

# Resource Summary Report

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## Genome Resources for Yeast Chromosomes

RRID:SCR\_015005

Type: Tool

### Proper Citation

Genome Resources for Yeast Chromosomes (RRID:SCR\_015005)

### Resource Information

**URL:** <http://gryc.inra.fr>

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**Description:** Database which provides annotated sequence data for the genomes of basidio and ascomycete yeasts. The resources provided include genetic element pages, data sets for downloading, quick and advanced searches, facilities for BLAST comparisons, and a genome browser powered by JBrowse from GMOD.

**Abbreviations:** GRYC

**Synonyms:** Genome Resources for Yeast Chromosomes (GRYC)

**Resource Type:** data or information resource, database

**Keywords:** yeast, single celled eukaryote, annotated genome, basidio yeast, ascomycete yeast

**Availability:** Available for download

**Resource Name:** Genome Resources for Yeast Chromosomes

**Resource ID:** SCR\_015005

**Record Creation Time:** 20220129T080323+0000

**Record Last Update:** 20260806T054614+0000

### Ratings and Alerts

No rating or validation information has been found for Genome Resources for Yeast Chromosomes.

No alerts have been found for Genome Resources for Yeast Chromosomes.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Bigey F, et al. (2023) Insights into the Genomic and Phenotypic Landscape of the Oleaginous Yeast *Yarrowia lipolytica*. *Journal of fungi* (Basel, Switzerland), 9(1).

Gorczyca M, et al. (2023) Transcription factors enhancing synthesis of recombinant proteins and resistance to stress in *Yarrowia lipolytica*. *Applied microbiology and biotechnology*, 107(15), 4853.

Kubiak-Szymendera M, et al. (2022) Hyperosmolarity adversely impacts recombinant protein synthesis by *Yarrowia lipolytica*-molecular background revealed by quantitative proteomics. *Applied microbiology and biotechnology*, 106(1), 349.

Celińska E, et al. (2022) "Fight-flight-or-freeze" - how *Yarrowia lipolytica* responds to stress at molecular level? *Applied microbiology and biotechnology*, 106(9-10), 3369.

Onésime D, et al. (2022) A unique, newly discovered four-member protein family involved in extracellular fatty acid binding in *Yarrowia lipolytica*. *Microbial cell factories*, 21(1), 200.

Navarrete C, et al. (2022) DebaryOmics: an integrative -omics study to understand the halophilic behaviour of *Debaryomyces hansenii*. *Microbial biotechnology*, 15(4), 1133.

Hapeta P, et al. (2021) A 37-amino acid loop in the *Yarrowia lipolytica* hexokinase impacts its activity and affinity and modulates gene expression. *Scientific reports*, 11(1), 6412.

Madzak C, et al. (2021) *Yarrowia lipolytica* Strains and Their Biotechnological Applications: How Natural Biodiversity and Metabolic Engineering Could Contribute to Cell Factories Improvement. *Journal of fungi* (Basel, Switzerland), 7(7).

Larroude M, et al. (2021) *Yarrowia lipolytica* chassis strains engineered to produce aromatic amino acids via the shikimate pathway. *Microbial biotechnology*, 14(6), 2420.

Hassing EJ, et al. (2021) Elimination of aromatic fusel alcohols as by-products of *Saccharomyces cerevisiae* strains engineered for phenylpropanoid production by 2-oxo-acid decarboxylase replacement. *Metabolic engineering communications*, 13, e00183.

Delaveau T, et al. (2021) Yap5 Competes With Hap4 for the Regulation of Iron Homeostasis Genes in the Human Pathogen *Candida glabrata*. *Frontiers in cellular and infection microbiology*, 11, 731988.

Maciaszczyk-Dziubinska E, et al. (2020) The ancillary N-terminal region of the yeast AP-1 transcription factor Yap8 contributes to its DNA binding specificity. *Nucleic acids research*, 48(10), 5426.

Denecker T, et al. (2020) Functional networks of co-expressed genes to explore iron homeostasis processes in the pathogenic yeast *Candida glabrata*. *NAR genomics and bioinformatics*, 2(2), lqaa027.

Kumar K, et al. (2020) Histone H4 dosage modulates DNA damage response in the pathogenic yeast *Candida glabrata* via homologous recombination pathway. *PLoS genetics*, 16(3), e1008620.

Gu Y, et al. (2020) Refactoring Ehrlich Pathway for High-Yield 2-Phenylethanol Production in *Yarrowia lipolytica*. *ACS synthetic biology*, 9(3), 623.

Lajus S, et al. (2020) Engineering the Yeast *Yarrowia lipolytica* for Production of Polylactic Acid Homopolymer. *Frontiers in bioengineering and biotechnology*, 8, 954.

Gounot JS, et al. (2020) High Complexity and Degree of Genetic Variation in *Brettanomyces bruxellensis* Population. *Genome biology and evolution*, 12(6), 795.

Bellut K, et al. (2020) *Lachancea fermentati* Strains Isolated From Kombucha: Fundamental Insights, and Practical Application in Low Alcohol Beer Brewing. *Frontiers in microbiology*, 11, 764.

Boisramé A, et al. (2019) Exon junction complex components Y14 and Mago still play a role in budding yeast. *Scientific reports*, 9(1), 849.

Pracharova P, et al. (2019) *Geotrichum candidum* gene expression and metabolite accumulation inside the cells reflect the strain oxidative stress sensitivity and ability to produce flavour compounds. *FEMS yeast research*, 19(1).