

Resource Summary Report

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Hifiasm

RRID:SCR_021069

Type: Tool

Proper Citation

Hifiasm (RRID:SCR_021069)

Resource Information

URL: <https://github.com/chhy123/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: sequence analysis software, software resource, data analysis software, software application, 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: 20260820T054917+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 584 mentions in open access literature.

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

Ma Z, et al. (2026) Population genomics reveals association of transposable elements variants with climatic adaptation in wild Amur grape. *Nature communications*, 17(1).

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

Fasham J, et al. (2026) Palindrome-mediated 16p13.3 triplications cause a recognizable neurodegenerative disorder with ataxia. *American journal of human genetics*, 113(1), 221.

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3 (Bethesda, Md.)*, 16(2).

Novo M, et al. (2026) ERGA-BGE Genome of *Ailoscolex lacteospumous* Bouch??, 1969 - the enigmatic milky worm endemic to the Pyrenees. *Open research Europe*, 6, 26.

Cadena CD, et al. (2026) New genomic resources and the historical demography of the Tourmaline Sunangel (Trochilidae, *Heliangelus exortis*) in the Colombian Andes. *The Journal of heredity*, 117(4), 868.

Young ND, et al. (2026) Chromosome-scale nuclear genome and proteome of *Anoplocephala perfoliata* elucidate lineage-specific features of a 'neglected' equine tapeworm. *BMC genomics*, 27(1), 201.

Wang P, et al. (2026) Telomere-to-telomere gap-free genome assembly of the *Opsariichthys evolans* (Cypriniformes: Cyprinidae). *Scientific data*, 13(1), 263.

Yulfo-Soto GE, et al. (2026) First genome and transcription factor profile for *Asimina triloba*, a native North American fruit tree. *The plant genome*, 19(1), e70181.

Liu P, et al. (2026) Telomere-to-telomere genome of *Stylosanthes guianensis* uncovers symbiotic adaptation to phosphorus-deficient soils. *Genome biology*, 27(1).

Liang S, et al. (2026) Full-length haplotype reconstruction of CD36 by long-read sequencing: uncovers a novel structural variant. *BMC genomics*, 27(1).

Tao X, et al. (2026) Co-occurrence of mcr-9 and bla NDM-1 in carbapenem-resistant *Enterobacter hormaechei* from burn patients. *Frontiers in cellular and infection microbiology*, 16, 1742596.

Mao X, et al. (2026) Sex chromosome evolution mediated by a large inversion and a possible switch of the sex determination gene. *Genome biology*, 27(1).

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

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. *Plant communications*, 7(1), 101581.

Passos GS, et al. (2026) Genomic and secondary metabolites of the marine cyanobacterium *Capilliphycus salinus* ALCB114379. *Journal of phycology*, 62(3), 904.

Huang Y, et al. (2026) The near-complete genome assembly of allotetraploid *Pennisetum purpureum* 'Purple' reveals the genetic and epigenetic landscape of centromeres. *Horticulture research*, 13(2), uhaf301.

Wang Y, et al. (2026) Haplotype-resolved genome assembly of the colored calla lily (*Zantedeschia elliottiana*) provides new insights into the evolution of the family Araceae. *Molecular horticulture*, 6(1), 12.

Zhou P, et al. (2026) The telomere-to-telomere haplotype genome provides in-depth insights into the molecular mechanisms of the anthocyanin deficiency phenotype in *Prunus mume*. *Molecular horticulture*, 6(1), 8.

Zhou H, et al. (2026) Pangenome analysis reveals the genetic mechanism underlying high-altitude adaptation in Qinghai-Xizang (Tibet) Plateau *Rhododendron*. *Journal of integrative plant biology*, 68(7), 2166.