Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

YeTFaSCo

RRID:SCR_006893
Type: Tool

Proper Citation

YeTFaSCo (RRID:SCR_006893)

Resource Information

URL: http://yetfasco.ccbr.utoronto.ca/

Proper Citation: YeTFaSCo (RRID:SCR_006893)

Description: Collection of all available transcription factor (TF) specificities for the yeast Saccharomyces cerevisiae in Position Frequency Matrix (PFM) or Position Weight Matrix (PWM) formats. The specificities are evaluated for quality using several metrics. With this website, you can scan sequences with the motifs to find where potential binding sites lie, inspect precomputed genome-wide binding sites, find which TFs have similar motifs to one you have found, and download the collection of motifs. Submissions are welcome.

Abbreviations: YeTFaSCo

Synonyms: Yeast Transcription Factor Specificity Compendium, YeTFaSCo: The Yeast Transcription Factor Specificity Compendium

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

Defining Citation: PMID:22102575

Keywords: transcription factor, binding site, sequence, yeast, motif, gene, genome, protein, protein complex

Funding: Ontario Graduate Scholarship awards ;
Canadian Institutes of Health Research Operating Grant MOP-490425;
Canadian Institutes of Health Research Operating Grant MOP-86705

Availability: Acknowledgement requested

Resource Name: YeTFaSCo

Resource ID: SCR_006893

Alternate IDs: nlx_151611, OMICS_01861

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250426T055907+0000

Ratings and Alerts

No rating or validation information has been found for YeTFaSCo.

No alerts have been found for YeTFaSCo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Shen Y, et al. (2025) Improving the generalization of protein expression models with mechanistic sequence information. Nucleic acids research, 53(3).

Vaknin I, et al. (2024) A universal system for boosting gene expression in eukaryotic cell-lines. Nature communications, 15(1), 2394.

Maués DB, et al. (2023) Overexpression of the Transcription Factor Azf1 Reveals Novel Regulatory Functions and Impacts ?-Glucosidase Production in Trichoderma reesei. Journal of fungi (Basel, Switzerland), 9(12).

Parab L, et al. (2022) Transcription factor binding process is the primary driver of noise in gene expression. PLoS genetics, 18(12), e1010535.

Conti MM, et al. (2022) Repression of essential cell cycle genes increases cellular fitness. PLoS genetics, 18(8), e1010349.

Mormino M, et al. (2021) Development of an Haa1-based biosensor for acetic acid sensing in Saccharomyces cerevisiae. FEMS yeast research, 21(6).

Becerra-Rodríguez C, et al. (2021) Yeast Plasma Membrane Fungal Oligopeptide Transporters Display Distinct Substrate Preferences despite Their High Sequence Identity. Journal of fungi (Basel, Switzerland), 7(11).

Panchy NL, et al. (2020) Improved recovery of cell-cycle gene expression in Saccharomyces cerevisiae from regulatory interactions in multiple omics data. BMC genomics, 21(1), 159.

Tam J, et al. (2020) Regulated repression governs the cell fate promoter controlling yeast meiosis. Nature communications, 11(1), 2271.

Krieger G, et al. (2020) Independent evolution of transcript abundance and gene regulatory dynamics. Genome research, 30(7), 1000.

Triandafillou CG, et al. (2020) Transient intracellular acidification regulates the core transcriptional heat shock response. eLife, 9.

Devia J, et al. (2020) Transcriptional Activity and Protein Levels of Horizontally Acquired Genes in Yeast Reveal Hallmarks of Adaptation to Fermentative Environments. Frontiers in genetics, 11, 293.

Kim S, et al. (2019) A combination of transcription factors mediates inducible interchromosomal contacts. eLife, 8.

Castro DM, et al. (2019) Multi-study inference of regulatory networks for more accurate models of gene regulation. PLoS computational biology, 15(1), e1006591.

Chen H, et al. (2018) The Genotype-Phenotype Relationships in the Light of Natural Selection. Molecular biology and evolution, 35(3), 525.

Rawal Y, et al. (2018) Gcn4 Binding in Coding Regions Can Activate Internal and Canonical 5' Promoters in Yeast. Molecular cell, 70(2), 297.

Engel SR, et al. (2018) Updated regulation curation model at the Saccharomyces Genome Database. Database : the journal of biological databases and curation, 2018.

Quispe X, et al. (2017) Genetic basis of mycotoxin susceptibility differences between budding yeast isolates. Scientific reports, 7(1), 9173.

Siahpirani AF, et al. (2017) A prior-based integrative framework for functional transcriptional regulatory network inference. Nucleic acids research, 45(4), e21.

He BZ, et al. (2017) Evolution of reduced co-activator dependence led to target expansion of a starvation response pathway. eLife, 6.