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: 20260729T044119+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 414 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Arthur TD, et al. (2025) IFN? activates an immune-like regulatory network in the cardiac vascular endothelium. Journal of molecular and cellular cardiology plus, 11, 100289.

Messingschlager M, et al. (2025) DNA methylation changes during acute COVID-19 are associated with long-term transcriptional dysregulation in patients' airway epithelial cells. EMBO molecular medicine, 17(5), 923.

Minaeva M, et al. (2025) Specifying cellular context of transcription factor regulons for exploring context-specific gene regulation programs. NAR genomics and bioinformatics, 7(1), lqae178.

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

Zimmerlin L, et al. (2025) Proteogenomic reprogramming to a functional human blastomere-like stem cell state via a PARP-DUX4 regulatory axis. Cell reports, 44(5), 115671.

Liu JF, et al. (2025) Decoding m 6 Am by simultaneous transcription-start mapping and methylation quantification. bioRxiv : the preprint server for biology.

Lin Q, et al. (2025) Multifaceted analysis of noncoding and coding de novo variants implicates NOTCH signaling pathway in tetralogy of Fallot in Chinese population. HGG advances, 6(2), 100414.

Trang KB, et al. (2025) 3D genomic features across >50 diverse cell types reveal insights into the genomic architecture of childhood obesity. eLife, 13.

Saputra E, et al. (2025) Prediction of local convergent shifts in evolutionary rates with phyloConverge. Bioinformatics (Oxford, England), 41(7).

Win ZZ, et al. (2025) Characterization and identification of extrachromosomal circular DNA in cholangiocarcinoma. PloS one, 20(5), e0322173.

Petrucci-Nelson T, et al. (2025) Complex Genetics and Regulatory Drivers of Hypermobile Ehlers-Danlos Syndrome: Insights from Genome-Wide Association Study Meta-analysis. medRxiv : the preprint server for health sciences.

Fabo TN, et al. (2025) Interactions Between Dietary Metabolites and Regulatory Risk Variants for Human Colon Cancer. bioRxiv : the preprint server for biology.

Cappuccio G, et al. (2025) MECP2 Duplication Uncouples Mitochondrial and Purine Metabolism During neuronal maturation. bioRxiv : the preprint server for biology.

Jin YJ, et al. (2025) Phosphorylation of endothelial histone H3.3 serine 31 by PKN1 links flow-induced signaling to proatherogenic gene expression. Nature cardiovascular research, 4(2), 180.

Linder J, et al. (2025) Predicting RNA-seq coverage from DNA sequence as a unifying model of gene regulation. Nature genetics, 57(4), 949.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. iScience, 28(3), 112081.

Frömel R, et al. (2025) Design principles of cell-state-specific enhancers in hematopoiesis. Cell, 188(12), 3202.

Zibetti C, et al. (2025) Molecular Determinants of the Human Retinal Pigment Epithelium Cell Fate and Potential Pharmacogenomic Targets for Precision Medicine. International journal of molecular sciences, 26(12).

Duan ??? G, et al. (2025) Lineage-associated Human Divergently-paired Genes Exhibit Structural and Regulatory Characteristics. Genomics, proteomics & bioinformatics, 23(4).

Zhou J, et al. (2025) Human Body Single-Cell Atlas of 3D Genome Organization and DNA Methylation. bioRxiv : the preprint server for biology.