

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

ChIP-Atlas

RRID:SCR_015511

Type: Tool

Proper Citation

ChIP-Atlas (RRID:SCR_015511)

Resource Information

URL: <http://chip-atlas.org/>

Proper Citation: ChIP-Atlas (RRID:SCR_015511)

Description: Database for visualizing and making use of public ChIP-seq data. ChIP-Atlas covers almost all public ChIP-seq experiments and data submitted to the SRA (Sequence Read Archives) in NCBI, DDBJ, or ENA.

Resource Type: data or information resource, database, software resource, web application

Keywords: chip-seq, sequence read archive, sequencing, FASEB list

Availability: Freely Available

Resource Name: ChIP-Atlas

Resource ID: SCR_015511

License: Creative Commons Attribution-Share Alike 4.0 International

License URLs: <https://dbarchive.biosciencedbc.jp/en/chip-atlas/lic.html>

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260829T182500+0000

Ratings and Alerts

No rating or validation information has been found for ChIP-Atlas.

No alerts have been found for ChIP-Atlas.

Data and Source Information

Usage and Citation Metrics

We found 477 mentions in open access literature.

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

Ishikawa A, et al. (2026) IL-15 and IL-21 synergy improves anti-tumor efficacy of iPSC-derived cytotoxic T cells in solid tumors. *Molecular therapy : the journal of the American Society of Gene Therapy*.

Wu N, et al. (2026) Arginine deprivation enhances ASS1-negative glioblastoma radiosensitivity via epigenetic silencing of DNA repair genes. *Cell death & disease*.

Zeineldin M, et al. (2026) ADH1C Down-Regulation Is a Key Hypoxia Response in Colon Epithelium. *The American journal of pathology*, 196(4), 853.

Larabee JL, et al. (2026) Clostridioides difficile TcdB induces expression of its receptor (CSPG4) through a noncanonical Hippo signaling mechanism. *The Journal of biological chemistry*, 302(2), 111137.

Meng Q, et al. (2026) A generic reference defined by consensus peaks for single-cell ATAC-seq data analysis. *Nature communications*, 17(1).

Roskams-Hieter B, et al. (2026) baal-nf identifies motif-disrupting variants that decrease transcription factor binding affinity. *Genome biology*, 27(1), 24.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Gerlach I, et al. (2026) Actl1R inhibition improves motor outcome and preserves muscle fibers after experimental autoimmune neuritis. *Acta neuropathologica communications*, 14(1).

Li X, et al. (2026) Nuclear Lipin1 recruits HDAC2 to epigenetically repress SREBP1-dependent lipid synthesis and myelination in hypoxic preterm white matter injury. *Stem cell reports*, 21(4), 102853.

Perkins B, et al. (2026) Dnmt3a-dependent de novo DNA methylation enforces lineage commitment and preserves functionality of memory Th1 and Tfh cells. *Cell reports*, 45(3), 117062.

Xia J, et al. (2026) FOXA2 promotes the occurrence and development of osteosarcoma cells by regulating ferroptosis through the Rheb/mTOR axis. *World journal of surgical oncology*, 24(1).

Wen J, et al. (2026) A new mRNA antigen vaccine induces potent B and T cell responses and in vivo protection against SARS-CoV-2. *bioRxiv : the preprint server for biology*.

Dogiparthi VR, et al. (2026) Predictive modeling of signal-responsive cis-elements in human red blood cell precursors. *Nucleic acids research*, 54(10).

Vanneste D, et al. (2026) MafB is a conserved transcriptional regulator of macrophage development and functional identity across tissues and species. *Immunity*, 59(3), 559.

Takhaveev V, et al. (2026) Click-code-seq reveals strand biases of DNA oxidation and depurination in human genome. *Nature chemical biology*, 22(5), 716.

Nasr MM, et al. (2026) PRDM16 Regulates Prostate Cancer Cell Dormancy and Prevents Bone Metastatic Outgrowth. *Cancer research*, 86(3), 604.

Esposito DV, et al. (2026) A non-coding ABO regulatory variant associated with VWF levels, thrombosis risk, and COVID-19 severity is topologically linked to ADAMTS13 in endothelial cells. *HGG advances*, 7(1), 100550.

Zhang W, et al. (2026) Recovering gene regulatory networks in single-cell multi-omics data with PRISM-GRN. *Genome research*, 36(1), 142.

Xing L, et al. (2026) Transcriptional activation of PPP1R14C by KLF7 unleashes CDK1 activity to promote lung squamous cell carcinoma. *Scientific reports*, 16(1).

Patel NG, et al. (2026) A non-canonical EZH2/TRIM28 epigenetic axis drives heparan sulfate remodeling and melanoma metastasis. *bioRxiv : the preprint server for biology*.