

Resource Summary Report

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CisGenome

RRID:SCR_001558

Type: Tool

Proper Citation

CisGenome (RRID:SCR_001558)

Resource Information

URL: <http://www.biostat.jhsph.edu/~hji/cisgenome/index.htm>

Proper Citation: CisGenome (RRID:SCR_001558)

Description: Integrated software tool for tiling array, ChIP-seq, genome and cis-regulatory element analysis.

Synonyms: CisGenome v2.0

Resource Type: data analysis tool

Defining Citation: [PMID:18978777](#)

Keywords: sequencing software, chip seq, downstream analysis, chip analysis, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: CisGenome

Resource ID: SCR_001558

Alternate IDs: OMICS_00423, biotools:cisgenome

Alternate URLs: <https://bio.tools/cisgenome>

Old URLs: <http://biogibbs.stanford.edu/~jihk/CisGenome/index.htm>

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260912T195527+0000

Ratings and Alerts

No rating or validation information has been found for CisGenome.

No alerts have been found for CisGenome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1. *Molecular cancer*, 25(1).

Post GA, et al. (2025) Cell type- and species-specific regulation of hepatic lncRNAs by TCDD-activated aryl hydrocarbon receptor. *Scientific reports*, 15(1), 37322.

Hu K, et al. (2024) Mecp2 promotes the anti-inflammatory effect of alpinetin via epigenetic modification crosstalk. *Journal of cellular and molecular medicine*, 28(13), e18510.

Itoh Y, et al. (2024) Analysis of the DNA-binding properties of TGF- β -activated Smad complexes unveils a possible molecular basis for cellular context-dependent signaling. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 38(15), e23877.

Hosseinzadeh L, et al. (2024) The androgen receptor interacts with GATA3 to transcriptionally regulate a luminal epithelial cell phenotype in breast cancer. *Genome biology*, 25(1), 44.

Haghani V, et al. (2024) Improving rigor and reproducibility in chromatin immunoprecipitation assay data analysis workflows with Rocketchip. *bioRxiv : the preprint server for biology*.

Ma J, et al. (2023) A microbiota-epigenetic circuit controls systematic circadian programs in the gut epithelium. *Frontiers in systems biology*, 3.

Zhao M, et al. (2023) NF- κ B subunits direct kinetically distinct transcriptional cascades in antigen receptor-activated B cells. *Nature immunology*, 24(9), 1552.

Fang Y, et al. (2023) DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence. *Nucleic acids research*, 51(5), 2046.

Nagata K, et al. (2022) Runx2 and Runx3 differentially regulate articular chondrocytes during surgically induced osteoarthritis development. *Nature communications*, 13(1), 6187.

Marchal C, et al. (2022) Context-dependent CpG methylation directs cell-specific binding of transcription factor ZBTB38. *Epigenetics*, 17(13), 2122.

Lui JC, et al. (2022) A neomorphic variant in SP7 alters sequence specificity and causes a high-turnover bone disorder. *Nature communications*, 13(1), 700.

Liao CG, et al. (2022) Active demethylation upregulates CD147 expression promoting non-small cell lung cancer invasion and metastasis. *Oncogene*, 41(12), 1780.

Hojo H, et al. (2022) Runx2 regulates chromatin accessibility to direct the osteoblast program at neonatal stages. *Cell reports*, 40(10), 111315.

Lex RK, et al. (2022) GLI transcriptional repression is inert prior to Hedgehog pathway activation. *Nature communications*, 13(1), 808.

Li J, et al. (2021) Mechanism of forkhead transcription factors binding to a novel palindromic DNA site. *Nucleic acids research*, 49(6), 3573.

Shin HM, et al. (2021) Chromatin accessibility of circulating CD8⁺ T cells predicts treatment response to PD-1 blockade in patients with gastric cancer. *Nature communications*, 12(1), 975.

Pei J, et al. (2021) Multi-omics integration identifies key upstream regulators of pathomechanisms in hypertrophic cardiomyopathy due to truncating MYBPC3 mutations. *Clinical epigenetics*, 13(1), 61.

Kanazawa S, et al. (2021) Mesenchymal stromal cells in the bone marrow niche consist of multi-populations with distinct transcriptional and epigenetic properties. *Scientific reports*, 11(1), 15811.

Pei J, et al. (2020) H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. *Clinical epigenetics*, 12(1), 106.