

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 resource, software application

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

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

Funding: NHGRI U54 HG004570;
NHGRI RC1HG005334;
NIEHS R01 ES024995;
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NIMH U01 MH105578;
NSF 0905968;
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CAREER Award

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: 20250429T055943+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 42 mentions in open access literature.

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

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.

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.

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.

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

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.

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

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

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.

Bai D, et al. (2022) Aberrant H3K4me3 modification of epiblast genes of extraembryonic tissue causes placental defects and implantation failure in mouse IVF embryos. *Cell reports*, 39(5), 110784.

Liu Z, et al. (2022) Large-scale chromatin reorganization reactivates placenta-specific genes that drive cellular aging. *Developmental cell*, 57(11), 1347.

Cui M, et al. (2022) Integrative analysis of omics summary data reveals putative mechanisms linked to different cell populations in systemic lupus erythematosus. *Genomics*, 114(4), 110435.

Janas JA, et al. (2022) Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. *Molecular cell*, 82(24), 4627.

Karlow JA, et al. (2022) Developmental Pathways Are Epigenetically Reprogrammed during Lung Cancer Brain Metastasis. *Cancer research*, 82(15), 2692.

Yokobayashi S, et al. (2021) Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. *Cell reports*, 37(5), 109909.

Du Q, et al. (2021) DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. *Cell reports*, 36(12), 109722.