

# 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

**Record Last Update:** 20260731T043036+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1451 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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

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

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.

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

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.

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.

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.

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

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.

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.

Wang X, et al. (2025) Diversity, functions, and antibiotic resistance genes of bacteria and fungi are examined in the bamboo plant phyllosphere that serve as food for the giant pandas. *International microbiology : the official journal of the Spanish Society for Microbiology*, 28(4), 751.

Zhao SY, et al. (2025) Rhizosphere microbiome metagenomics in PGPR-mediated alleviation of combined stress from polypropylene microplastics and Cd in hybrid *Pennisetum*. *Frontiers in microbiology*, 16, 1549043.

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.

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