

Resource Summary Report

Generated by [dkNET](#) on Sep 8, 2026

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

Resource Name: Hiclib

Resource ID: SCR_005535

Alternate IDs: OMICS_00521

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260905T132537+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 22 mentions in open access literature.

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

Haase MAB, et al. (2026) Ancient co-option of LTR retrotransposons as yeast centromeres. *Nature*, 651(8107), 1004.

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.

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

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

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.