

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

TFBS

RRID:SCR_015774

Type: Tool

Proper Citation

TFBS (RRID:SCR_015774)

Resource Information

URL: <http://tfbs.genereg.net/>

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Description: Perl software for transcription factor binding site detection and analysis. It implements classes for the representation of objects encountered in analysis of these protein-binding sites.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:12176838](#), [DOI:10.1093/bioinformatics/18.8.1135](#)

Keywords: protein-binding, transcription factor, factor binding, binding site detection, transcription analysis, perl, bio.tools

Availability: Free, Available for download, No longer in development

Resource Name: TFBS

Resource ID: SCR_015774

Alternate IDs: biotools:tfbs, OMICS_20526

Alternate URLs: <https://github.com/ComputationalRegulatoryGenomicsICL/TFBS>, <https://bio.tools/tfbs>, <https://sources.debian.org/src/libtfbs-perl/>

License: Mozilla Public License Version 2.0 (MPL-2.0)

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260905T132759+0000

Ratings and Alerts

No rating or validation information has been found for TFBS.

No alerts have been found for TFBS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Pereira MF, et al. (2025) YY1 mutations disrupt corticogenesis through a cell type specific rewiring of cell-autonomous and non-cell-autonomous transcriptional programs. *Molecular psychiatry*, 30(8), 3413.

Zhou Y, et al. (2025) Transcriptional activation of MACF1 by NR2F1 drives WNT-mediated focal adhesion and metastasis in lung adenocarcinoma. *European journal of medical research*, 30(1), 988.

Pereira MF, et al. (2024) YY1 mutations disrupt corticogenesis through a cell-type specific rewiring of cell-autonomous and non-cell-autonomous transcriptional programs. *bioRxiv* : the preprint server for biology.

Serrano-Ron L, et al. (2021) Reconstruction of lateral root formation through single-cell RNA sequencing reveals order of tissue initiation. *Molecular plant*, 14(8), 1362.

Frez-Muñoz L, et al. (2021) The Food Identity of Countries Differs Between Younger and Older Generations: A Cross-Sectional Study in American, European and Asian Countries. *Frontiers in nutrition*, 8, 653039.

Lou X, et al. (2019) Comprehensive analysis of five long noncoding RNAs expression as competing endogenous RNAs in regulating hepatoma carcinoma. *Cancer medicine*, 8(12), 5735.

Joseph PV, et al. (2019) Comprehensive and Systematic Analysis of Gene Expression Patterns Associated with Body Mass Index. *Scientific reports*, 9(1), 7447.

Jiang L, et al. (2019) LightCpG: a multi-view CpG sites detection on single-cell whole genome sequence data. *BMC genomics*, 20(1), 306.

Kumasaka N, et al. (2019) High-resolution genetic mapping of putative causal interactions between regions of open chromatin. *Nature genetics*, 51(1), 128.

Nguyen QH, et al. (2018) Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. *GigaScience*, 7(3), 1.

Osato N, et al. (2018) Characteristics of functional enrichment and gene expression level of human putative transcriptional target genes. *BMC genomics*, 19(Suppl 1), 957.

Huh I, et al. (2018) Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. *PLoS computational biology*, 14(10), e1006451.

Alam T, et al. (2017) FARN: knowledgebase of inferred functions of non-coding RNA transcripts. *Nucleic acids research*, 45(5), 2838.

Li S, et al. (2017) Quantifying deleterious effects of regulatory variants. *Nucleic acids research*, 45(5), 2307.

van der Meulen SB, et al. (2016) Transcriptome landscape of *Lactococcus lactis* reveals many novel RNAs including a small regulatory RNA involved in carbon uptake and metabolism. *RNA biology*, 13(3), 353.

Ren C, et al. (2016) iFORM: Incorporating Find Occurrence of Regulatory Motifs. *PloS one*, 11(12), e0168607.

Kural KC, et al. (2016) Pathways of aging: comparative analysis of gene signatures in replicative senescence and stress induced premature senescence. *BMC genomics*, 17(Suppl 14), 1030.

Sweeney T, et al. (2016) The application of transcriptomic data in the authentication of beef derived from contrasting production systems. *BMC genomics*, 17(1), 746.

Liu Y, et al. (2016) Genetic variants in ERBB4 is associated with chronic hepatitis B virus infection. *Oncotarget*, 7(4), 4981.

Hernando-Herraez I, et al. (2015) The interplay between DNA methylation and sequence divergence in recent human evolution. *Nucleic acids research*, 43(17), 8204.