

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: software resource, software application, data processing software

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

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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 1451 mentions in open access literature.

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

Zhang C, et al. (2026) Multi-omics reveals gut microbiota-mediated environmental adaptation in Mallards and domesticated Shaoxing ducks. *Poultry science*, 105(1), 106177.

Kosmopoulos JC, et al. (2026) Ecosystem health shapes viral ecology in peatland soils. *Nature microbiology*, 11(1), 142.

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.

Grimwood RM, et al. (2026) A Novel Crustavirus as a Candidate Aetiology of Tail Fan Necrosis in New Zealand Red Rock Lobsters, *Jasus edwardsii*. *Journal of fish diseases*, 49(2), e70033.

Jin S, et al. (2026) Microbial collagenase activity is linked to oral-gut translocation in advanced chronic liver disease. *Nature microbiology*, 11(1), 211.

Guo X, et al. (2026) Diversity and Ecological Potentials of Marine Viruses Inhabiting Continental Shelf Seas. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e11707.

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. *NPJ biofilms and microbiomes*, 11(1), 142.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. GigaByte (Hong Kong, China), 2025, gigabyte161.

Wang S, et al. (2025) Deterministic succession patterns in the rumen and fecal microbiome associate with host metabolic shifts in peripartum dairy cattle. GigaScience, 14.

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. Current biology : CB, 35(5), 1061.

Li W, et al. (2025) Benchmarking and optimizing qualitative and quantitative pipelines in environmental metatranscriptomics using mixture controlling experiments. ISME communications, 5(1), ycaf090.

Chen XX, et al. (2025) Microbial dysbiosis with tryptophan metabolites alteration in lower respiratory tract is associated with clinical responses to anti-PD-1 immunotherapy in advanced non-small cell lung cancer. Cancer immunology, immunotherapy : CII, 74(4), 140.

Gao Y, et al. (2025) Benchmarking short-read metagenomics tools for removing host contamination. GigaScience, 14.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. Microbiome, 13(1), 200.

Wei Y, et al. (2025) Effects of oil pollution on the growth and rhizosphere microbial community of *Calamagrostis epigejos*. Scientific reports, 15(1), 1278.

Bard NW, et al. (2025) Teknonaturalist: A Snakemake Pipeline for Assessing Fungal Diversity From Plant Genome Bycatch. Molecular ecology resources, 25(3), e14056.

Zhang Y, et al. (2025) Gut Commensal *Barnesiella Intestinihominis* Ameliorates Hyperglycemia and Liver Metabolic Disorders. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(8), e2411181.

Yin Q, et al. (2025) Ecological dynamics of Enterobacteriaceae in the human gut microbiome across global populations. Nature microbiology, 10(2), 541.

Feng Y, et al. (2025) Regional antimicrobial resistance gene flow among the One Health sectors in China. Microbiome, 13(1), 3.