

Resource Summary Report

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Cistrome

RRID:SCR_000242

Type: Tool

Proper Citation

Cistrome (RRID:SCR_000242)

Resource Information

URL: <http://cistrome.org>

Proper Citation: Cistrome (RRID:SCR_000242)

Description: Web based integrative platform for transcriptional regulation studies.

Synonyms: Galaxy Cistrome

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:21859476](#)

Keywords: Transcriptional, regulation, Chip, data, analysis, genome, gene, expression, motif, mining, bio.tools

Funding: Dana-Farber Cancer Institute High Tech and Campaign Technology Fund ;
National Basic Research Program of China ;
NHGRI HG004069;
NIDDK DK074967;
NIDDK DK062434

Availability: Free, Freely available

Resource Name: Cistrome

Resource ID: SCR_000242

Alternate IDs: SCR_017663, biotools:cistrome, OMICS_02173

Alternate URLs: <http://cistrome.org/ap/root>, <https://bio.tools/cistrome>

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260805T044005+0000

Ratings and Alerts

No rating or validation information has been found for Cistrome.

No alerts have been found for Cistrome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Likasitwatanakul P, et al. (2025) Chemical Perturbations Impacting Histone Acetylation Govern Colorectal Cancer Differentiation. Gastroenterology.

Wierbi??owicz K, et al. (2025) Parp7 generates an ADP-ribosyl degron that controls negative feedback of androgen signaling. The EMBO journal, 44(17), 4720.

Li Z, et al. (2023) The EstroGene Database Reveals Diverse Temporal, Context-Dependent, and Bidirectional Estrogen Receptor Regulomes in Breast Cancer. Cancer research, 83(16), 2656.

Tsai JW, et al. (2022) FOXR2 Is an Epigenetically Regulated Pan-Cancer Oncogene That Activates ETS Transcriptional Circuits. Cancer research, 82(17), 2980.

Lyu Q, et al. (2022) A small proportion of X-linked genes contribute to X chromosome upregulation in early embryos via BRD4-mediated transcriptional activation. Current biology : CB, 32(20), 4397.

Helbling JC, et al. (2021) Combined Gene Expression and Chromatin Immunoprecipitation From a Single Mouse Hippocampus. Current protocols, 1(2), e33.

Ma Z, et al. (2018) Epigenetic drift of H3K27me3 in aging links glycolysis to healthy longevity in Drosophila. eLife, 7.

Villalba-Benito L, et al. (2017) Overexpression of DNMT3b target genes during Enteric Nervous System development contribute to the onset of Hirschsprung disease. Scientific reports, 7(1), 6221.

Bose DA, et al. (2017) RNA Binding to CBP Stimulates Histone Acetylation and Transcription. Cell, 168(1-2), 135.

Lee JE, et al. (2017) Brd4 binds to active enhancers to control cell identity gene induction in adipogenesis and myogenesis. Nature communications, 8(1), 2217.

Zhou L, et al. (2017) BTBD18 Regulates a Subset of piRNA-Generating Loci through Transcription Elongation in Mice. Developmental cell, 40(5), 453.

Rubel CA, et al. (2016) A Gata2-Dependent Transcription Network Regulates Uterine Progesterone Responsiveness and Endometrial Function. *Cell reports*, 17(5), 1414.

Crowe EP, et al. (2016) Changes in the Transcriptome of Human Astrocytes Accompanying Oxidative Stress-Induced Senescence. *Frontiers in aging neuroscience*, 8, 208.

Cugusi S, et al. (2015) The Drosophila Helicase Maleless (MLE) is Implicated in Functions Distinct From its Role in Dosage Compensation. *Molecular & cellular proteomics : MCP*, 14(6), 1478.

Yu B, et al. (2015) Epigenetic Alterations in Density Selected Human Spermatozoa for Assisted Reproduction. *PloS one*, 10(12), e0145585.

Yi P, et al. (2015) Structure of a biologically active estrogen receptor-coactivator complex on DNA. *Molecular cell*, 57(6), 1047.