

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

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: 20250430T055748+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 4620 mentions in open access literature.

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

Dubey AP, et al. (2025) KRB72 facilitates ATPase-dependent editing progression through a structural roadblock in mitochondrial A6 mRNA. *Nucleic acids research*, 53(2).

Glaría E, et al. (2025) Liver X Receptors and Inflammatory-Induced C/EBP β Selectively Cooperate to Control CD38 Transcription. *Journal of innate immunity*, 17(1), 56.

Albers-Warlé KI, et al. (2025) Postoperative Innate Immune Dysregulation, Proteomic, and Monocyte Epigenomic Changes After Colorectal Surgery: A Substudy of a Randomized Controlled Trial. *Anesthesia and analgesia*, 140(1), 185.

Tanaka A, et al. (2025) Integrative analysis of ATAC-seq and RNA-seq for cells infected by human T-cell leukemia virus type 1. *PLoS computational biology*, 21(1), e1012690.

Faraji F, et al. (2025) YAP-driven malignant reprogramming of oral epithelial stem cells at single cell resolution. *Nature communications*, 16(1), 498.

Le S, et al. (2025) Integrated analysis of chromatin and transcriptomic profiling of the striatum after cerebral hypoperfusion in mice. *BMC genomics*, 26(1), 71.

Hai C, et al. (2025) Loss of Myostatin Affects m6A Modification but Not Semen

Characteristics in Bull Spermatozoa. International journal of molecular sciences, 26(2).

Mestre-Fos S, et al. (2025) eIF3 engages with 3'-UTR termini of highly translated mRNAs. eLife, 13.

Zhang R, et al. (2025) c-JUN: a chromatin repressor that limits mesoderm differentiation in human pluripotent stem cells. Nucleic acids research, 53(3).

Zhao M, et al. (2025) Genetic variation in IL-4 activated tissue resident macrophages determines strain-specific synergistic responses to LPS epigenetically. Nature communications, 16(1), 1030.

Oviedo JM, et al. (2025) Schistosoma mansoni antigen induced innate immune memory features mitochondrial biogenesis and can be inhibited by ovarian produced hormones. bioRxiv : the preprint server for biology.

Xiao R, et al. (2025) Deciphering Transcription in Cryptosporidium parvum: Polycistronic Gene Expression and Chromatin Accessibility. bioRxiv : the preprint server for biology.

Yang LX, et al. (2025) Alleviation of liver fibrosis by inhibiting a non-canonical ATF4-regulated enhancer program in hepatic stellate cells. Nature communications, 16(1), 524.

Funasaki S, et al. (2025) Protocol for transcriptomic and epigenomic analyses of tip-like endothelial cells using scRNA-seq and ChIP-seq. STAR protocols, 6(1), 103326.

Nohara K, et al. (2025) Acquired sperm hypomethylation by gestational arsenic exposure is re-established in both the paternal and maternal genomes of post-epigenetic reprogramming embryos. Epigenetics & chromatin, 18(1), 4.

Sen S, et al. (2025) Distinct structural and functional heterochromatin partitioning of lamin B1 and lamin B2 revealed using genome-wide nicking enzyme epitope targeted DNA sequencing. Nucleic acids research, 53(2).

Lorzadeh A, et al. (2025) Motif distribution and DNA methylation underlie distinct Cdx2 binding during development and homeostasis. Nature communications, 16(1), 929.

Zhang L, et al. (2025) The transcription factor CREB regulates epithelial-mesenchymal transition of lens epithelial cells by phosphorylation-dependent and phosphorylation-independent mechanisms. The Journal of biological chemistry, 301(1), 108064.

Liao F, et al. (2025) The role of FOXK2-FBXO32 in breast cancer tumorigenesis: Insights into ribosome-associated pathways. Thoracic cancer, 16(1), e15482.

Angarola BL, et al. (2025) Comprehensive single-cell aging atlas of healthy mammary tissues reveals shared epigenomic and transcriptomic signatures of aging and cancer. Nature aging, 5(1), 122.