

Resource Summary Report

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tfbstools

RRID:SCR_024260

Type: Tool

Proper Citation

tfbstools (RRID:SCR_024260)

Resource Information

URL: <https://bioconductor.org/packages/TFBSTools/>

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Description: Software R package for analysis and manipulation of transcription factor binding sites. It includes matrices conversion between Position Frequency Matirx (PFM), Position Weight Matirx (PWM) and Information Content Matrix (ICM). It can also scan putative TFBS from sequence/alignment, query JASPAR database and provides a wrapper of de novo motif discovery software.

Synonyms: TFBSTools

Resource Type: software toolkit, software resource

Defining Citation: [PMID:26794315](#)

Keywords: analysis and manipulation of transcription factor binding sites, transcription factor binding sites analysis, transcription factor binding sites manipulation,

Availability: Free, Available for download, Freely available,

Resource Name: tfbstools

Resource ID: SCR_024260

Alternate IDs: OMICS_11082

Alternate URLs: <https://sources.debian.org/src/r-bioc-tfbstools/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260803T040903+0000

Ratings and Alerts

No rating or validation information has been found for tfbstools.

No alerts have been found for tfbstools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Tamaki R, et al. (2025) Cell-free DNA-based inference of the activities of 370 + transcription factors mirrors their activities in tumors. BMC genomics, 26(1), 892.

Ver Heul AM, et al. (2025) RAG suppresses group 2 innate lymphoid cells. eLife, 13.

Gao Y, et al. (2025) Multimodal analyses reveal genes driving electrophysiological maturation of neurons in the primate prefrontal cortex. Neuron, 113(15), 2490.

Köhne M, et al. (2025) Satb1 directs the differentiation of TH17 cells through suppression of IL-2 expression. Cell reports, 44(7), 115866.

Kentro JA, et al. (2024) Conserved transcription factors coordinate synaptic gene expression through repression. bioRxiv : the preprint server for biology.

Yan F, et al. (2024) Single-cell multiomics decodes regulatory programs for mouse secondary palate development. Nature communications, 15(1), 821.

McAllan L, et al. (2023) Integrative genomic analyses in adipocytes implicate DNA methylation in human obesity and diabetes. Nature communications, 14(1), 2784.

Shi W, et al. (2023) Integration of risk variants from GWAS with SARS-CoV-2 RNA interactome prioritizes FUBP1 and RAB2A as risk genes for COVID-19. Scientific reports, 13(1), 19194.

Taavitsainen S, et al. (2021) Single-cell ATAC and RNA sequencing reveal pre-existing and persistent cells associated with prostate cancer relapse. Nature communications, 12(1), 5307.

Györfi AH, et al. (2021) Engrailed 1 coordinates cytoskeletal reorganization to induce myofibroblast differentiation. The Journal of experimental medicine, 218(9).

Giacomini DA, et al. (2020) Coexpression Clusters and Allele-Specific Expression in Metabolism-Based Herbicide Resistance. Genome biology and evolution, 12(12), 2267.

Assouvie A, et al. (2020) A genetic variant controls interferon- γ gene expression in human myeloid cells by preventing C/EBP- β binding on a conserved enhancer. PLoS genetics,

16(11), e1009090.

Funikov SY, et al. (2020) Adaptation of gene loci to heterochromatin in the course of *Drosophila* evolution is associated with insulator proteins. *Scientific reports*, 10(1), 11893.

Inoue D, et al. (2019) Spliceosomal disruption of the non-canonical BAF complex in cancer. *Nature*, 574(7778), 432.

Youn A, et al. (2019) BiFET: sequencing Bias-free transcription factor Footprint Enrichment Test. *Nucleic acids research*, 47(2), e11.

Su CH, et al. (2016) Regulation of IL-20 Expression by Estradiol through KMT2B-Mediated Epigenetic Modification. *PloS one*, 11(11), e0166090.