

Resource Summary Report

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HOMER

RRID:SCR_010881

Type: Tool

Proper Citation

HOMER (RRID:SCR_010881)

Resource Information

URL: <http://homer.ucsd.edu/>

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Description: Software tools for Motif Discovery and next-gen sequencing analysis. Used for analyzing ChIP-Seq, GRO-Seq, RNA-Seq, DNase-Seq, Hi-C and numerous other types of functional genomics sequencing data sets. Collection of command line programs for unix style operating systems written in Perl and C++.

Abbreviations: HOMER

Synonyms: HOMER, Hypergeometric Optimization of Motif EnRichment, Homer, Homer v4.5

Resource Type: data analysis software, software application, software resource, sequence analysis software, data processing software

Defining Citation: [PMID:20513432](#)

Keywords: motif, discovery, next, generation, sequencing, analysis, genomic, data

Funding: NURSA consortium grant ;
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Resource Name: HOMER

Resource ID: SCR_010881

Alternate IDs: OMICS_00483

Alternate URLs: <http://biowhat.ucsd.edu/homer/index.html>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190418+0000

Ratings and Alerts

No rating or validation information has been found for HOMER.

No alerts have been found for HOMER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5370 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Chen Y, et al. (2026) The transcription factor CUX1 exerts opposing roles in human and mouse adipocyte differentiation. *Molecular metabolism*, 103, 102290.

Arai M, et al. (2026) Oral antigen exposure under costimulation blockade induces Treg cells to establish immune tolerance. *The Journal of experimental medicine*, 223(3).

Xiao L, et al. (2026) Small Extracellular Vesicles From Human Amniotic Membrane Mesenchymal Stem Cells Rejuvenate Senescent ?? Cells and Cure Age-Related Diabetes in Mice. *Aging cell*, 25(1), e70327.

Sinke L, et al. (2026) DNA methylation of genes involved in lipid metabolism drives adiponectin levels and metabolic disease. *Diabetologia*, 69(1), 127.

Zarodniuk M, et al. (2026) Mechanical compression induces neuronal apoptosis, reduces synaptic activity, and promotes glial neuroinflammation in mice and humans. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2513172122.

Santos M, et al. (2026) Comprehensive Mapping of Functional Enhancers in Chinese Hamster Ovary Cells. *Biotechnology and bioengineering*, 123(1), 196.

Kama Y, et al. (2026) Notch interaction with RUNX factors regulates initiation of the T-lineage program. *The Journal of experimental medicine*, 223(2).

Mao L, et al. (2026) Super-enhancer-driven core transcription factor FOXP1 delays endothelial cell senescence via phase separation-mediated SESN3 activation. *Theranostics*, 16(3), 1386.

Blanch TE, et al. (2026) Age-Dependent Chromatin Remodeling Drives Inflammatory Dysregulation in Tendon Cells. *bioRxiv : the preprint server for biology*.

Xu Y, et al. (2026) From degraded to deciphered: Applying ATAC-seq to forensic molecular diagnosis under degradation conditions. *Forensic science international*, 379, 112789.

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. *Molecular cell*, 86(1), 24.

Liu B, et al. (2025) TaTCP6 is required for efficient and balanced utilization of nitrate and phosphorus in wheat. *Nature communications*, 16(1), 1683.

Zhang X, et al. (2025) PerR functions as a redox-sensing transcription factor regulating metal homeostasis in the thermoacidophilic archaeon *Saccharolobus islandicus* REY15A. *Nucleic acids research*, 53(1).

Cayford J, et al. (2025) Chromatin changes associated with neutrophil extracellular trap formation in whole blood reflect complex immune signaling. *Frontiers in immunology*, 16, 1515430.

Wang C, et al. (2025) Multi-omics analysis reveals critical cis-regulatory roles of transposable elements in livestock genomes. *iScience*, 28(3), 112049.

Wang Q, et al. (2025) METTL3-mediated m⁶A modification of pri-miRNA-31 promotes hypertrophic scar progression. *Acta biochimica et biophysica Sinica*, 57(7), 1106.

Wang J, et al. (2025) Multi-omics analysis reveals Jianpi formula-derived bioactive peptide-YG-22 potentially inhibited colorectal cancer via regulating epigenetic reprogram and signal pathway regulation. *Frontiers in genetics*, 16, 1560172.

Chen R, et al. (2025) Chemotherapy-Mediated Induction of PD-L1 via SEI1 Facilitates Myeloma Immune Evasion. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(19), e2411082.

Zhang B, et al. (2025) KLF6-mediated recruitment of the p300 complex enhances H3K23su and cooperatively upregulates SEMA3C with FOSL2 to drive 5-FU resistance in colon cancer cells. *Experimental & molecular medicine*, 57(3), 667.

Liu J, et al. (2025) FOXO4-SP6 axis controls surface epithelium commitment by mediating epigenomic remodeling. *Stem cell reports*, 20(4), 102445.