

Resource Summary Report

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ChIP-seq

RRID:SCR_001237

Type: Tool

Proper Citation

ChIP-seq (RRID:SCR_001237)

Resource Information

URL: <https://gitlab.sib.swiss/EPD/chipseq>

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Description: Set of software modules for performing common ChIP-seq data analysis tasks across the whole genome, including positional correlation analysis, peak detection, and genome partitioning into signal-rich and signal-poor regions. The tools are designed to be simple, fast and highly modular. Each program carries out a well-defined data processing procedure that can potentially fit into a pipeline framework. ChIP-Seq is also freely available on a Web interface.

Abbreviations: ChIP-seq

Synonyms: ChIP-seq - Tools for the analysis of ChIP-seq data

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

Defining Citation: [PMID:27863463](#)

Keywords: high-throughput sequencing, chromatin immuno precipitation, chip-seq, genome, c

Availability: Free, Available for download, Freely available

Resource Name: ChIP-seq

Resource ID: SCR_001237

Alternate IDs: OMICS_02103

Alternate URLs: <https://epd.expasy.org/chipseq/>, <https://chip-seq.sourceforge.net/>

License: GNU General Public License, v3

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Ratings and Alerts

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

No alerts have been found for ChIP-seq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7500 mentions in open access literature.

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

Qin Z, et al. (2026) Deciphering epigenetic regulation in cardiac developmental toxicity: Mechanisms and implications (Review). Molecular medicine reports, 33(2).

Noel L, et al. (2026) Benchmarking large language models for identifying transcription factor regulatory interactions. Bioinformatics (Oxford, England), 42(1).

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. Science advances, 12(1), eady2539.

Silva-Llanes I, et al. (2026) GASDERMIN D-mediated pyroptosis as a therapeutic target in TAU-dependent frontotemporal dementia mouse model. Journal of biomedical science, 33(1), 6.

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

Gan Y-X, et al. (2026) HERV6196 as an enhancer with oncogenic potential in rectal cancer. Microbiology spectrum, 14(1), e0078825.

Telonis AG, et al. (2026) Synergistic intragenic epigenetic deregulation by IDH2 and SRSF2 mutations causes mis-splicing of key transcriptional regulators. Science advances, 12(1), eadu8292.

Bonnet J, et al. (2026) Histone modification cross-talk and protein complex diversification confer plasticity to Polycomb repression. Genes & development, 40(1-2), 43.

Johnson NR, et al. (2026) Antagonistic regulation of nitrogen and drought signaling mediated by NIN-like protein 7 transcription factor in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 123(1), e2509904122.

Zhou Z, et al. (2026) H3K27 Acetylation-driven IGF2BP2 Mutates during the Aging of MSCs, thereby Influencing Osteogenic Differentiation and Bone Aging. *International journal of biological sciences*, 22(1), 142.

Tao M, et al. (2026) Enhancer-mediated NR2F2 recruitment activates BGN to promote tumor growth and shape tumor microenvironment in papillary thyroid cancer. *Theranostics*, 16(1), 298.

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).

Chen YY, et al. (2026) Single-nucleus multiomics of murine gonads reveals transcriptional regulatory network underlying supporting lineage differentiation. *Science advances*, 12(1), eaea7403.

Liang Y, et al. (2026) DMTF1 up-regulation rescues proliferation defect of telomere dysfunctional neural stem cells via the SWI/SNF-E2F axis. *Science advances*, 12(1), eady5905.

Ma WH, et al. (2026) Targeting PTPN13 with 11-amino-acid peptides of C-terminal APC prevents immune evasion of colorectal cancer. *Cell research*, 36(1), 72.

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.

Shin GS, et al. (2025) Lamin B1 regulates RNA splicing factor expression by modulating the spatial positioning and chromatin interactions of the ETS1 gene locus. *Animal cells and systems*, 29(1), 149.

Timmer LT, et al. (2025) Cardiomyocyte SORBS2 expression increases in heart failure and regulates integrin interactions and extracellular matrix composition. *Cardiovascular research*, 121(4), 585.

Wan J, et al. (2025) Comprehensive mapping of genetic variation at Epromoters reveals pleiotropic association with multiple disease traits. *Nucleic acids research*, 53(4).

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).