

Resource Summary Report

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ScerTF

RRID:SCR_006121

Type: Tool

Proper Citation

ScerTF (RRID:SCR_006121)

Resource Information

URL: <http://stormo.wustl.edu/ScerTF>

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Description: Catalog of over 1,200 position weight matrices (PWMs) for 196 different yeast transcription factors (TFs). They've curated 11 literature sources, benchmarked the published position-specific scoring matrices against in-vivo TF occupancy data and TF deletion experiments, and combined the most accurate models to produce a single collection of the best performing weight matrices for *Saccharomyces cerevisiae*. ScerTF is useful for a wide range of problems, such as linking regulatory sites with transcription factors, identifying a transcription factor based on a user-input matrix, finding the genes bound/regulated by a particular TF, and finding regulatory interactions between transcription factors. Enter a TF name to find the recommended matrix for a particular TF, or enter a nucleotide sequence to identify all TFs that could bind a particular region.

Abbreviations: ScerTF

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

Defining Citation: [PMID:22140105](#)

Keywords: binding site, transcription factor, regulatory site, gene, regulation, regulatory interaction, matrix, nucleotide sequence, dna sequence, yeast, position weight matrix, bio.tools

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Resource Name: ScerTF

Resource ID: SCR_006121

Alternate IDs: biotools:scertf, nlx_151599, OMICS_00542

Alternate URLs: <http://ural.wustl.edu/ScerTF>, <https://bio.tools/scertf>

Old URLs: <http://ural.wustl.edu/TFDB/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260905T132547+0000

Ratings and Alerts

No rating or validation information has been found for ScerTF.

No alerts have been found for ScerTF.

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 [Kravitz](#) .

Xu H, et al. (2023) Chance promoter activities illuminate the origins of eukaryotic intergenic transcriptions. Nature communications, 14(1), 1826.

Recio PS, et al. (2023) Zinc cluster transcription factors frequently activate target genes using a non-canonical half-site binding mode. Nucleic acids research, 51(10), 5006.

Grah R, et al. (2020) The relation between crosstalk and gene regulation form revisited. PLoS computational biology, 16(2), e1007642.

Renganaath K, et al. (2020) Systematic identification of cis-regulatory variants that cause gene expression differences in a yeast cross. eLife, 9.

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.

Liu J, et al. (2020) Quantitative analysis of transcription factor binding and expression using calling cards reporter arrays. Nucleic acids research, 48(9), e50.

Freddolino PL, et al. (2018) Stochastic tuning of gene expression enables cellular adaptation in the absence of pre-existing regulatory circuitry. eLife, 7.

Sorrells TR, et al. (2018) Intrinsic cooperativity potentiates parallel cis-regulatory evolution. eLife, 7.

Datta V, et al. (2018) Detection of cooperatively bound transcription factor pairs using ChIP-seq peak intensities and expectation maximization. *PloS one*, 13(7), e0199771.

Rossi MJ, et al. (2017) Correspondence: DNA shape is insufficient to explain binding. *Nature communications*, 8, 15643.

Zhou S, et al. (2017) Developmentally regulated internal transcription initiation during meiosis in budding yeast. *PloS one*, 12(11), e0188001.

Spivak AT, et al. (2016) Combinatorial Cis-regulation in *Saccharomyces* Species. *G3* (Bethesda, Md.), 6(3), 653.

Lardenois A, et al. (2015) The conserved histone deacetylase Rpd3 and its DNA binding subunit Ume6 control dynamic transcript architecture during mitotic growth and meiotic development. *Nucleic acids research*, 43(1), 115.

Tsai ZT, et al. (2015) Contribution of Sequence Motif, Chromatin State, and DNA Structure Features to Predictive Models of Transcription Factor Binding in Yeast. *PLoS computational biology*, 11(8), e1004418.

Gomar-Alba M, et al. (2015) The C-terminal region of the Hot1 transcription factor binds GGGACAAA-related sequences in the promoter of its target genes. *Biochimica et biophysica acta*, 1849(12), 1385.

Zentner GE, et al. (2015) ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. *Nature communications*, 6, 8733.

Gopinath RK, et al. (2014) The Hsp90-dependent proteome is conserved and enriched for hub proteins with high levels of protein-protein connectivity. *Genome biology and evolution*, 6(10), 2851.

Costanzo MC, et al. (2014) *Saccharomyces* genome database provides new regulation data. *Nucleic acids research*, 42(Database issue), D717.

Haynes BC, et al. (2013) Mapping functional transcription factor networks from gene expression data. *Genome research*, 23(8), 1319.