

Resource Summary Report

Generated by [ASWG](#) on Aug 24, 2026

tfbstools

RRID:SCR_024260

Type: Tool

Proper Citation

tfbstools (RRID:SCR_024260)

Resource Information

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

Proper Citation: tfbstools (RRID:SCR_024260)

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 resource, software toolkit

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: 20260821T194257+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 24 mentions in open access literature.

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

Dabak T, et al. (2026) The genetic basis of mimicry in the snowy bumble bee (*Bombus niveatus*) in Anatolia with insights from a color polymorphic gynandromorph. *PLoS genetics*, 22(3), e1012060.

Liang X, et al. (2026) Predicting enhancer-gene links from single-cell multi-omics data by integrating prior Hi-C information. *Nucleic acids research*, 54(9).

Suresh V, et al. (2026) Molecular dynamics of Brodmann Area 22 in development and autism. *bioRxiv : the preprint server for biology*.

Zhu I, et al. (2026) High-resolution map of chromatin accessibility - insights into the focused binding of a large number of transcription factors. *Epigenetics & chromatin*, 19(1).

Fan H, et al. (2026) Single-cell transcriptomic and chromatin accessibility atlas of peripheral blood mononuclear cells reveals immune cell heterogeneity and breed-specific characteristics in Duroc and Meishan pigs. *BMC genomics*, 27(1).

Chen LW, et al. (2026) Maternal obesity induces activator protein 1-mediated inflammatory response to impair embryonic neurogenesis. *The Journal of physiology*, 604(7), 3159.

Baweja B, et al. (2025) hsa-let-7b-5p-associated BUB1/TMPO-AS1 ceRNA axis identified as a potential biomarker in lung adenocarcinoma. *Cell division*, 21(1), 2.

Amblard I, et al. (2025) A dual enhancer-attenuator element ensures transient Cdx2 expression during mouse posterior body formation. *Developmental cell*.

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).

Assouvie A, et al. (2020) A genetic variant controls interferon- γ gene expression in human myeloid cells by preventing C/EBP- γ binding on a conserved enhancer. *PLoS genetics*, 16(11), e1009090.

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