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

Proper Citation: MycoCosm (RRID:SCR_005312)

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

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

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250519T204318+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 223 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in Colletotrichum fungi. GigaScience, 13.

Qi Z, et al. (2024) Adaptive advantages of restorative RNA editing in fungi for resolving survival-reproduction trade-offs. Science advances, 10(1), eadk6130.

Iacovelli R, et al. (2024) Discovery and Heterologous Expression of Functional 4-O-Dimethylallyl-l-tyrosine Synthases from Lichen-Forming Fungi. Journal of natural products, 87(9), 2243.

Chen W, et al. (2024) Phylogenomics analysis of velvet regulators in the fungal kingdom. Microbiology spectrum, 12(2), e0371723.

Zhao H, et al. (2024) Substrate specificity mapping of fungal CAZy AA3_2 oxidoreductases.

Biotechnology for biofuels and bioproducts, 17(1), 47.

Zhang X, et al. (2024) Insights into the efficient degradation mechanism of extracellular proteases mediated by Purpureocillium lilacinum. Frontiers in microbiology, 15, 1404439.

Trieu TA, et al. (2024) Myo5B plays a significant role in the hyphal growth and virulence of the human pathogenic fungus Mucor lusitanicus. Microbiology (Reading, England), 170(7).

Stajich JE, et al. (2024) Signatures of transposon-mediated genome inflation, host specialization, and photoentrainment in Entomophthora muscae and allied entomophthoralean fungi. eLife, 12.

Popošek LL, et al. (2024) New Insights into Interactions between Mushroom Aegerolysins and Membrane Lipids. Toxins, 16(3).

Klauer RR, et al. (2024) Hydrophobins from Aspergillus mediate fungal interactions with microplastics. bioRxiv : the preprint server for biology.

Longsaward R, et al. (2024) In silico analysis of secreted effectorome of the rubber tree pathogen Rigidoporus microporus highlights its potential virulence proteins. Frontiers in microbiology, 15, 1439454.

Hasegawa N, et al. (2024) Random forest machine-learning algorithm classifies white- and brown-rot fungi according to the number of the genes encoding Carbohydrate-Active enZyme families. Applied and environmental microbiology, 90(7), e0048224.

Dubinkina V, et al. (2024) A transcriptomic atlas of acute stress response to low pH in multiple Issatchenkia orientalis strains. Microbiology spectrum, 12(1), e0253623.

Rosas-Paz M, et al. (2024) Nitrogen limitation-induced adaptive response and lipogenesis in the Antarctic yeast Rhodotorula mucilaginosa M94C9. Frontiers in microbiology, 15, 1416155.

LeBlanc C, et al. (2024) Conservation of function without conservation of amino acid sequence in intrinsically disordered transcriptional activation domains. bioRxiv : the preprint server for biology.

Molinelli L, et al. (2024) Methionine oxidation of carbohydrate-active enzymes during white-rot wood decay. Applied and environmental microbiology, 90(3), e0193123.

Plett JM, et al. (2024) Sesquiterpenes of the ectomycorrhizal fungus Pisolithus microcarpus alter root growth and promote host colonization. Mycorrhiza, 34(1-2), 69.

Mascarin GM, et al. (2024) CRISPR-Cas9-mediated enhancement of Beauveria bassiana virulence with overproduction of oosporein. Fungal biology and biotechnology, 11(1), 21.

Stonoha-Arther C, et al. (2024) Rhizosphere microbial community structure in high-producing, low-input switchgrass families. PloS one, 19(10), e0308753.