

Resource Summary Report

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ChromHMM

RRID:SCR_018141

Type: Tool

Proper Citation

ChromHMM (RRID:SCR_018141)

Resource Information

URL: <http://compbio.mit.edu/ChromHMM/>

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Description: Software tool for chromatin state discovery and characterization. Used for chromatin state discovery and genome annotation of non coding genome using epigenomic information across one or multiple cell types. Combines multiple genome wide epigenomic maps, and uses combinatorial and spatial mark patterns to infer complete annotation for each cell type. Provides automated enrichment analysis of resulting annotations.

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

Defining Citation: [PMID:29120462](#), [PMID:22373907](#)

Keywords: Chromatin state discovery, chromatin characterization, genome annotation, non coding genome, epigenomic, cell, annotation, analysis, pattern

Funding: Alfred P. Sloan Fellowship ;
CAREER Award ;
NHGRI RC1HG005334;
NHGRI U01 HG007912;
NHGRI U54 HG004570;
NIEHS R01 ES024995;
NIMH U01 MH105578;
NSF 0905968

Availability: Free, Available for download, Freely available

Resource Name: ChromHMM

Resource ID: SCR_018141

Alternate IDs: OMICS_03490

Alternate URLs: <https://sources.debian.org/src/chromhmm/>

License: GPL 3

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T132831+0000

Ratings and Alerts

No rating or validation information has been found for ChromHMM.

No alerts have been found for ChromHMM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

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

Hilgart E, et al. (2026) DNA Methylation Stochasticity Is Linked to Transcriptional Variability and Convergent Epigenetic Disruption across Genetic Subtypes of Acute Myeloid Leukemia. Cancer research, 86(13), 3325.

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. Cancer research, 85(1), 32.

Aramburu O, et al. (2025) Multiomics uncovers the epigenomic and transcriptomic response to viral and bacterial stimulation in turbot. GigaScience, 14.

Pan H, et al. (2025) Super-enhancers orchestrate transcriptional dysregulation and metabolic reprogramming in uveal melanoma. Communications biology, 8(1), 951.

Atienza Párraga A, et al. (2025) Combinatorial DNMTs and EZH2 inhibition reprograms the H3K27me3 and DNAm-mediated onco-epigenome to suppress multiple myeloma proliferation. Scientific reports, 15(1), 31568.

Grimm SL, et al. (2025) CA-125 as a Biomarker in Renal Medullary Carcinoma: Integrated Molecular Profiling, Functional Characterization, and Prospective Clinical Validation. Clinical cancer research : an official journal of the American Association for Cancer

Research, 31(6), 1057.

Liao H, et al. (2024) Whole-Genome DNA Methylation Profiling of Intrahepatic Cholangiocarcinoma Reveals Prognostic Subtypes with Distinct Biological Drivers. *Cancer research*, 84(11), 1747.

Graham MK, et al. (2024) The TERT Promoter is Polycomb-Repressed in Neuroblastoma Cells with Long Telomeres. *Cancer research communications*, 4(6), 1533.

Lee HM, et al. (2024) Epigenome Reprogramming Through H3K27 and H3K4 Trimethylation as a Resistance Mechanism to DNA Methylation Inhibition in BRAFV600E-Mutated Colorectal Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(22), 5166.

Jamge B, et al. (2023) Histone variants shape chromatin states in Arabidopsis. *eLife*, 12.

Fischer A, et al. (2023) In vivo interrogation of regulatory genomes reveals extensive quasi-insufficiency in cancer evolution. *Cell genomics*, 3(3), 100276.

Brown AC, et al. (2023) Comprehensive epigenomic profiling reveals the extent of disease-specific chromatin states and informs target discovery in ankylosing spondylitis. *Cell genomics*, 3(6), 100306.

Milevskiy MJG, et al. (2023) Three-dimensional genome architecture coordinates key regulators of lineage specification in mammary epithelial cells. *Cell genomics*, 3(11), 100424.

Hillje R, et al. (2022) Time makes histone H3 modifications drift in mouse liver. *Aging*, 14(12), 4959.

Hsieh TS, et al. (2022) Enhancer-promoter interactions and transcription are largely maintained upon acute loss of CTCF, cohesin, WAPL or YY1. *Nature genetics*, 54(12), 1919.

Ji F, et al. (2022) Computational workflow for integrative analyses of DNA replication timing, epigenomic, and transcriptomic data. *STAR protocols*, 3(4), 101827.

Ren R, et al. (2022) Characterization and perturbation of CTCF-mediated chromatin interactions for enhancing myogenic transdifferentiation. *Cell reports*, 40(7), 111206.

Li X, et al. (2022) A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. *American journal of human genetics*, 109(3), 446.

Wu LY, et al. (2022) Dynamic chromatin state profiling reveals regulatory roles of auxin and cytokinin in shoot regeneration. *Developmental cell*, 57(4), 526.