

Resource Summary Report

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HiC-Pro

RRID:SCR_017643

Type: Tool

Proper Citation

HiC-Pro (RRID:SCR_017643)

Resource Information

URL: <https://github.com/nservant/HiC-Pro>

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Description: Software tool as optimized and flexible pipeline for Hi-C data processing. Used to process Hi-C data, from raw fastq files, paired end Illumina data, to normalized contact maps.

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

Defining Citation: [PMID:26619908](#)

Keywords: Hi-C, data, raw, fastq, file, paired, Illumina, normalized, contact, map, bio.tools

Funding: France Genomique National infrastructure ;
Labex Deep ;
European Research Council ;
ERC Advanced Investigator award ;
European Commission ;
ABS4NGS project ;
National Human Genome Research Institute ;
Paris Alliance of Cancer Research Institutes ;
Howard Hughes Medical Institute

Availability: Free, Available for download, Freely available

Resource Name: HiC-Pro

Resource ID: SCR_017643

Alternate IDs: biotools:hic-pro

Alternate URLs: <https://bio.tools/hic-pro>

License: BSD-3 Licence

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260801T190745+0000

Ratings and Alerts

No rating or validation information has been found for HiC-Pro.

No alerts have been found for HiC-Pro.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 206 mentions in open access literature.

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

Do C, et al. (2025) Binding domain mutations provide insight into CTCF's relationship with chromatin and its contribution to gene regulation. *Cell genomics*, 5(4), 100813.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Maestri D, et al. (2025) EBNA leader protein orchestrates chromatin architecture remodeling during Epstein-Barr virus-induced B cell transformation. *Nucleic acids research*, 53(12).

Deng WA, et al. (2025) Chromosome-level genome assembly and annotation of the pygmy grasshopper *Gibbotettix parvipulvillus*. *Scientific data*, 12(1), 1119.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, *Phthonandria atrilineata*. *Scientific data*, 12(1), 186.

Karagyzova T, et al. (2025) HIRA defines early replication initiation zones independently of their genome compartment. *Nature communications*, 16(1), 9715.

Liu H, et al. (2025) Conservation and variability of long-range interactions in structurally diverse maize genomes. *Nature communications*, 16(1), 10105.

Liu Y, et al. (2025) Reference genome provide insights into sex determination of silver aworana (*Osteoglossum bicirrhosum*). *BMC biology*, 23(1), 29.

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

He B, et al. (2025) Deep Insight into the genome of a major rice pest, *Scripophaga incertulas*. *Scientific data*, 12(1), 642.

Ren L, et al. (2025) Chromosome-level genome assembly of the synanthropic fly *Chrysomya megacephala*: insights into oviposition location. *BMC genomics*, 26(1), 442.

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

Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the protandrous hermaphrodite Asian seabass (*Lates calcarifer*). *Scientific data*, 12(1), 1457.

Cao J, et al. (2025) Chromosome-level genome assembly of Jaguar guapote (*Parachromis manguensis*) by massive parallel sequencing. *Scientific data*, 12(1), 411.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Hu Y, et al. (2025) Highly contiguous genome of the medicinal plant *Sarcandra glabra* (Thunb.) Nakai. *Scientific data*, 12(1), 1508.

Gill R, et al. (2025) Dissecting regulatory non-coding GWAS loci reveals fibroblast causal genes with pathophysiological relevance to heart failure. *Nature communications*, 16(1), 9020.

Lim TY, et al. (2025) Pore-C sequencing identifies episome-driven chromosome conformation perturbations differentiating pneumococcal epigenetic variants. *PLoS pathogens*, 21(8), e1013392.

Xia H, et al. (2025) Chromosome-level genome assembly of the *Rhizoctonia solani*. *Scientific data*, 12(1), 1053.

Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (*Engraulis japonicus*). *Scientific data*, 12(1), 134.