

Resource Summary Report

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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/>

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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: data processing software, software resource, software toolkit, 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

Funding:

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: 20250525T032127+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 59 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Kong T, et al. (2025) RSK1 is an exploitable dependency in myeloproliferative neoplasms and secondary acute myeloid leukemia. Nature communications, 16(1), 492.

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.

Stanojevi? D, et al. (2024) Rockfish: A transformer-based model for accurate 5-methylcytosine prediction from nanopore sequencing. Nature communications, 15(1), 5580.

Nakata Y, et al. (2024) PTIP epigenetically regulates DNA damage-induced cell cycle arrest by upregulating PRDM1. Scientific reports, 14(1), 17987.

Scelfo A, et al. (2024) Tunable DNMT1 degradation reveals DNMT1/DNMT3B synergy in DNA methylation and genome organization. The Journal of cell biology, 223(4).

Mohammed J, et al. (2024) A common cis-regulatory variant impacts normal-range and disease-associated human facial shape through regulation of PKDCC during chondrogenesis. eLife, 13.

Murphy AE, et al. (2024) Predicting cell type-specific epigenomic profiles accounting for distal genetic effects. Nature communications, 15(1), 9951.

Zainu A, et al. (2024) FIGNL1-FIRRM is essential for meiotic recombination and prevents

DNA damage-independent RAD51 and DMC1 loading. *Nature communications*, 15(1), 7015.

Ang DA, et al. (2024) Aberrant non-canonical NF- κ B signalling reprograms the epigenome landscape to drive oncogenic transcriptomes in multiple myeloma. *Nature communications*, 15(1), 2513.

Qiao X, et al. (2024) Diversifying the anthracycline class of anti-cancer drugs identifies aclarubicin for superior survival of acute myeloid leukemia patients. *Molecular cancer*, 23(1), 120.

Prajapati HK, et al. (2024) Nucleosome dynamics render heterochromatin accessible in living human cells. *bioRxiv : the preprint server for biology*.

Caeiro LD, et al. (2024) Methylation of histone H3 lysine 36 is a barrier for therapeutic interventions of head and neck squamous cell carcinoma. *Genes & development*, 38(1-2), 46.

Coronado-Zamora M, et al. (2023) Transposons contribute to the functional diversification of the head, gut, and ovary transcriptomes across *Drosophila* natural strains. *Genome research*, 33(9), 1541.

Rogers BB, et al. (2023) MAPT expression is mediated by long-range interactions with cis - regulatory elements. *bioRxiv : the preprint server for biology*.

Son KH, et al. (2023) Integrative mapping of the dog epigenome: Reference annotation for comparative intertissue and cross-species studies. *Science advances*, 9(27), eade3399.

Caeiro LD, et al. (2023) Methylation of histone H3 lysine 36 is a barrier for therapeutic interventions of head and neck squamous cell carcinoma. *bioRxiv : the preprint server for biology*.

Liu T, et al. (2023) Enhancer Coamplification and Hijacking Promote Oncogene Expression in Liposarcoma. *Cancer research*, 83(9), 1517.

Yang BA, et al. (2023) Three-dimensional chromatin re-organization during muscle stem cell aging. *Aging cell*, 22(4), e13789.

Fixsen BR, et al. (2023) SALL1 enforces microglia-specific DNA binding and function of SMADs to establish microglia identity. *Nature immunology*, 24(7), 1188.

Singh I, et al. (2023) Intrinsic epigenetic state of primary osteosarcoma drives metastasis. *bioRxiv : the preprint server for biology*.