Resource Summary Report

Generated by dkNET on Apr 29, 2025

Hiclib

RRID:SCR_005535
Type: Tool

Proper Citation

Hiclib (RRID:SCR_005535)

Resource Information

URL: http://mirnylab.bitbucket.org/hiclib/index.html

Proper Citation: Hiclib (RRID:SCR_005535)

Description: An Software resource

Abbreviations: Hiclib

Resource Type: software resource

Funding:

Resource Name: Hiclib

Resource ID: SCR_005535

Alternate IDs: OMICS_00521

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014254+0000

Ratings and Alerts

No rating or validation information has been found for Hiclib.

No alerts have been found for Hiclib.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Li B, et al. (2024) Proximal telomeric decompaction due to telomere shortening drives FOXC1-dependent myocardial senescence. Nucleic acids research, 52(11), 6269.

Rahman S, et al. (2023) Lineage specific 3D genome structure in the adult human brain and neurodevelopmental changes in the chromatin interactome. Nucleic acids research, 51(20), 11142.

Huang YF, et al. (2023) High-Resolution 3D Genome Map of Brucella Chromosomes in Exponential and Stationary Phases. Microbiology spectrum, 11(2), e0429022.

Wang L, et al. (2023) Morphine Re-arranges Chromatin Spatial Architecture of Primate Cortical Neurons. Genomics, proteomics & bioinformatics, 21(3), 551.

Li CX, et al. (2022) Three-Dimensional Genome Map of the Filamentous Fungus Penicillium oxalicum. Microbiology spectrum, 10(3), e0212121.

Ma Z, et al. (2021) High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. Nature genetics, 53(9), 1385.

Golov AK, et al. (2021) Sensitivity of cohesin-chromatin association to high-salt treatment corroborates non-topological mode of loop extrusion. Epigenetics & chromatin, 14(1), 36.

Wasim A, et al. (2021) A Hi-C data-integrated model elucidates E. coli chromosome's multiscale organization at various replication stages. Nucleic acids research, 49(6), 3077.

Zuo W, et al. (2021) Stage-resolved Hi-C analyses reveal meiotic chromosome organizational features influencing homolog alignment. Nature communications, 12(1), 5827.

Hu B, et al. (2021) Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature communications, 12(1), 3968.

Zhou Y, et al. (2020) Modeling and analysis of Hi-C data by HiSIF identifies characteristic promoter-distal loops. Genome medicine, 12(1), 69.

Guin K, et al. (2020) Spatial inter-centromeric interactions facilitated the emergence of evolutionary new centromeres. eLife, 9.

Zhou Y, et al. (2019) Temporal dynamic reorganization of 3D chromatin architecture in hormone-induced breast cancer and endocrine resistance. Nature communications, 10(1), 1522.

Li M, et al. (2019) A Sir2-regulated locus control region in the recombination enhancer of Saccharomyces cerevisiae specifies chromosome III structure. PLoS genetics, 15(8), e1008339.

He M, et al. (2018) Genome-Wide Chromatin Structure Changes During Adipogenesis and Myogenesis. International journal of biological sciences, 14(11), 1571.

Fudenberg G, et al. (2017) FISH-ing for captured contacts: towards reconciling FISH and 3C. Nature methods, 14(7), 673.

Mora A, et al. (2016) In the loop: promoter-enhancer interactions and bioinformatics. Briefings in bioinformatics, 17(6), 980.

Galazka JM, et al. (2016) Neurospora chromosomes are organized by blocks of importin alpha-dependent heterochromatin that are largely independent of H3K9me3. Genome research, 26(8), 1069.

Wang XT, et al. (2015) Structural heterogeneity and functional diversity of topologically associating domains in mammalian genomes. Nucleic acids research, 43(15), 7237.

Yao L, et al. (2015) Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. Critical reviews in biochemistry and molecular biology, 50(6), 550.