

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: data analysis service, data or information resource, database, service resource, production service resource, analysis 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: 20260801T190305+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 [ASWG](#) .

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.

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

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.

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.

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.