

Resource Summary Report

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HiTC

RRID:SCR_013175

Type: Tool

Proper Citation

HiTC (RRID:SCR_013175)

Resource Information

URL: <http://www.bioconductor.org/packages//2.10/bioc/html/HiTC.html>

Proper Citation: HiTC (RRID:SCR_013175)

Description: Software package to explore high-throughput "C" data such as 5C or Hi-C.

Abbreviations: HiTC

Resource Type: software resource

Resource Name: HiTC

Resource ID: SCR_013175

Alternate IDs: OMICS_00524

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260808T190020+0000

Ratings and Alerts

No rating or validation information has been found for HiTC.

No alerts have been found for HiTC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Powell SK, et al. (2026) 3D genetic architecture of schizophrenia risk across three neuronal subtypes. *Molecular psychiatry*, 31(4), 2216.

Pulecio J, et al. (2026) Functional chromatin signatures premark future lineage-specific enhancers. *Cell genomics*, 6(5), 101189.

Hou C, et al. (2025) RNA polymerase I is essential for driving the formation of 3D genome in early embryonic development in mouse, but not in human. *Genome medicine*, 17(1), 57.

Zhang K, et al. (2025) The 3D genome of plasma cells in multiple myeloma. *Scientific reports*, 15(1), 19331.

Li Z, et al. (2025) KDM4C inhibition blocks tumor growth in basal breast cancer by promoting cathepsin L-mediated histone H3 cleavage. *Nature genetics*, 57(6), 1463.

Pilatowski-Herzing E, et al. (2025) Capturing chromosome conformation in Crenarchaea. *Molecular microbiology*, 123(2), 101.

Warburton A, et al. (2025) Human papillomavirus genomes associate with active host chromatin during persistent viral infection. *PLoS pathogens*, 21(9), e1013454.

Menozi L, et al. (2025) Three-dimensional diffractive acoustic tomography. *Nature communications*, 16(1), 1149.

Vu?i?evi? D, et al. (2025) Sensitive dissection of a genomic regulatory landscape using bulk and targeted single-cell activation. *Cell genomics*, 5(10), 100984.

Liu J, et al. (2025) Evolution of chromosomes and nuclear architectures of amniotes. *Nature communications*, 17(1), 737.

Xu X, et al. (2025) 3D genome landscape of primary and metastatic colorectal carcinoma reveals the regulatory mechanism of tumorigenic and metastatic gene expression. *Communications biology*, 8(1), 365.

Song WL, et al. (2025) Telomere-to-telomere genome assembly and 3D chromatin architecture of *Centella asiatica* insight into evolution and genetic basis of triterpenoid saponin biosynthesis. *Horticulture research*, 12(5), uhaf037.

Tavallae G, et al. (2025) Mapping the 3D genome architecture. *Computational and structural biotechnology journal*, 27, 89.

Kaplan SJ, et al. (2024) CRISPR screening uncovers a long-range enhancer for *ONECUT1* in pancreatic differentiation and links a diabetes risk variant. *Cell reports*, 43(8), 114640.

Chen W, et al. (2024) Two telomere-to-telomere gapless genomes reveal insights into *Capsicum* evolution and capsaicinoid biosynthesis. *Nature communications*, 15(1), 4295.

Han MC, et al. (2024) The first Korean carbon-ion radiation therapy facility: current status of the Heavy-ion Therapy Center at the Yonsei Cancer Center. *Radiation oncology journal*, 42(4), 295.

Shu J, et al. (2024) Genome-wide screening and functional validation of methylation barriers near promoters. *Nucleic acids research*, 52(9), 4857.

Chen B, et al. (2024) Stratifying TAD boundaries pinpoints focal genomic regions of regulation, damage, and repair. *Briefings in bioinformatics*, 25(4).

Badel C, et al. (2024) Chromosome architecture in an archaeal species naturally lacking structural maintenance of chromosomes proteins. *Nature microbiology*, 9(1), 263.

Rengifo Rojas C, et al. (2024) Biallelic non-productive enhancer-promoter interactions precede imprinted expression of *Kcnk9* during mouse neural commitment. *HGG advances*, 5(2), 100271.