

Resource Summary Report

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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 SCORes, , Transcription-Factor Motif Discovery from Importance Scores

Resource Type: software resource, source code

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

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: 20260813T055319+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

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Liu BB, et al. (2026) Multiomics and deep learning dissect regulatory syntax in human development. *Nature*, 653(8116), 1240.

Dickm??nken H, et al. (2026) Evaluating single-cell ATAC-seq atlasing technologies using sequence-to-function modeling. *Nature communications*, 17(1).

Cowley CJ, et al. (2026) Distinctive DNA sequence features define epigenetic longevity of inflammatory memory. *Science (New York, N.Y.)*, 391(6792), eadz6830.

Metzl-Raz E, et al. (2025) Deep learning the dynamic regulatory sequence code of cardiac organoid differentiation. *bioRxiv : the preprint server for biology*.

Vorontsov IE, et al. (2025) Cross-platform motif discovery and benchmarking to explore binding specificities of poorly studied human transcription factors. *Communications biology*, 8(1), 1545.

Hagihara Y, et al. (2025) Precise modulation of BRG1 levels reveals features of mSWI/SNF dosage sensitivity. *Nature genetics*, 57(9), 2250.

Naqvi S, et al. (2025) Transfer learning reveals sequence determinants of the quantitative response to transcription factor dosage. *Cell genomics*, 5(3), 100780.

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*.

Dalal K, et al. (2025) Interpreting regulatory mechanisms of Hippo signaling through a deep learning sequence model. *Cell genomics*, 5(4), 100821.

Ma XR, et al. (2024) Molecular convergence of risk variants for congenital heart defects leveraging a regulatory map of the human fetal heart. *medRxiv : the preprint server for health sciences*.

Vorontsov IE, et al. (2024) Cross-platform DNA motif discovery and benchmarking to explore binding specificities of poorly studied human transcription factors. *bioRxiv : the preprint server for biology*.

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