

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

Defining Citation: [PMID:20513432](#)

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

Funding: Foundation Leducq Transatlantic Network 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: 20260829T182357+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 5929 mentions in open access literature.

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

Liang W, et al. (2026) Evolutionary Analysis of Transcriptional Regulation Mediated by Cdx2 in Rodents. Cell proliferation, 59(3), e70103.

Droll SH, et al. (2026) Skin Epidermal Progenitor Maintenance by the SRCAP-H2A.Z Axis Downstream to Extracellular Signal-Regulated Kinase and mTOR Signaling. The Journal of investigative dermatology, 146(2), 509.

Paldi F, et al. (2026) Transient histone deacetylase inhibition induces cellular memory of gene expression and 3D genome folding. Nature genetics, 58(2), 404.

Chen Q, et al. (2026) An integrated multi-omics and network analysis of neutrophil differentiation from initial- to late-stage. Genome biology, 27(1).

Stokes MS, et al. (2026) NAD⁺ sensing by PARP7 regulates the C/EBP β -dependent transcription program during adipogenesis. Cell reports, 45(2), 116929.

Akagha MJ, et al. (2026) IFN γ 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).

Biswas D, et al. (2026) Techno-economic optimization, sensitivity analysis and stability evaluation of a high-renewable hybrid microgrid for rural Bangladesh. Scientific reports, 16(1).

Vandenbempt V, et al. (2026) PTPN2 deficiency amplifies inflammatory signalling and impairs functional maturation of human stem cell-derived islets. Stem cell research &

therapy, 17(1).

Lai C, et al. (2026) Olig2 acts as an inducible barrier to in vivo astrocyte-to-neuron conversion. *Nature communications*, 17(1).

Zhao Y, et al. (2026) Overexpression of the pioneer transcription factor Nr5a2 promotes the development of mouse somatic cell nuclear transfer embryos. *PLoS biology*, 24(1), e3003611.

Capella-Monsonís H, et al. (2026) Matrix-bound nanovesicles as epigenetic modulators of myeloid cells. *Science advances*, 12(7), eadx9159.

Van HT, et al. (2026) Chromatin modifiers KMT2D, BAF, and p300 are required for de novo binding of transcription factors on enhancers. *bioRxiv : the preprint server for biology*.

Samuel BER, et al. (2026) Integrative profiling of transcriptome and H3K27ac modification reveals changes associated with BCG-induced trained immunity in bovine immune cells. *Scientific reports*, 16(1).

Gao S, et al. (2026) ZFP42 maintains stemness and rhythmic transcription in human epidermal stem and progenitor cells via CRY1. *Communications biology*, 9(1).

Shao C, et al. (2026) Mutant p53 binds and controls estrogen receptor activity to drive endocrine resistance in ovarian cancer. *Genes & development*, 40(3-4), 199.

Wang L, et al. (2026) Predictive prioritization of enhancers associated with pancreatic disease risk. *Cell genomics*, 6(1), 101040.

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).

Yoshimoto D, et al. (2026) Downregulation of HLA Class I Expression through HLA-A DNA Methylation Is Associated with Reduced CD8+ T-cell Infiltration in Cervical Cancer. *Cancer immunology research*, 14(1), 77.

Pasco ST, et al. (2026) Challenge Specific Modulation of Responses to Adjuvant-Induced Innate Immune Memory. *Immunology*, 177(2), 254.