

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: software application, data analysis software, software resource, 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 [nidm-terms](#) .

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.

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).

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.

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.

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.

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

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.

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.

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.

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).

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.

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.

Dimitriu MA, et al. (2025) NanoTag is an improved method to map interactions between DNA and proteins not requiring IgG. *Scientific reports*, 15(1), 28672.

Garg J, et al. (2025) Bromodomain proteins IBD1 and IBD2 link histone acetylation to SWR1- and INO80-mediated H2A.Z regulation in *Tetrahymena*. *Epigenetics & chromatin*, 18(1), 51.

Guo J, et al. (2025) The SAS chromatin-remodeling complex mediates inflorescence-specific chromatin accessibility for transcription factor binding. *Nucleic acids research*, 53(8).

Zhang Y, et al. (2025) Integrated Computational and Functional Screening Identifies G9a Inhibitors for SETD2-mutant Leukemia. *Genomics, proteomics & bioinformatics*, 23(2).