

Resource Summary Report

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Yeast Search for Transcriptional Regulators And Consensus Tracking

RRID:SCR_006076

Type: Tool

Proper Citation

Yeast Search for Transcriptional Regulators And Consensus Tracking
(RRID:SCR_006076)

Resource Information

URL: <http://www.yeastract.com>

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Description: A curated repository of more than 206000 regulatory associations between transcription factors (TF) and target genes in *Saccharomyces cerevisiae*, based on more than 1300 bibliographic references. It also includes the description of 326 specific DNA binding sites shared among 113 characterized TFs. Further information about each Yeast gene has been extracted from the *Saccharomyces* Genome Database (SGD). For each gene the associated Gene Ontology (GO) terms and their hierarchy in GO was obtained from the GO consortium. Currently, YEASTRACT maintains a total of 7130 terms from GO. The nucleotide sequences of the promoter and coding regions for Yeast genes were obtained from Regulatory Sequence Analysis Tools (RSAT). All the information in YEASTRACT is updated regularly to match the latest data from SGD, GO consortium, RSA Tools and recent literature on yeast regulatory networks. YEASTRACT includes DISCOVERER, a set of tools that can be used to identify complex motifs found to be over-represented in the promoter regions of co-regulated genes. DISCOVERER is based on the MUSA algorithm. These algorithms take as input a list of genes and identify over-represented motifs, which can then be compared with transcription factor binding sites described in the YEASTRACT database.

Abbreviations: YEASTRACT

Resource Type: data or information resource, database

Defining Citation: [PMID:24170807](#), [PMID:20972212](#), [PMID:18032429](#), [PMID:16381908](#)

Keywords: yeast, gene, regulatory association, transcription factor, target gene, genomic, transcription regulation, transcription, web service, bio.tools, FASEB list

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Availability: Free

Resource Name: Yeast Search for Transcriptional Regulators And Consensus Tracking

Resource ID: SCR_006076

Alternate IDs: nif-0000-03652, OMICS_00547, biotools:yeastract

Alternate URLs: <https://bio.tools/yeastract>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260829T182943+0000

Ratings and Alerts

No rating or validation information has been found for Yeast Search for Transcriptional Regulators And Consensus Tracking.

No alerts have been found for Yeast Search for Transcriptional Regulators And Consensus Tracking.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 130 mentions in open access literature.

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

Moreira V, et al. (2026) Impaired Acetyl-CoA Compartmentalization Drives a Futile Lipogenic-Oxidative Cycle in N88S Seipinopathy. *Cells*, 15(5).

Li MT, et al. (2026) Transcriptomics-guided identification of engineering targets for improving salt tolerance in *Saccharomyces cerevisiae*. *Microbial cell factories*, 25(1).

Li R, et al. (2026) Sugar stress attenuates fruity aroma in sweet wine by suppressing ethyl ester biosynthesis: Insights from integrated sensory, metabolome, and transcriptomic analyses. *Food chemistry: X*, 34, 103580.

Chen RR, et al. (2025) Identification of key transcription factors, including DAL80 and CRZ1, involved in heat and ethanol tolerance in *Saccharomyces cerevisiae*.

Biotechnology for biofuels and bioproducts, 18(1), 50.

Avogo EW, et al. (2025) Bioinformatics analysis identifies Mot2 protein as a potential regulator of autophagy in *Saccharomyces cerevisiae*. *microPublication biology*, 2025.

Sasikumar S, et al. (2025) Genome-scale metabolic modelling identifies reactions mediated by SNP-SNP interactions associated with yeast sporulation. *NPJ systems biology and applications*, 11(1), 50.

Zuo W, et al. (2025) Engineering artificial cross-species promoters with different transcriptional strengths. *Synthetic and systems biotechnology*, 10(1), 49.

Garc??a-Mart??nez J, et al. (2025) Global changes in synthesis rates and mRNA stabilities during adaptive responses to cell wall stress in yeast. *Scientific reports*, 15(1), 25260.

Maksiutenko EM, et al. (2024) Gene Expression Analysis of Yeast Strains with a Nonsense Mutation in the eRF3-Coding Gene Highlights Possible Mechanisms of Adaptation. *International journal of molecular sciences*, 25(12).

Mota MN, et al. (2024) Shared and more specific genetic determinants and pathways underlying yeast tolerance to acetic, butyric, and octanoic acids. *Microbial cell factories*, 23(1), 71.

Pontes A, et al. (2024) Tracking alternative versions of the galactose gene network in the genus *Saccharomyces* and their expansion after domestication. *iScience*, 27(2), 108987.

Lin X, et al. (2024) Novel transcriptional regulation of the GAP promoter in *Pichia pastoris* towards high expression of heterologous proteins. *Microbial cell factories*, 23(1), 206.

Holyavkin C, et al. (2023) Genomic, transcriptomic, and metabolic characterization of 2-Phenylethanol-resistant *Saccharomyces cerevisiae* obtained by evolutionary engineering. *Frontiers in microbiology*, 14, 1148065.

Bari KA, et al. (2023) Tra1 controls the transcriptional landscape of the aging cell. *G3 (Bethesda, Md.)*, 13(1).

Park ZM, et al. (2023) Kar4 is Required for the Normal Pattern of Meiotic Gene Expression. *bioRxiv : the preprint server for biology*.

Das D, et al. (2023) Insights into the identification and evolutionary conservation of key genes in the transcriptional circuits of meiosis initiation and commitment in budding yeast. *FEBS open bio*, 13(12), 2290.

Sing CN, et al. (2022) Identification of a modulator of the actin cytoskeleton, mitochondria, nutrient metabolism and lifespan in yeast. *Nature communications*, 13(1), 2706.

Yang G, et al. (2022) Transcription Factors in *Aureobasidium* spp.: Classification, Regulation and a Newly Built Database. *Journal of fungi (Basel, Switzerland)*, 8(10).

Liska O, et al. (2022) TFLink: an integrated gateway to access transcription factor-target gene interactions for multiple species. *Database : the journal of biological databases and curation*, 2022.

Cheng C, et al. (2022) Deletion of NGG1 in a recombinant *Saccharomyces cerevisiae* improved xylose utilization and affected transcription of genes related to amino acid metabolism. *Frontiers in microbiology*, 13, 960114.