

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>

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260905T133154+0000

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 261 mentions in open access literature.

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

Barata-Antunes C, et al. (2026) Endocytosis of the *Saccharomyces cerevisiae* Jen1 monocarboxylate-proton symporter under mildly alkaline conditions: a mechanism to prevent metabolite loss? *Microbial cell factories*, 25(1).

Yates AD, et al. (2026) Ensembl 2026. *Nucleic acids research*, 54(D1), D1053.

Zaccaria T, et al. (2026) Exploring the Habitability of the Outer Solar System Icy Moons for the Extremotolerant Yeast *Rhodotorula frigidicola*. *Environmental microbiology*, 28(2), e70260.

Gu A, et al. (2026) Differential gene expression to heat stress drives thermotolerance, pathogenicity, and reproduction in *Fusarium head blight* pathogens: from transcriptomic profiling to functional validation. *BMC plant biology*, 26(1).

Chen T, et al. (2026) Functional analysis of target of rapamycin in regulating mycelial growth and development in *Penicillium italicum*. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(3), 345.

Ozketen AC, et al. (2026) The proteome study of germinated *Puccinia triticina* urediniospores reveals a novel effector protein required for virulence. *Scientific reports*, 16(1).

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.

Lang X, et al. (2026) FungiSNC: An integrated database for fungi small non-coding RNAs based on high-throughput sequencing. *Journal of advanced research*, 84, 187.

Cheng Z, et al. (2026) Knockout of *SsArl1* Leading to Enhanced Virulence in *Sclerotinia sclerotiorum*. *Journal of fungi (Basel, Switzerland)*, 12(6).

Ye W, et al. (2026) PolyAseqTrap: a universal tool for genome-wide identification and quantification of polyadenylation sites from different 3' end sequencing data. *Genome biology*, 27(1).

Kumar V, et al. (2026) Host-Induced Silencing of *Rhizoctonia solani* 5-Enolpyruvylshikimate-3-Phosphate Synthase Impairs Its Virulence in Rice. *Plant biotechnology journal*, 24(6), 3573.

Phan-Canh T, et al. (2026) *Candida auris* skin tropism and antifungal resistance are mediated by carbonic anhydrase Nce103. *Nature microbiology*, 11(2), 461.

Tsiouri O, et al. (2026) Comparative analysis towards the identification of genome wide characteristics of a beneficial fungal endophyte. *Scientific reports*, 16(1).

Murayama H, et al. (2026) Structure of ergosteryl-aspartate synthase reveals how an entrapped tRNA is used like a prosthetic swinging arm in the synthesis of aminoacylated sterols. *Nature communications*, 17(1).

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.

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.

Li R, et al. (2025) Differential Gene Expression in *Fusarium* Head Blight Pathogens Facilitates Root Infection of Wheat, Maize, and Soybean. *Plants (Basel, Switzerland)*, 14(16).

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

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.

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.