

Resource Summary Report

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HapHiC

RRID:SCR_026284

Type: Tool

Proper Citation

HapHiC (RRID:SCR_026284)

Resource Information

URL: <https://github.com/zengxiaofei/HapHiC>

Proper Citation: HapHiC (RRID:SCR_026284)

Description: Software fast, reference-independent, allele-aware scaffolding tool based on Hi-C data. Allele-aware scaffolding tool that uses Hi-C data to scaffold haplotype-phased genome assemblies into chromosome-scale pseudomolecules.

Resource Type: software resource, software application, source code

Defining Citation: [PMID:39103456](#)

Keywords: reference-independent, allele-aware scaffolding tool, performance on chromosome assignment, contig ordering and orientation, Hi-C data, scaffold haplotype-phased genome assemblies, chromosome-scale pseudomolecules,

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: HapHiC

Resource ID: SCR_026284

License: BSD-3-Clause

Record Creation Time: 20250115T053334+0000

Record Last Update: 20260804T043845+0000

Ratings and Alerts

No rating or validation information has been found for HapHiC.

No alerts have been found for HapHiC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Guan DL, et al. (2025) Chromosome-level genome assembly and annotation of the predatory stink bug *Eocanthecona furcellata*. *Scientific data*, 12(1), 1920.

Xiao TW, et al. (2025) Chromosome-scale genome assembly of *Sauvagesia rhodoleuca* (Ochnaceae) provides insights into its genome evolution and demographic history. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(5).

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. *GigaScience*, 14.

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

Roberts NG, et al. (2025) Chromosome-level haplotype-resolved genome assembly of the linguliform brachiopod *Discradisca antillarum* (d'Orbigny, 1845). *G3 (Bethesda, Md.)*, 15(12).

Hu X, et al. (2025) A Chromosome-scale Genome Assembly for the Broad-leaved Bamboo *Indocalamus tessellatus*. *Scientific data*, 12(1), 1706.

Moon SJ, et al. (2025) Haplotype-resolved chromosome-level genome sequence of *Elsholtzia splendens* (Nakai ex F.Maek.). *Scientific data*, 12(1), 827.

Bing H, et al. (2025) Chromosome-level genome assembly of the obligate cave loach *Troglonectes daqikongensis*. *Scientific data*, 12(1), 1918.

Yang Y, et al. (2025) A Chromosome-Scale Genome of *Trametes versicolor* and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene Biosynthesis. *Journal of fungi (Basel, Switzerland)*, 11(1).

Park H, et al. (2025) Chromosome-level Genome Assembly of the Halophytic Turfgrass *Zoysia macrostachya*. *Scientific data*, 12(1), 1335.

Moore ML, et al. (2025) Hybridization and low-light adaptability in California eelgrass (*Zostera* spp.). *Nature plants*, 11(11), 2409.

Yang Y, et al. (2025) Haplotype-resolved genome assembly of the leading cultivar of jujube (*Ziziphus jujuba* Mill. 'Huizao'). *Scientific data*, 12(1), 1800.

Zheng Q, et al. (2024) Chromosome-level genome assembly and annotation of Barbel chub *Squaliobarbus curriculus*. *Scientific data*, 11(1), 1453.