

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 28, 2025

TF-Modisco

RRID:SCR_024811

Type: Tool

Proper Citation

TF-Modisco (RRID:SCR_024811)

Resource Information

URL: <https://github.com/kundajelab/tfmodisco>

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Description: Software application as algorithm for identifying motifs from basepair-level importance scores computed on genomic sequence data.

Synonyms: TF MOTif Discovery from Importance SCOrs, , Transcription-Factor Motif Discovery from Importance Scores

Resource Type: source code, software resource

Keywords: identifying motifs from basepair-level importance scores, genomic sequence data,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: TF-Modisco

Resource ID: SCR_024811

License: MIT license

Record Creation Time: 20240103T212525+0000

Record Last Update: 20250428T054431+0000

Ratings and Alerts

No rating or validation information has been found for TF-Modisco .

No alerts have been found for TF-Modisco .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Pampari A, et al. (2025) ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants. bioRxiv : the preprint server for biology.

Taskiran II, et al. (2024) Cell-type-directed design of synthetic enhancers. Nature, 626(7997), 212.