crops and a Novel Species. *Journal of fungi (Basel, Switzerland)*, 12(6).

Ganjoloo N, et al. (2026) Reintroduction of lignin-modifying enzymes in the brown-rot fungus *Gloeophyllum trabeum* restores ligninolytic activities but diminishes lignocellulose degradation. *Fungal biology and biotechnology*, 13(1).

Cole J, et al. (2025) Comparative genomic analysis of a metagenome-assembled genome reveals distinctive symbiotic traits in a *Mucoromycotina* fine root endophyte arbuscular mycorrhizal fungus. *BMC genomics*, 26(1), 967.

Busse W, et al. (2025) Super-resolution imaging of native fluorescent photoreceptors in chytrid fungal eyes. *The EMBO journal*, 44(14), 4088.

Ezzedine JA, et al. (2025) Snow- and ice-ecosystem cleaning capability of the pucciniomycotinous yeast *Phenoliferia psychropholica*. *Communications biology*, 8(1), 1084.

Jin GT, et al. (2025) A de novo Gene Promotes Seed Germination Under Drought Stress in *Arabidopsis*. *Molecular biology and evolution*, 42(1).

Mondo SJ, et al. (2025) Consecutive low-frequency shifts in A/T content denote nucleosome positions across microeukaryotes. *iScience*, 28(5), 112472.

Lax C, et al. (2025) Symmetric adenine methylation is an essential DNA modification in the early-diverging fungus *Rhizopus microsporus*. *Nature communications*, 16(1), 3843.