

Resource Summary Report

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CHiCAGO

RRID:SCR_014941

Type: Tool

Proper Citation

CHiCAGO (RRID:SCR_014941)

Resource Information

URL: <http://regulatorygenomicsgroup.org/chicago>

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Description: Statistical pipeline for detecting significant chromosomal interactions in Capture Hi-C data. CHiCAGO uses a convolution background model accounting for both random Brownian collisions between chromatin fragments and technical noise. CHiCAGO then performs a p-value weighting procedure based on the expected true positive rates at different distance ranges, with scores representing soft-thresholded -log weighted p-values., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Capture HiC Analysis of Genomic Organisation, Capture HiC Analysis of Genomic Organization, CHiCAGO: Capture HiC Analysis of Genomic Organisation

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

Defining Citation: [PMID:27306882](#)

Keywords: capture hi-c, capture hi-c data, chic, brownian collisions, chromatin, p-value weighting, genomic organization, genome, statistical analysis, bio.tools

Funding: BBSRC ;
MRC UK ;
EMBL

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CHiCAGO

Resource ID: SCR_014941

Alternate IDs: biotools:chicago

Alternate URLs: <https://bitbucket.org/chicagoTeam/chicago>, <https://bio.tools/chicago>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260912T195823+0000

Ratings and Alerts

No rating or validation information has been found for CHiCAGO.

No alerts have been found for CHiCAGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 163 mentions in open access literature.

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

Trang KB, et al. (2025) 3D genomic features across >50 diverse cell types reveal insights into the genomic architecture of childhood obesity. *eLife*, 13.

Salamone IM, et al. (2025) Shared loci but distinct variants underlie genetic architecture of allergic diseases. *medRxiv : the preprint server for health sciences*.

Cho H, et al. (2025) Chromosome-level genome assembly and improved annotation of onion genome (*Allium cepa* L.). *Scientific data*, 12(1), 336.

Ray-Jones H, et al. (2025) Genetic coupling of enhancer activity and connectivity in gene expression control. *Nature communications*, 16(1), 970.

Madrid A, et al. (2025) Whole genome methylation sequencing in blood from persons with mild cognitive impairment and dementia due to Alzheimer's disease identifies cognitive status. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14474.

Su C, et al. (2025) scMultiMap: Cell-type-specific mapping of enhancers and target genes from single-cell multimodal data. *Nature communications*, 16(1), 3941.

Liu Y, et al. (2025) Chromatin interaction maps of human arterioles reveal mechanisms for the genetic regulation of blood pressure. *Nature communications*, 16(1), 6577.

Raynal F, et al. (2025) Global chromatin reorganization and regulation of genes with specific evolutionary ages during differentiation and cancer. *Nucleic acids research*, 53(4).

Morgens DW, et al. (2025) Enhancers and genome conformation provide complex transcriptional control of a herpesviral gene. *Molecular systems biology*, 21(1), 30.

Achinger-Kawecka J, et al. (2024) The potential of epigenetic therapy to target the 3D epigenome in endocrine-resistant breast cancer. *Nature structural & molecular biology*, 31(3), 498.

Serra F, et al. (2024) p53 rapidly restructures 3D chromatin organization to trigger a transcriptional response. *Nature communications*, 15(1), 2821.

Thakur R, et al. (2024) Mapping chromatin interactions at melanoma susceptibility loci and cell-type specific dataset integration uncovers distant gene targets of cis-regulation. *medRxiv : the preprint server for health sciences*.

Rivera IS, et al. (2024) GWAS and 3D chromatin mapping identifies multicancer risk genes associated with hormone-dependent cancers. *PLoS genetics*, 20(11), e1011490.

Liu Y, et al. (2024) Chromatin interaction maps of human arterioles reveal new mechanisms for the genetic regulation of blood pressure. *bioRxiv : the preprint server for biology*.

Feng AC, et al. (2024) The transcription factor NF- κ B orchestrates nucleosome remodeling during the primary response to Toll-like receptor 4 signaling. *Immunity*, 57(3), 462.

Raynal F, et al. (2024) Global chromatin reorganization and regulation of genes with specific evolutionary ages during differentiation and cancer. *bioRxiv : the preprint server for biology*.

Hansen P, et al. (2024) Using paired-end read orientations to assess technical biases in capture Hi-C. *NAR genomics and bioinformatics*, 6(4), lqae156.

Giménez-Llorente D, et al. (2024) STAG2 loss in Ewing sarcoma alters enhancer-promoter contacts dependent and independent of EWS::FLI1. *EMBO reports*, 25(12), 5537.

Madrid A, et al. (2024) Whole genome methylation sequencing in blood from persons with mild cognitive impairment and dementia due to Alzheimer's disease identifies cognitive status. *bioRxiv : the preprint server for biology*.

Lin S, et al. (2024) TargetGene: a comprehensive database of cell-type-specific target genes for genetic variants. *Nucleic acids research*, 52(D1), D1072.