

Resource Summary Report

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MEGAHIT

RRID:SCR_018551

Type: Tool

Proper Citation

MEGAHIT (RRID:SCR_018551)

Resource Information

URL: <https://github.com/voutcn/megahit>

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Description: Software tool as Next Generation Sequencing assembler. Optimized for metagenomes, but also works well on generic single genome assembly (small or mammalian size) and single cell assembly. Can assemble genome sequences from metagenomic datasets of hundreds of Giga base-pairs in time and memory efficient manner on single server.

Synonyms: MEGAHIT v0.1

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

Defining Citation: [PMID:25609793](#), [PMID:27012178](#)

Keywords: NGS metagenome, Next Generation Sequencing assembler, metagenome, genome assembly, genome sequence, metagenomic dataset, giga base pairs, bio.tools

Funding: Hong Kong GRF ;
Innovation and Technology Fund

Availability: Free, Available for download, Freely available

Resource Name: MEGAHIT

Resource ID: SCR_018551

Alternate IDs: OMICS_07234, biotools:megahit

Alternate URLs: <https://bio.tools/megahit>, <https://sources.debian.org/src/megahit/>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260905T133055+0000

Ratings and Alerts

No rating or validation information has been found for MEGAHit.

No alerts have been found for MEGAHit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1897 mentions in open access literature.

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

Sinha A, et al. (2026) Prophage induction contributes to alterations in the gut phageome during intestinal inflammation. *Cell reports*, 45(7), 117491.

Ma S, et al. (2026) Metabolic interactions drive microbial community succession and functional expression of Nongxiangxing (Strong-flavor) daqu. *Journal of advanced research*, 84, 109.

Jeon JY, et al. (2026) Short-Read Pangenomes and Their Potential Utility in Population and Conservation Genomics. *Molecular ecology resources*, 26(1), e70060.

Yun Y, et al. (2026) Gut microbiome plasticity explains the altitudinal distribution pattern and adaptability in a small mammal species (*Apodemus draco*). *Microbiology spectrum*, 14(1), e0238825.

Ren QD, et al. (2026) Pomegranate peel extract alleviates diabetic retinopathy by suppressing the PI3K/AKT/HIF-1 α /VEGF pathway and gut microbiota modulation. *Journal of advanced research*, 85, 137.

Jia X, et al. (2026) Integrative analysis of rumen microbiota and host multi-organ interactions underlying feed conversion efficiency in Hu sheep. *Journal of animal science and biotechnology*, 17(1), 19.

Kang L, et al. (2026) Genomic evidence of HMPV resurgence in Beijing: Clade B2 triggers the 2024 winter epidemic peak. *Virologica Sinica*, 41(1), 48.

Li C, et al. (2026) Altered rumen bacterial flora is associated with increased lipogenesis of adipose tissue in obese dairy cows before calving. *Microbiome*, 14(1), 66.

Zheng J, et al. (2026) Integrated metabolomics and metagenomics uncover pathogenic mechanisms of *Fusarium* wilt and faba bean defense responses. *NPJ science of food*,

10(1), 25.

Lin Y, et al. (2026) Intermittent fasting inhibits Tp53-driven glioma through gut microbiota-mediated methionine-m6A regulation. *Nature communications*, 17(1), 1804.

Zhuang GC, et al. (2026) Atmospheric deposition enhances marine methane production and emissions from global oceans. *Nature communications*, 17(1), 1811.

Daryani NE, et al. (2026) Characterizing the gut virome in ulcerative colitis and crohn's disease: signatures of disease severity. *Virology journal*, 23(1), 46.

Li M, et al. (2026) Rumen microbiota modulates metabolic stress in high-yield dairy cows: insights from early to peak lactation. *Microbiome*, 14(1), 61.

Alvarado DA, et al. (2026) Effects of Soluble Corn Fiber Consumption on Executive Functions and Gut Microbiota in Middle to Older Age Adults: A Randomized Controlled Crossover Trial. *The Journal of nutrition*, 156(5), 101473.

Valenzuela-Diaz S, et al. (2026) Impact of phage enrichment on the observed infant gut phageome. *Microbiology spectrum*, 14(5), e0215325.

Wang J, et al. (2026) Earthworm gut microbiome promotes biodegradation of albendazole in soil. *Crop health*, 4(1).

Xie Y, et al. (2026) Metagenome-assembled genomes from the gut microbiome of spontaneous diabetic macaques provide insights into microbes associated with type 2 diabetes mellitus. *BMC microbiology*, 26(1).

Chen S, et al. (2026) Metatranscriptomics profiling reveals rodent- and shrew-borne viral diversity and evolutionary relationships in Guangzhou, China. *Virologica Sinica*, 41(1), 35.

Chen JM, et al. (2026) Microbiota-derived IPA mitigates post-stroke neuroinflammation by inhibiting TREM2-dependent pyroptosis. *Journal of neuroinflammation*, 23(1), 47.

Ran X, et al. (2026) Differences in metavirome among *Aedes albopictus*, *Culex tritaeniorhynchus*, and *Anopheles sinensis* in Jiangxi Province, China. *Parasites & vectors*, 19(1), 14.