

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

Genolevures

RRID:SCR_013173

Type: Tool

Proper Citation

Genolevures (RRID:SCR_013173)

Resource Information

URL: <http://cbi.labri.fr/Genolevures>

Proper Citation: Genolevures (RRID:SCR_013173)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 24,2023. It provides annotated sequence data and classifications for the genomes of eighteen species of hemiascomycete yeasts, including nine complete genomes. The Gnolevures web resources provides genetic element pages, orthologs defined by syntenic homology, protein families, a genome browser for interspecies comparison, and data sets for downloading. An advanced search facility permits a number of criterion-based and full text queries. Classification data, including protein families and orthologs, and the most up-to-date genome annotations, are for the most part not available in general-purpose sequence data bases such as EMBL/GenBank/DDBJ.

Synonyms: Gnolevures

Resource Type: data or information resource, database

Keywords: hemiascomycete yeast, protein family

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Genolevures

Resource ID: SCR_013173

Alternate IDs: nif-0000-21161, nif-0000-02862, SCR_013203

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260912T195759+0000

Ratings and Alerts

No rating or validation information has been found for Genolevures.

No alerts have been found for Genolevures.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Champeimont R, et al. (2014) SPoRE: a mathematical model to predict double strand breaks and axis protein sites in meiosis. BMC bioinformatics, 15(1), 391.

Pereira I, et al. (2014) Characterization of new polyol/H⁺ symporters in *Debaryomyces hansenii*. PloS one, 9(2), e88180.

Beopoulos A, et al. (2012) Identification and characterization of DGA2, an acyltransferase of the DGAT1 acyl-CoA:diacylglycerol acyltransferase family in the oleaginous yeast *Yarrowia lipolytica*. New insights into the storage lipid metabolism of oleaginous yeasts. Applied microbiology and biotechnology, 93(4), 1523.

Ueno K, et al. (2011) Intestinal resident yeast *Candida glabrata* requires Cyb2p-mediated lactate assimilation to adapt in mouse intestine. PloS one, 6(9), e24759.

Koren A, et al. (2010) Epigenetically-inherited centromere and neocentromere DNA replicates earliest in S-phase. PLoS genetics, 6(8), e1001068.

Dobrynin K, et al. (2010) Characterization of two different acyl carrier proteins in complex I from *Yarrowia lipolytica*. Biochimica et biophysica acta, 1797(2), 152.

Brustolini OJ, et al. (2009) Computational analysis of the interaction between transcription factors and the predicted secreted proteome of the yeast *Kluyveromyces lactis*. BMC bioinformatics, 10, 194.

Lelandais G, et al. (2008) Genome adaptation to chemical stress: clues from comparative transcriptomics in *Saccharomyces cerevisiae* and *Candida glabrata*. Genome biology, 9(11), R164.

Roetzer A, et al. (2008) *Candida glabrata* environmental stress response involves *Saccharomyces cerevisiae* Msn2/4 orthologous transcription factors. Molecular microbiology, 69(3), 603.

Hogues H, et al. (2008) Transcription factor substitution during the evolution of fungal ribosome regulation. Molecular cell, 29(5), 552.

Morgner N, et al. (2008) Subunit mass fingerprinting of mitochondrial complex I. *Biochimica et biophysica acta*, 1777(10), 1384.

Sherman D, et al. (2006) Genolevures complete genomes provide data and tools for comparative genomics of hemiascomycetous yeasts. *Nucleic acids research*, 34(Database issue), D432.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.