Resource Summary Report

Generated by ASWG on Aug 3, 2026

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

Defining Citation: PMID:20513432

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

Funding: NURSA consortium grant ;
NIH HC088093;
NIDDK DK063491;
NCI CA52599;
NIGMS P50 GM081892;
Foundation Leducq Transatlantic Network Grant

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: 20260803T040554+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 ASWG .

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 m 6A 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.