

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

[tfmodisco-lite](#)

RRID:SCR_026709

Type: Tool

Proper Citation

tfmodisco-lite (RRID:SCR_026709)

Resource Information

URL: <https://github.com/jmschrei/tfmodisco-lite>

Proper Citation: tfmodisco-lite (RRID:SCR_026709)

Description: Software tool as lite implementation of tfmodisco, a motif discovery algorithm for genomics experiments. Rewrite of the original TF-MoDISCo code.

Resource Type: software toolkit, software resource, source code

Keywords: lite implementation of tfmodisco, motif discovery algorithm, genomics experiments

Availability: Free, Available for download, Freely available

Resource Name: tfmodisco-lite

Resource ID: SCR_026709

License: MIT license

Record Creation Time: 20250407T215450+0000

Record Last Update: 20260814T043133+0000

Ratings and Alerts

No rating or validation information has been found for tfmodisco-lite.

No alerts have been found for tfmodisco-lite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Cetnarowska A, et al. (2026) Extensive enhancer crosstalk controls PPARG2 activation during adipogenesis. *Nature communications*, 17(1).

Lin J, et al. (2026) EPInformer: scalable and integrative prediction of gene expression from promoter-enhancer sequences with multimodal epigenomic profiles. *Nature communications*, 17(1).

Zamboni M, et al. (2026) The regulatory code of injury-responsive enhancers enables precision cell-state targeting in the CNS. *Nature neuroscience*, 29(2), 337.

Chao KH, et al. (2025) Predicting dynamic expression patterns in budding yeast with a fungal DNA language model. *bioRxiv : the preprint server for biology*.

Taslim TH, et al. (2025) Global cis-regulatory landscape of double-stranded DNA viruses. *bioRxiv : the preprint server for biology*.

Liu BB, et al. (2025) An automated ATAC-seq method reveals sequence determinants of transcription factor dose response in the open chromatin. *bioRxiv : the preprint server for biology*.

Marderstein AR, et al. (2025) Mapping the regulatory effects of common and rare non-coding variants across cellular and developmental contexts in the brain and heart. *bioRxiv : the preprint server for biology*.

Weilert M, et al. (2025) Widespread low-affinity motifs enhance chromatin accessibility and regulatory potential in mESCs. *bioRxiv : the preprint server for biology*.

Agarwal V, et al. (2025) Massively parallel characterization of transcriptional regulatory elements. *Nature*, 639(8054), 411.

Chao KH, et al. (2025) Predicting dynamic expression patterns in budding yeast with a fungal DNA language model. *Research square*.

Phan MHQ, et al. (2025) Conservation of regulatory elements with highly diverged sequences across large evolutionary distances. *Nature genetics*, 57(6), 1524.

Karollus A, et al. (2024) Species-aware DNA language models capture regulatory elements and their evolution. *Genome biology*, 25(1), 83.

Kathail P, et al. (2024) Current genomic deep learning models display decreased performance in cell type-specific accessible regions. *Genome biology*, 25(1), 202.