Resource Summary Report

Generated by RRID on Apr 28, 2025

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.

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

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

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: Free, Available for download, Requires R package Delaporte v2.3.0

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: 20250428T053847+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 157 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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

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

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

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.

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

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.

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.

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.

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.

Conery M, et al. (2024) GWAS-informed data integration and non-coding CRISPRi screen illuminate genetic etiology of bone mineral density. 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.

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.

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.

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.

Buyukcelebi K, et al. (2024) Integrating leiomyoma genetics, epigenomics, and single-cell transcriptomics reveals causal genetic variants, genes, and cell types. Nature communications, 15(1), 1169.

Li J, et al. (2024) Mechanosensitive super-enhancers regulate genes linked to atherosclerosis in endothelial cells. The Journal of cell biology, 223(3).

Pollex T, et al. (2024) Enhancer-promoter interactions become more instructive in the transition from cell-fate specification to tissue differentiation. Nature genetics, 56(4), 686.

Steinhauser S, et al. (2024) The transcription factor ZNF469 regulates collagen production in liver fibrosis. bioRxiv : the preprint server for biology.

Breen C, et al. (2024) Whole genome methylation sequencing in blood identifies extensive differential DNA methylation in late-onset dementia due to Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(2), 1050.