

Resource Summary Report

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MIPS Neurospora crassa Genome Database

RRID:SCR_007794

Type: Tool

Proper Citation

MIPS Neurospora crassa Genome Database (RRID:SCR_007794)

Resource Information

URL: <http://mips.helmholtz-muenchen.de/genre/proj/ncrassa/>

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Description: A database of the molecular structure and functional network of the entirely sequenced, filamentous fungus *Neurospora crassa*. The underlying sequence is the release 7 of the high quality draft sequence of the Broad Institute. The goal is to provide a comprehensive genome database in the Genome Research Environment in parallel with other fungal genomes to enable in depth fungal comparative analysis. The database contains the manually modelled gene set generated in the German *Neurospora* genome project and is combined with Broad calls from release 7 version 3.

Synonyms: MNCDB, MIPS

Resource Type: data or information resource, database

Keywords: fungus

Resource Name: MIPS Neurospora crassa Genome Database

Resource ID: SCR_007794

Alternate IDs: nif-0000-03151

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260905T133145+0000

Ratings and Alerts

No rating or validation information has been found for MIPS Neurospora crassa Genome Database.

No alerts have been found for MIPS Neurospora crassa Genome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Hu W, et al. (2014) Bioinformatic and biochemical characterizations of C-S bond formation and cleavage enzymes in the fungus *Neurospora crassa* ergothioneine biosynthetic pathway. *Organic letters*, 16(20), 5382.

Samils N, et al. (2013) Sex-linked transcriptional divergence in the hermaphrodite fungus *Neurospora tetrasperma*. *Proceedings. Biological sciences*, 280(1764), 20130862.

Mähs A, et al. (2012) The essential phosphoinositide kinase MSS-4 is required for polar hyphal morphogenesis, localizing to sites of growth and cell fusion in *Neurospora crassa*. *PloS one*, 7(12), e51454.

Akman OE, et al. (2012) Digital clocks: simple Boolean models can quantitatively describe circadian systems. *Journal of the Royal Society, Interface*, 9(74), 2365.

González-Fernández R, et al. (2010) Proteomics of plant pathogenic fungi. *Journal of biomedicine & biotechnology*, 2010, 932527.

Nowrousian M, et al. (2010) De novo assembly of a 40 Mb eukaryotic genome from short sequence reads: *Sordaria macrospora*, a model organism for fungal morphogenesis. *PLoS genetics*, 6(4), e1000891.