Resource Summary Report

Generated by NIF on May 25, 2025

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

Defining Citation: PMID:10487868

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

Funding:

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: 20250525T030823+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 19 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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 transfomation 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.