

Resource Summary Report

Generated by T1D on Sep 5, 2026

Genolevures: Genomic Exploration of the Hemiascomycete Yeasts

RRID:SCR_013203

Type: Tool

Proper Citation

Genolevures: Genomic Exploration of the Hemiascomycete Yeasts (RRID:SCR_013203)

Resource Information

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

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Description: Gnolevures 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. It also provides exploratory tools and curated data sets relative to nine complete and seven partial genome sequences determined and manually annotated by the Gnolevures Consortium, to facilitate comparative genomic studies of Hemiascomycete yeasts. The 2008 update to the Gnolevures database provides four new genomes in complete (subtelomere to subtelomere) chromosome sequences, 50 000 protein-coding and tRNA genes, and in silico analyses for each gene element. A key element is a novel classification of conserved multi-species protein families and their use in detecting synteny, gene fusions and other aspects of genome remodeling in evolution. The purpose is to release high-quality curated data from complete genomes, with a focus on the relations between genes, genomes and proteins. It is a large-scale comparative genomics project between *Saccharomyces cerevisiae* and other yeast species representative of the various branches of the Hemiascomycetous class. They sequence and manually curate both complete genomes and random genomic libraries. It addresses basic questions concerning molecular evolution: species-specific and class-specific genes, distribution of genes among functional families, rate of divergence, mechanisms of chromosome shuffling. With their relative small genome size, yeasts offer a unique opportunity for exploring eukaryotic genome evolution by comparative analysis of several species. Sponsors: French National center for Scientific Research (CNRS) (GDR 2354, partial); French National Research Agency (ANR) (ANR-05-BLAN-0331; GENARISE, partial); Rgion Aquitaine (Ple de Recherche en Informatique) (2005-1306001AB, partial) and ACI IMPBIO (IMPB114, partial) (Gnolevures En Ligne). Funding

for open access charge: CNRS GDR 2354.

Synonyms: Genolevures

Resource Type: data or information resource, database

Keywords: element, evolution, family, fungal genome databases, fusion, genetic, chromosome, classification, coding, comparison, genome, genomic, hemiascomycete, homology, interspecies, mechanism, ortholog, protein, saccharomyces cerevisiae, sequence, size, specie, subtelomere, trna, yeast

Resource Name: Genolevures: Genomic Exploration of the Hemiascomycete Yeasts

Resource ID: SCR_013203

Alternate IDs: nif-0000-21161

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260903T235214+0000

Ratings and Alerts

No rating or validation information has been found for Genolevures: Genomic Exploration of the Hemiascomycete Yeasts.

No alerts have been found for Genolevures: Genomic Exploration of the Hemiascomycete Yeasts.

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 [T1D](#).

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.

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.

Lavoie H, et al. (2010) Evolutionary tinkering with conserved components of a transcriptional regulatory network. *PLoS biology*, 8(3), e1000329.

Nikolaou E, et al. (2009) Phylogenetic diversity of stress signalling pathways in fungi. *BMC evolutionary biology*, 9, 44.

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.

Fang ZA, et al. (2009) Gene responses to oxygen availability in *Kluyveromyces lactis*: an insight on the evolution of the oxygen-responding system in yeast. *PloS one*, 4(10), e7561.

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.

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.

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

Miele V, et al. (2008) DNA physical properties determine nucleosome occupancy from yeast to fly. *Nucleic acids research*, 36(11), 3746.

Gupta R, et al. (2007) Ubiquitination screen using protein microarrays for comprehensive identification of Rsp5 substrates in yeast. *Molecular systems biology*, 3, 116.