

Resource Summary Report

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Fungal C-values Database

RRID:SCR_002726

Type: Tool

Proper Citation

Fungal C-values Database (RRID:SCR_002726)

Resource Information

URL: <http://www.zbi.ee/fungal-genomesize/>

Proper Citation: Fungal C-values Database (RRID:SCR_002726)

Description: Database for scientists interested in fungal genomics. Multiple species are included, and the database provides information on DNA C-values and genomic size. It also gives information derived from electrophoresis experiments and genome sequencing projects. The database accepts data submissions. We appreciate receiving published offprints, preprints, and personal communications providing C-value estimates for fungi.

Synonyms: Fungal Genome Size Database

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

Defining Citation: [PMID:17090588](#)

Keywords: fungal c-value, fungal genome, fungus, c-value

Availability: Free, Freely available

Resource Name: Fungal C-values Database

Resource ID: SCR_002726

Alternate IDs: nif-0000-02857

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260817T040325+0000

Ratings and Alerts

No rating or validation information has been found for Fungal C-values Database.

No alerts have been found for Fungal C-values Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Sanzani SM, et al. (2025) Rapid and Accurate Detection of the Most Common Bee Pathogens; Nosema ceranae, Aspergillus flavus, Paenibacillus larvae and Black Queen Cell Virus. Insects, 16(8).

Fernández P, et al. (2024) A 160 Gbp fern genome shatters size record for eukaryotes. iScience, 27(6), 109889.

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

Jung H, et al. (2020) Twelve quick steps for genome assembly and annotation in the classroom. PLoS computational biology, 16(11), e1008325.

Dominguez Del Angel V, et al. (2018) Ten steps to get started in Genome Assembly and Annotation. F1000Research, 7.

Donnart T, et al. (2017) Filamentous ascomycete genomes provide insights into Copia retrotransposon diversity in fungi. BMC genomics, 18(1), 410.

Cross H, et al. (2017) Fungal diversity and seasonal succession in ash leaves infected by the invasive ascomycete Hymenoscyphus fraxineus. The New phytologist, 213(3), 1405.

Tavares S, et al. (2014) Genome size analyses of Pucciniales reveal the largest fungal genomes. Frontiers in plant science, 5, 422.

Garcia S, et al. (2014) Recent updates and developments to plant genome size databases. Nucleic acids research, 42(Database issue), D1159.

Zhang H, et al. (2012) Total centromere size and genome size are strongly correlated in ten grass species. Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology, 20(4), 403.

Sun C, et al. (2012) LTR retrotransposons contribute to genomic gigantism in plethodontid salamanders. Genome biology and evolution, 4(2), 168.

Anderson JL, et al. (2011) Population genetics of the aquatic fungus *Tetracladium marchalianum* over space and time. *PloS one*, 6(1), e15908.

Shi S, et al. (2010) Screening of Cell Cycle-Related Genes of *Pleurotus eryngii* Using Yeast Mutant Strains. *Mycobiology*, 38(1), 70.

Gregory TR, et al. (2007) Eukaryotic genome size databases. *Nucleic acids research*, 35(Database issue), D332.