

Resource Summary Report

Generated by T1D on Jul 30, 2026

Hifiasm

RRID:SCR_021069

Type: Tool

Proper Citation

Hifiasm (RRID:SCR_021069)

Resource Information

URL: <https://github.com/chhyip123/hifiasm>

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Description: Software tool as haplotype resolved de novo assembler for PacBio Hifi reads. Can assemble human genome in several hours. Introduces new graph binning algorithm and achieves haplotype resolved assembly given trio data. Takes advantage of long high fidelity sequence reads to represent haplotype information in phased assembly graph. Preserves contiguity of all haplotypes.

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

Defining Citation: [PMID:33526886](#)

Keywords: PacBio Hifi reads, haplotype resolved de novo assembler, trio data, long high fidelity sequence reads,

Funding: NHGRI R01 HG010040;
NHGRI U01 HG010961;
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Availability: Free, Available for download, Freely available

Resource Name: Hifiasm

Resource ID: SCR_021069

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260729T044501+0000

Ratings and Alerts

No rating or validation information has been found for Hifiasm.

No alerts have been found for Hifiasm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 544 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. *G3* (Bethesda, Md.), 16(1).

Liang Y, et al. (2025) The giant genome of lily provides insights into the hybridization of cultivated lilies. *Nature communications*, 16(1), 45.

Simmons NB, et al. (2025) The genome sequence of *Glossophaga mutica* (Chiroptera, Phyllostomidae, Glossophaginae; Merriam, 1898). *Wellcome open research*, 10, 174.

Crowley LM, et al. (2025) The genome sequence of a snail-killing fly, *Dichetophora obliterata* (Fabricius, 1805). *Wellcome open research*, 10, 176.

Zhang S, et al. (2025) A High-Quality Reference Genome and Comparative Genomics of the Widely Farmed Banded Cricket (*Gryllodes sigillatus*) Identifies Selective Breeding Targets. *Ecology and evolution*, 15(3), e71134.

Sivell O, et al. (2025) The genome sequence of the Small Red Damselfly, *Ceriagrion tenellum* (de Villers, 1789). *Wellcome open research*, 10, 79.

Sivell D, et al. (2025) The genome sequence of the click beetle, *Ampedus sanguinolentus sanguinolentus* (Schrank, 1776). *Wellcome open research*, 10, 96.

Geiser MF, et al. (2025) The genome sequence of a flea beetle, *Neocrepidodera transversa* (Marsham, 1802). *Wellcome open research*, 10, 62.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte* (Hong Kong, China), 2025, gigabyte149.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. *GigaScience*, 14.

Wang P, et al. (2025) A chromosome-level genome assembly and annotation of the *Pseudorasbora elongata* (Cypriniformes: Cyprinidae). *Scientific data*, 12(1), 554.

Sivell D, et al. (2025) The genome sequence of a carabid beetle, *Carabus problematicus* Herbst, 1786. Wellcome open research, 10, 59.

Wangwiwatsin A, et al. (2025) The genome sequence of the liver fluke *Opisthorchis viverrini* (Poirier, 1886) Stiles & Hassall, 1896. Wellcome open research, 10, 1.

Li X, et al. (2025) A high-quality chromosome-level genome assembly of *Eucalyptus globulus* Labill. Scientific data, 12(1), 1093.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. Frontiers in zoology, 22(1), 7.

Boyes D, et al. (2025) The genome sequence of the Warty Knot-Horn moth, *Acrobasis repandana* Fabricius, 1798. Wellcome open research, 10, 50.

Xie S, et al. (2025) Extreme heterochiasmy and high rates of sex-reversed recombination result in large yet homomorphic sex chromosomes in the Emei moustache toad. Genome research, 35(6), 1325.

Lin SH, et al. (2025) Unraveling forensic timelines using molecular markers in *Phormia regina* maggots. bioRxiv : the preprint server for biology.

Jiang X, et al. (2025) A chromosome-level genome assembly of the aphid *Semiaphis heraclei* (Takahashi). Scientific data, 12(1), 770.

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