

Resource Summary Report

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Ensembl Fungi

RRID:SCR_008681

Type: Tool

Proper Citation

Ensembl Fungi (RRID:SCR_008681)

Resource Information

URL: <http://fungi.ensembl.org/index.html>

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Description: The Ensembl Genomes project produces genome databases for important species from across the taxonomic range, using the Ensembl software system. Five sites are now available, one of which is Ensembl Fungi, which houses fungal species.

Sponsors: EnsemblFungi is a project run by EMBL - EBI to maintain annotation on selected genomes, based on the software developed in the Ensembl project developed jointly by the EBI and the Wellcome Trust Sanger Institute.

Synonyms: EnsemblFungi

Resource Type: data or information resource, database

Keywords: fungus, database, genome, software, specie, taxonomic, FASEB list

Resource Name: Ensembl Fungi

Resource ID: SCR_008681

Alternate IDs: nif-0000-33718, r3d100011196

Alternate URLs: <https://doi.org/10.17616/R3RK74>, <https://doi.org/10.17616/R3RK74>

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Ratings and Alerts

No rating or validation information has been found for Ensembl Fungi.

No alerts have been found for Ensembl Fungi.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 218 mentions in open access literature.

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

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Zhu B, et al. (2025) Multi-kingdom microbial changes and their associations with the clinical characteristics in schizophrenia patients. *Translational psychiatry*, 15(1), 228.

Sun D, et al. (2025) FgMsn2, a zinc finger transcription factor, regulates stress responses, pathogenicity and metabolism in wheat scab fungus *Fusarium graminearum*. *Stress biology*, 5(1), 54.

Moonjely S, et al. (2025) Comparative transcriptomics reveal contrasting strategies between a fungal plant pathogen and an endophyte during initial host colonization. *Microbiology spectrum*, 13(8), e0022625.

Zhang X, et al. (2025) Global characterization of GH3 family glycoside hydrolase genes in *Fusarium verticillioides* and functional analysis of FvGH3-6. *Frontiers in microbiology*, 16, 1543210.

Tomaz da Silva P, et al. (2025) Nucleotide dependency analysis of genomic language models detects functional elements. *Nature genetics*, 57(10), 2589.

Zhang L, et al. (2025) Intestinal fungal signatures and their impact on immune checkpoint inhibitor efficacy: a multi-cohort meta-analysis. *NPJ biofilms and microbiomes*, 11(1), 188.

Jiang Y, et al. (2025) High-resolution microbiome analysis of host-rich samples using 2bRAD-M without host depletion. *NPJ biofilms and microbiomes*, 11(1), 223.

Papp LA, et al. (2025) Transcriptome changes of fission yeast cells exposed to fumonisin B1 or co-cultured with *Fusarium verticillioides*. *Applied microbiology and biotechnology*, 109(1), 211.

Lu P, et al. (2025) Up-Frameshift Factors from Phytopathogenic Fungi Play a Crucial Role in Nonsense-Mediated mRNA Decay. *Journal of fungi (Basel, Switzerland)*, 11(6).

Yang Y, et al. (2025) Systematic identification of secondary bile acid production genes in global microbiome. *mSystems*, 10(1), e0081724.

Pimentel MF, et al. (2025) Dual RNA-seq reveals transcriptome changes during *Fusarium virguliforme*-*Trichoderma afroharzianum* interactions. *PloS one*, 20(1), e0310850.

Zhang S, et al. (2025) Molecular Characterisation of the Peroxidase Gene Family in *Botrytis cinerea* and the Role of BcPRD7 in Virulence. *Molecular plant pathology*, 26(4), e70079.

Navasca A, et al. (2025) Dispensable genome and segmental duplications drive the genome plasticity in *Fusarium solani*. *Frontiers in fungal biology*, 6, 1432339.

Muro EM, et al. (2025) The emergence of eukaryotes as an evolutionary algorithmic phase transition. *Proceedings of the National Academy of Sciences of the United States of America*, 122(13), e2422968122.

Ding Y, et al. (2025) The ortholog of human DNAJC9 promotes histone H3-H4 degradation and is counteracted by Asf1 in fission yeast. *Nucleic acids research*, 53(3).

Moreno-Rodríguez A, et al. (2025) Evolutionary perspective of the CAG/CAA interplay coding for pure polyglutamine stretches in proteins. *NAR genomics and bioinformatics*, 7(2), lqaf075.

Pierre-Pierre N, et al. (2025) SsMet1 is a critical gene in methionine biosynthesis in *Sclerotinia sclerotiorum*. *Frontiers in fungal biology*, 6, 1563395.

Pacheco R, et al. (2025) In vitro RNA-mediated gene silencing of *Fusarium oxysporum* f.sp. *cubense* from Ecuador and assessment of RNAi molecule stability in banana plants. *BMC research notes*, 18(1), 185.

Zárate-Ortiz AI, et al. (2025) Secretion of antifungal metabolites contributes to the antagonistic activity of *Talaromyces oaxaquensis*. *Current research in microbial sciences*, 8, 100402.