Resource Summary Report

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HOCOMOCO

RRID:SCR_005409
Type: Tool

Proper Citation

HOCOMOCO (RRID:SCR_005409)

Resource Information

URL: http://autosome.ru/HOCOMOCO/

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Description: A comprehensive collection of human transcription factor binding sites models. DNA sequences of TF binding regions obtained by both pregenomic and high-throughput methods were collected from existing databases and other public data. The ChIPMunk software was used to construct positional weight matrices. Four motif discovery strategies were tested based on different motif shape priors including flat and periodic priors associated with DNA helix pitch. A quality rating was manually assigned to each model based on known binding preferences. An appropriate TFBS model was selected for each TF, with similar models selected for related TFs. In any case only one model per TF was selected unless there was additional evidence for two distinct binding models or different stable modes of dimerization. All TFBS models and initial binding segments data used for motif discovery were mapped to UniPROT IDs.

Abbreviations: HOCOMOCO

Synonyms: Homo Sapiens Comprehensive Model Collection (HOCOMOCO) of transcription factor (TF) binding models, Homo Sapiens Comprehensive Model Collection, Homo Sapiens Comprehensive Model Collection of transcription factor binding models

Resource Type: data or information resource, database

Defining Citation: PMID:23175603

Keywords: transcription factor, binding model, model, binding, FASEB list

Availability: Acknowledgement requested

Resource Name: HOCOMOCO

Resource ID: SCR_005409

Alternate IDs: OMICS_00537

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T200137+0000

Ratings and Alerts

No rating or validation information has been found for HOCOMOCO.

No alerts have been found for HOCOMOCO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 461 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Sato K, et al. (2026) Aberrant Hippo-YAP/TEAD Signaling Drives Malignant Transcriptional Reprogramming in External Auditory Canal Squamous Cell Carcinoma. Cancer research communications, 6(2), 260.

Liu H, et al. (2026) C9orf72 hexanucleotide repeat RNA drives transcriptional dysregulation through genome-wide DNA:RNA hybrid G-quadruplexes. Neuron, 114(6), 1045.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. Cancer discovery, 16(2), 296.

Foidart P, et al. (2026) Whole-genome doubling drives immune evasion by silencing antigen presentation. Cancer cell, 44(7), 1418.

Lapohos O, et al. (2026) AmalgaMo: flexible DNA motif merging. Bioinformatics advances, 6(1), vbag043.

Daniel NM, et al. (2026) FOXO1 transcription factor modulates airway epithelial responses to viral infection. PloS one, 21(4), e0345169.

Meng Q, et al. (2026) A generic reference defined by consensus peaks for single-cell ATAC-seq data analysis. Nature communications, 17(1).

Yuan X, et al. (2026) Fusobacterium nucleatum promotes tumor extravasation and metastasis in head and neck cancer via TLR4/MYB/ESPN axis. Communications biology, 9(1).

Qvist P, et al. (2026) BRD1 haploinsufficiency alters early neuronal programming and disrupts maturation in human induced glutamatergic neurons. Research square.

Zhigulev A, et al. (2026) Rare regulatory mutations disrupt mesenchymal molecular programs driving endocardial cushion formation in bicuspid aortic valve. Nature communications, 17(1).

Herrle N, et al. (2026) The transaminase-?-amidase pathway senses oxidative stress to control glutamine metabolism and ?-ketoglutarate levels in endothelial cells. The EMBO journal, 45(3), 820.

O'Brien A, et al. (2026) Integrative screening identifies functional variants and VNTRs underlying GWAS signals at the 5p15.33 multi-cancer susceptibility locus. medRxiv : the preprint server for health sciences.

Geis L, et al. (2026) Probing transcription factor subsets in gene regulatory networks. Algorithms for molecular biology : AMB, 21(1).

Chang L, et al. (2026) Single-cell Multiome Analysis of Chromatin State and Transcriptome in the Human Basal Ganglia. bioRxiv : the preprint server for biology.

Akagha MJ, et al. (2026) IFN? shapes macrophage inflammatory responses by STAT1 isoform-specific epigenetic and transcriptional mechanisms. BMC genomics, 27(1).

Lauber M, et al. (2026) Navigating the landscape of direct cellular reprogramming with DiReG. NPJ systems biology and applications, 12(1).

Agarwal G, et al. (2026) Inherited resilience to clonal hematopoiesis by modifying stem cell RNA regulation. Science (New York, N.Y.), 391(6780), 52.

Comerford M, et al. (2026) Mapping the gene regulatory landscape of archaic hominin introgression in modern Papuans. PLoS genetics, 22(3), e1012067.

Lapohos O, et al. (2026) Refining sequence-to-expression modelling with chromatin accessibility. Bioinformatics (Oxford, England), 42(5).

Eryilmaz G, et al. (2026) Dose-dependent IFN programs in myeloid cells after mRNA and adenovirus COVID-19 vaccination. JCI insight, 11(4).