

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[hifiasm-meta](#)

RRID:SCR_022771

Type: Tool

Proper Citation

hifiasm-meta (RRID:SCR_022771)

Resource Information

URL: <https://github.com/xfengnefx/hifiasm-meta>

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Description: Software tool as metagenome assembler that exploits high accuracy of recent data. De novo metagenome assembler, based on haplotype resolved de novo assembler for PacBio Hifi reads. Workflow consists of optional read selection, sequencing error correction, read overlapping, string graph construction and graph cleaning.

Synonyms: hifiasm_meta

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

Defining Citation: [PMID:35534630](#)

Keywords: Error correction, read overlapping, hifiasm, haplotype resolved de novo assembler, PacBio Hifi reads

Funding: NHGRI R01HG010040;
NHGRI U01HG010971

Availability: Free, Available for download, Freely available

Resource Name: hifiasm-meta

Resource ID: SCR_022771

License: MIT License

Record Creation Time: 20220922T050155+0000

Record Last Update: 20260804T043748+0000

Ratings and Alerts

No rating or validation information has been found for hifiasm-meta.

No alerts have been found for hifiasm-meta.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Ni M, et al. (2025) Epigenetic phase variation in the gut microbiome enhances bacterial adaptation. bioRxiv : the preprint server for biology.

Zhang Y, et al. (2022) Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. GigaScience, 11.