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

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;
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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: 20260729T044441+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 47 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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.

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 DNAme-mediated onco-epigenome to suppress multiple myeloma proliferation. Scientific reports, 15(1), 31568.

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

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.

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

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.

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

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.

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.