

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: 20260919T195610+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 [nidm-terms](#).

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.

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

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.

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.

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.

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.

Liu S, et al. (2026) A comparative study of the gut microbiome and fecal metabolome in hypertensive patients from middle-temperate and tropical cities of China: Daqing and

Haikou. *Frontiers in microbiology*, 17, 1801806.

Stach TL, et al. (2026) Complex compositional and metabolic response of river sediment microbiomes to multiple anthropogenic stressors. *ISME communications*, 6(1), ycaf079.

Zhang J, et al. (2026) Gut microbiota dysbiosis drives depression-like behavior in adolescent rats via lysine-regulated mTOR autophagy pathway. *Translational psychiatry*, 16(1).

Ballaben AS, et al. (2026) One Health Genomic Perspective on *Pseudomonas aeruginosa*: A Neglected Reservoir of Last-Resort Resistance Genes. *Current microbiology*, 83(7).

Wei D, et al. (2026) The crayfish-rice coculture model contributes to regulating the soil fertility of rice fields and maintaining the stability of soil microbial community composition and function. *Advanced biotechnology*, 4(2).

Hernández-Velázquez R, et al. (2026) Metagenomic insight into the diversity and biogeochemical functions of microbial communities in the maar tropical Lake Atexcac. *Microbiology (Reading, England)*, 172(6).

Yi J, et al. (2026) *M. globosa* promotes lung cancer progression and M2 macrophage polarization through oxidative phosphorylation. *NPJ precision oncology*, 10(1).

Husz LH, et al. (2026) Phenotypic and Genomic Analysis of Antimicrobial Resistance in *Escherichia coli* Isolated from Food-Transport Containers Used in Institutional Catering. *Antibiotics (Basel, Switzerland)*, 15(4).

Paietta EN, et al. (2026) Mammal-infecting DNA viruses identified in lemurs and rodents in Madagascar mirror the evolutionary history of their hosts. *Microbial genomics*, 12(5).

Duan J, et al. (2026) Metagenomic analysis suggests that tomato root-knot nematode infestation disrupts rhizosphere microbial networks, consistent with reduced disease suppression. *Frontiers in microbiology*, 17, 1798902.

Wang F, et al. (2026) Ecological and evolutionary dynamics of the oral microbiome across childhood. *bioRxiv : the preprint server for biology*.

Yang W, et al. (2026) Alterations in the gut virome of children with allergic rhinitis: enrichment of pro-inflammatory bacteriophages and depletion of fungal viruses. *Microbiology spectrum*, 14(4), e0327625.