Resource Summary Report

Generated by NIF on Sep 12, 2026

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: 20260905T132752+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 NIF .

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.

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.

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.

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-?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.