

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

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: 20260725T190745+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 83 mentions in open access literature.

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

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

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.

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

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.

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

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

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.

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.

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.

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

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

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

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

Zhang Y, et al. (2024) Telomere-to-telomere Citrullus super-pangenome provides direction for watermelon breeding. *Nature genetics*, 56(8), 1750.

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.

van Roozendaal H, et al. (2024) Process and outcome evaluation of a social norms approach intervention on alcohol use among Flemish university students: a quasi-experimental study. *Archives of public health = Archives belges de sante publique*, 82(1), 45.

Zhao SG, et al. (2024) Integrated analyses highlight interactions between the three-dimensional genome and DNA, RNA and epigenomic alterations in metastatic prostate cancer. *Nature genetics*, 56(8), 1689.

Chen WJ, et al. (2023) Single-cell RNA-seq integrated with multi-omics reveals SERPINE2 as a target for metastasis in advanced renal cell carcinoma. *Cell death & disease*, 14(1), 30.