

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline

RRID:SCR_021323

Type: Tool

Proper Citation

ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline
(RRID:SCR_021323)

Resource Information

URL: <https://github.com/ENCODE-DCC/chip-seq-pipeline2/>

Proper Citation: ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline (RRID:SCR_021323)

Description: Software tool as ChIP-seq pipeline for processing ChIP-seq reads, aligning to reference genome, peak calling, and IDR analysis of replicate data according to ENCODE standards.

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

Defining Citation: [PMID:22955991](#)

Keywords: ChIP-seq pipeline, processing ChIP-seq reads, aligning to reference genome, peak calling, IDR analysis, replicate data, ENCODE standards

Availability: Free, Available for download, Freely available

Resource Name: ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline

Resource ID: SCR_021323

License: MIT License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260814T043040+0000

Ratings and Alerts

No rating or validation information has been found for ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline.

No alerts have been found for ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 97 mentions in open access literature.

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

Wang X, et al. (2026) Boosting the detection of enhancer-promoter loops via normalization methods for chromatin interaction data. *Nature communications*, 17(1).

Yang Y, et al. (2026) Targeting Wnt/??-catenin and circadian regulator restores PRC2/EZH2-controlled chromatin bivalency and suppresses cell state diversity. *The Journal of clinical investigation*, 136(9).

Kucinski J, et al. (2026) HES3-dependent regulatory functions in development and fusion-positive rhabdomyosarcoma. *bioRxiv : the preprint server for biology*.

Gjoni K, et al. (2026) Machine learning-predicted chromatin organization landscape across pediatric tumors. *Scientific reports*, 16(1).

Wu M, et al. (2026) Targeting EBV-associated gastric cancer by lytic induction therapy with nanatinostat. *Tumour virus research*, 22, 200346.

Thienger P, et al. (2026) A Double-Negative Prostate Cancer Subtype Is Vulnerable to SWI/SNF-Targeting Degradable Molecules. *Cancer research*, 86(7), 1570.

Anglen T, et al. (2025) A gene regulatory element modulates myosin expression and controls cardiomyocyte response to stress. *bioRxiv : the preprint server for biology*.

Sun Z, et al. (2025) Genomic and Transcriptomic Signatures of SETD1A Disruption in Human Excitatory Neuron Development and Psychiatric Disease Risk. *bioRxiv : the preprint server for biology*.

Yang Y, et al. (2025) H3K18 lactylation potentiates microglial polarization via the TLR4 pathway in diabetes-induced cognitive impairment. *JCI insight*, 10(24).

Prajapati HK, et al. (2025) Nucleosome dynamics render heterochromatin accessible in living human cells. *Nature communications*, 16(1), 4577.

Tjalsma SJD, et al. (2025) Long-range enhancer-controlled genes are hypersensitive to regulatory factor perturbations. *Cell genomics*, 5(3), 100778.

Deka K, et al. (2025) Multiple myeloma associated long non-coding RNA PLUM confers chemoresistance by enhancing PRC2 mediated UPR pathway activation. *Nature communications*, 16(1), 8155.

Fang S, et al. (2025) The impact of haplotypes derived from Chinese pigs on genetic variation and economic traits in the Duroc breed. *Genetics, selection, evolution : GSE*, 57(1), 58.

Sun S, et al. (2025) Single-cell multiomics analysis reveals CTCF as a key regulator of lung morphogenesis and progenitor maintenance. *Nature communications*, 16(1), 10729.

Conrad RJ, et al. (2025) NRF2 supports non-small cell lung cancer growth independently of CBP/p300-enhanced glutathione synthesis. *EMBO reports*, 26(12), 3106.

Cooke EW, et al. (2025) H3K79 methylation and H3K36 tri-methylation synergistically regulate gene expression in pluripotent stem cells. *bioRxiv : the preprint server for biology*.

Nshanian M, et al. (2025) Short-chain fatty acid metabolites propionate and butyrate are unique epigenetic regulatory elements linking diet, metabolism and gene expression. *Nature metabolism*, 7(1), 196.

Zhou Z, et al. (2025) Robust regulatory interplay of enhancers, facilitators, and promoters in a native chromatin context. *bioRxiv : the preprint server for biology*.

Kagda MS, et al. (2025) Data navigation on the ENCODE portal. *Nature communications*, 16(1), 9592.

Yu M, et al. (2025) Integrative analysis of the 3D genome and epigenome in mouse embryonic tissues. *Nature structural & molecular biology*, 32(3), 479.