

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

Defining Citation: [PMID:26619908](#)

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

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

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: 20260919T195517+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 238 mentions in open access literature.

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

Huang R, et al. (2026) IAPeZ retrotransposons regulate the first lineage segregation in mouse pre-implantation development. Nucleic acids research, 54(11).

Wu H, et al. (2026) A high-quality chromosome-level genome assembly of the low chilling requirement mulberry, *Morus macroura*. Scientific data, 13(1).

Lin YT, et al. (2026) Glass scallop genome reveals key adaptations to deep-sea environments and ectosymbiosis. Nature communications, 17(1).

Liu G, et al. (2026) Extraordinary diversity of antiviral immune-related gene families across 38 bat species. BMC biology, 24(1).

Zhang X, et al. (2026) A telomere-to-telomere gap-free genome assembly of the protandrous maroon clownfish (*Premnas biaculeatus*). Scientific data, 13(1), 220.

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

Kawaguchi YW, et al. (2026) Improved genome assembly of whale shark, the world's biggest fish: revealing intragenomic heterogeneity in molecular evolution. GigaScience, 15.

Wang L, et al. (2026) Site-specific HPV18 integration facilitates cervical carcinogenesis through metabolic reprogramming-induced dysfunction of the SpHK1/S1P/S1PR1 pathway. Cell death & disease, 17(1), 24.

Wang S, et al. (2026) UniChrom: a universal deep learning architecture for cross-scale chromatin interaction prediction. BMC genomics, 27(1).

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

Chen Q, et al. (2026) Chromosome-level genome assembly and annotation of the critically endangered Siberian crane (*Leucogeranus leucogeranus*). *Scientific data*, 13(1).

Liu Z, et al. (2026) Genomic contraction of the LOX gene family limits jasmonic acid biosynthesis and contributes to delayed flower bud opening in honeysuckle (*Lonicera japonica*). *Horticulture research*, 13(6), uhag078.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Xie X, et al. (2026) Chromosome-level genome assembly of mud snail *Bullacta exarata*. *Scientific data*, 13(1).

Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.

Ye B, et al. (2026) Dual control of liver regeneration by Nr1d1 homeostasis and Klf2 checkpoint. *Cell death discovery*, 12(1).

Tang Y, et al. (2026) A chromosome level genome assembly of *Homatula variegata* from the Yangtze River basin. *Scientific data*, 13(1).

E Z, et al. (2026) Chromosome-level genome assembly of the longfin barb (*Acrossocheilus longipinnis*). *Scientific data*, 13(1).

Zhou C, et al. (2026) Chromosome-level genome assembly of the deep-sea solemyid bivalve *Acharax haimaensis*. *Scientific data*, 13(1).

Chen W, et al. (2026) A near telomere-to-telomere genome assembly of *Pterocryptis cochinchinensis*. *Scientific data*, 13(1).