

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, data processing software, software application, software resource, 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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195521+0000

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 8035 mentions in open access literature.

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

Clifton NE, et al. (2026) Setd1a Loss-of-function Disrupts Epigenetic Regulation of Ribosomal Genes via Altered DNA Methylation. Schizophrenia bulletin, 52(2).

Atri Roozbahani G, et al. (2026) Induction of cellular senescence by androgen receptor agonist or antagonist is mediated via two novel common DYRK1A-DREAM and cyclin G2 signaling pathways in castration-resistant prostate cancer. Journal of advanced research, 80, 371.

Yang L, et al. (2026) Transcription factor ATF3 aggravates kidney fibrosis by maintaining the state of histone H3 lysine 27 acetylation. Chinese medical journal, 139(2), 253.

Chavez J, et al. (2026) The Zinc-Finger Protein POGZ Associates with Polycomb Repressive Complex 1 to Regulate Bone Morphogenetic Protein Signaling During Neuronal Differentiation. Stem cell reviews and reports, 22(3), 1371.

Huang HN, et al. (2026) LDOC1 connects histone H2B monoubiquitination to tumor cell plasticity in non-small cell lung cancer. Cell communication and signaling : CCS, 24(1), 64.

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.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. Cancer discovery, 16(4), 800.

Shaheen MT, et al. (2026) The Lysine Demethylase KDM4C Is an Oncogenic Driver and Regulates ERK Activity in KRAS-Mutant Pancreatic Ductal Adenocarcinoma. Cancer research communications, 6(1), 245.

- Vivek AT, et al. (2026) Integrative multi-omics analysis widens annotation and functional insights into long non-coding RNAs of *Arabidopsis thaliana*. *Biology direct*, 21(1), 14.
- Tingvall-Gustafsson J, et al. (2026) B-lineage commitment is dependent on a reversible epigenetic switch. *Genes & development*, 40(3-4), 233.
- Kong F, et al. (2026) Differential effects of HDAC8 targeting on Foxp3+ Tregs and effector T cells promote antitumor immunity. *JCI insight*, 11(3).
- 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).
- Fan J, et al. (2026) PDX1 phosphorylation at S61 by mTORC1 links nutrient signaling to ? cell function and metabolic disease. *Cell reports*, 45(1), 116811.
- Gulla S, et al. (2026) MECOM Function Is Critical for AR-Driven Treatment-Resistant Prostate Cancer. *Cancer research*, 86(9), 2143.
- Yan X, et al. (2026) AKAP95 condensates regulate transcription and can be targeted in MLL-fusion driven oncogenesis. *Nature communications*, 17(1), 1457.
- Kortebi M, et al. (2026) Bacterial chromatin remodeling associated with transcription-induced domains at pathogenicity Islands. *Nature communications*, 17(1), 161.
- 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.
- Peña-Martínez EG, et al. (2026) Global Evaluation of Congenital Heart Disease-Associated Non-Coding Variants. *Research square*.
- Liu Y, et al. (2026) Functional variants at 1p36.23 confer risk of schizophrenia through modulating RERE. *Nature communications*, 17(1), 1742.