

Resource Summary Report

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HiCEXplorer

RRID:SCR_022111

Type: Tool

Proper Citation

HiCEXplorer (RRID:SCR_022111)

Resource Information

URL: <https://github.com/deeptools/HiCEXplorer>

Proper Citation: HiCEXplorer (RRID:SCR_022111)

Description: Software tool to analyse Hi-C and capture Hi-C data. Command line suite of tools to process, normalize and visualize Hi-C data.

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

Keywords: Hi-C, process, normalize, visualize, Hi-C data, capture Hi-C data

Availability: Free, Available for download, Freely available

Resource Name: HiCEXplorer

Resource ID: SCR_022111

License: GNU GPL v3.0

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260810T040748+0000

Ratings and Alerts

No rating or validation information has been found for HiCEXplorer.

No alerts have been found for HiCEXplorer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

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

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

de Souza Araujo N, et al. (2026) Retroelement expansions underlie genome evolution in stingless bees. *BMC genomics*, 27(1), 160.

Cheng Z, et al. (2026) A chromosome-level reference genome of an endangered plant *Craigia yunnanensis*. *Scientific data*, 13(1).

Kim S, et al. (2026) *Tetraopes* Milkweed Beetle Genomes Elucidate the Adaptive Basis of a Temperate Coevolutionary Radiation. *Molecular ecology resources*, 26(3), e70117.

Lan L, et al. (2026) Comparative Genomics Provide Insights Into Karyotype Evolution in Vespertilionid Bats (*Vespertilionidae*, Chiroptera). *Molecular ecology resources*, 26(3), e70129.

Chen N, et al. (2026) A Chromosome-Level Genome Assembly and Annotation of the Chinese Porcupine (*Hystrix hodgsoni*) Reveals the Expansion of Olfactory-Related Gene Families. *Genes*, 17(6).

Luo Y, et al. (2026) A chromosome-level genome assembly and multi-omics analyses provide insights into the biosynthesis of piperlongumine in *Piper sarmentosum*. *Communications biology*, 9(1), 170.

Liu X, et al. (2026) Going wild in banana breeding enables *Fusarium*-resistant hybrids with improved fruit quality. *Nature communications*, 17(1).

Moreno-Rodriguez T, et al. (2026) Convergent evolution of complex structural variants drives therapy resistance in metastatic prostate cancer. *Genome biology*, 27(1).

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Pellow R, et al. (2026) A wavelet-based approach generates quantitative, scale-free and hierarchical descriptions of 3D genome structures and new biological insights. *PLoS computational biology*, 22(1), e1013887.

Dong Y, et al. (2026) Structural variation drives enhancer hijacking via 3D genome disruption in ccRCC. *NPJ digital medicine*, 9(1), 85.

Grover A, et al. (2026) UniversalEPI: robust prediction of cell type-specific and differential chromatin interactions from DNA sequence and chromatin accessibility. *Nucleic acids research*, 54(10).

Rossini R, et al. (2026) Loss of multilevel 3D genome organization during breast cancer progression. *Genome research*, 36(1), 20.

Kabbe M, et al. (2026) Single-nucleus epigenomic profiling of the adult human central nervous system unveils epigenetic memory of developmental programs. *Nature neuroscience*, 29(4), 992.

Aggarwal N, et al. (2026) Integrated flexible DNA methylation-chromatin segmentation modeling enhances epigenomic state annotation. *Nucleic acids research*, 54(11).

Du J, et al. (2026) Chromosome-level genome assembly of the dwarf cattail *Typha minima*. *Scientific data*, 13(1), 231.

Wu J, et al. (2026) Hi-C for genome-wide detection of enhancer-hijacking rearrangements in routine lymphoid cancer biopsies. *Cell genomics*, 6(5), 101166.

Hasegawa K, et al. (2026) Age-related decline in nuclear envelope LINC complex drives neuronal aging via axon initial segment dysfunction. *EMBO reports*, 27(13), 3788.

Choubey P, et al. (2026) Cohesin complex cooperates with PU.1 at super-enhancers to regulate the differentiation and identity of conventional dendritic cells. *Cell reports*, 45(5), 117331.