

Resource Summary Report

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SCPD - Saccharomyces cerevisiae promoter database

RRID:SCR_004412

Type: Tool

Proper Citation

SCPD - Saccharomyces cerevisiae promoter database (RRID:SCR_004412)

Resource Information

URL: <http://rulai.cshl.edu/SCPD/>

Proper Citation: SCPD - Saccharomyces cerevisiae promoter database (RRID:SCR_004412)

Description: A promoter database of Saccharomyces cerevisiae. Users can explore the promoter regions of ~6000 genes and ORFs in yeast genome, annotate putative regulatory sites of all genes and ORFs, locate intergenic regions, and retrieve sequence of the promoter region. In regards to regulatory elements and transcription factors, users can provide information on transcriptionally related genes, browse matrix and consensus sequences, view the correlation between elements, observe binding affinity and expression, and look at genomewide distribution. SCPD also provides some simple but useful tools for promoter sequence analysis. Gene, consensus and matrix records may be submitted.

Abbreviations: SCPD

Synonyms: SCPD - The Promoter Database of Saccharomyces cerevisiae

Resource Type: analysis service resource, service resource, data or information resource, data repository, data analysis service, database, production service resource, storage service resource

Defining Citation: [PMID:10487868](#)

Keywords: promoter, gene, genome, orf, transcription factor binding site, transcriptional start site, transcription factor

Resource Name: SCPD - Saccharomyces cerevisiae promoter database

Resource ID: SCR_004412

Alternate IDs: OMICS_01867, nif-0000-03445

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260729T044101+0000

Ratings and Alerts

No rating or validation information has been found for SCPD - *Saccharomyces cerevisiae* promoter database.

No alerts have been found for SCPD - *Saccharomyces cerevisiae* promoter database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Tutaj H, et al. (2024) Extreme positive epistasis for fitness in monosomic yeast strains. *eLife*, 12.

Du HY, et al. (2023) Analysis of the Properties of 44 ABC Transporter Genes from Biocontrol Agent *Trichoderma asperellum* ACCC30536 and Their Responses to Pathogenic *Alternaria alternata* Toxin Stress. *Current issues in molecular biology*, 45(2), 1570.

Wanarska M, et al. (2022) A New Expression System Based on Psychrotolerant *Debaryomyces macquariensis* Yeast and Its Application to the Production of Cold-Active ?-d-Galactosidase from *Paracoccus* sp. 32d. *International journal of molecular sciences*, 23(19).

Kang XX, et al. (2021) The GATA type transcriptional factors regulate pullulan biosynthesis in *Aureobasidium melanogenum* P16. *International journal of biological macromolecules*, 192, 161.

Huang Z, et al. (2019) Identification of a Heat-Inducible Element of Cysteine Desulfurase Gene Promoter in *Lentinula edodes*. *Molecules (Basel, Switzerland)*, 24(12).

Gómez-Gallego T, et al. (2019) The *Rhizophagus irregularis* Genome Encodes Two CTR Copper Transporters That Mediate Cu Import Into the Cytosol and a CTR-Like Protein Likely Involved in Copper Tolerance. *Frontiers in plant science*, 10, 604.

Contreras G, et al. (2019) Oxidative stress and the presence of bacteria increase gene expression of the antimicrobial peptide aclasin, a fungal CS?? defensin in *Aspergillus clavatus*. *PeerJ*, 7, e6290.

- Hashim FA, et al. (2019) Review of Different Sequence Motif Finding Algorithms. *Avicenna journal of medical biotechnology*, 11(2), 130.
- Ben Amira M, et al. (2018) MIP diversity from *Trichoderma*: Structural considerations and transcriptional modulation during mycoparasitic association with *Fusarium solani* olive trees. *PloS one*, 13(3), e0193760.
- Yu W, et al. (2018) Functional analysis of eliciting plant response protein Epl1-Tas from *Trichoderma asperellum* ACCC30536. *Scientific reports*, 8(1), 7974.
- Chen YC, et al. (2017) Randomized CRISPR-Cas Transcriptional Perturbation Screening Reveals Protective Genes against Alpha-Synuclein Toxicity. *Molecular cell*, 68(1), 247.
- Ji S, et al. (2017) Properties analysis of transcription factor gene TasMYB36 from *Trichoderma asperellum* CBS433.97 and its heterogeneous transformation to improve antifungal ability of *Populus*. *Scientific reports*, 7(1), 12801.
- Xie X, et al. (2016) Arbuscular Mycorrhizal Symbiosis Requires a Phosphate Transceptor in the *Gigaspora margarita* Fungal Symbiont. *Molecular plant*, 9(12), 1583.
- Martani F, et al. (2015) The *Saccharomyces cerevisiae* poly(A) binding protein Pab1 as a target for eliciting stress tolerant phenotypes. *Scientific reports*, 5, 18318.
- Zhou Q, et al. (2014) Genomic and transcriptome analyses reveal that MAPK- and phosphatidylinositol-signaling pathways mediate tolerance to 5-hydroxymethyl-2-furaldehyde for industrial yeast *Saccharomyces cerevisiae*. *Scientific reports*, 4, 6556.
- Tan M, et al. (2012) An information transmission model for transcription factor binding at regulatory DNA sites. *Theoretical biology & medical modelling*, 9, 19.
- Elsztein C, et al. (2011) The resistance of the yeast *Saccharomyces cerevisiae* to the biocide polyhexamethylene biguanide: involvement of cell wall integrity pathway and emerging role for YAP1. *BMC molecular biology*, 12, 38.
- Wei W, et al. (2007) Comparative analysis of regulatory motif discovery tools for transcription factor binding sites. *Genomics, proteomics & bioinformatics*, 5(2), 131.
- Guan Q, et al. (2006) Impact of nonsense-mediated mRNA decay on the global expression profile of budding yeast. *PLoS genetics*, 2(11), e203.
- Hongay CF, et al. (2006) Antisense transcription controls cell fate in *Saccharomyces cerevisiae*. *Cell*, 127(4), 735.