Resource Summary Report

Generated by NIF on Apr 29, 2025

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 resource, software application

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: 20250429T060006+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 1024 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Li D, et al. (2025) Seed microbiomes promote Astragalus mongholicus seed germination through pathogen suppression and cellulose degradation. Microbiome, 13(1), 23.

Fang Y, et al. (2025) Genome-resolved year-round dynamics reveal a broad range of giant virus microdiversity. mSystems, 10(1), e0116824.

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

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

Midot F, et al. (2025) Temporal dynamics of soil microbial C and N cycles with GHG fluxes in the transition from tropical peatland forest to oil palm plantation. Applied and environmental microbiology, 91(1), e0198624.

Ding J, et al. (2025) Depth heterogeneity of lignin-degrading microbiome and organic carbon processing in mangrove sediments. NPJ biofilms and microbiomes, 11(1), 5.

Chuckran PF, et al. (2025) Codon bias, nucleotide selection, and genome size predict in situ bacterial growth rate and transcription in rewetted soil. Proceedings of the National Academy of Sciences of the United States of America, 122(3), e2413032122.

Peng Q, et al. (2025) Comparative metagenomics reveals the metabolic flexibility of coastal prokaryotic microbiomes contributing to lignin degradation. Biotechnology for biofuels and bioproducts, 18(1), 9.

Prattico C, et al. (2025) Identification of novel fructo-oligosaccharide bacterial consumers by pulse metatranscriptomics in a human stool sample. mSphere, 10(1), e0066824.

Yang JT, et al. (2025) Non-adapted bacterial infection suppresses plant reproduction. Science advances, 11(2), eads7738.

Modha S, et al. (2025) Expanding the genomic diversity of human anelloviruses. Virus evolution, 11(1), veaf002.

Liu Z, et al. (2025) Ecological features of microbial community linked to stochastic and deterministic assembly processes in acid mine drainage. Applied and environmental microbiology, 91(1), e0102824.

Ren M, et al. (2025) Duodenal-jejunal bypass ameliorates MASLD in rats by regulating gut microbiota and bile acid metabolism through FXR pathways. Hepatology communications, 9(2).

Zhuang Y, et al. (2025) Core microbe Bifidobacterium in the hindgut of calves improves the growth phenotype of young hosts by regulating microbial functions and host metabolism. Microbiome, 13(1), 13.

Inskeep WP, et al. (2025) Respiratory processes of early-evolved hyperthermophiles in sulfidic and low-oxygen geothermal microbial communities. Nature communications, 16(1), 277.

Li T, et al. (2025) Free-caged rearing modes regulate chicken intestinal metabolism by influencing gut microbial homeostasis. Poultry science, 104(1), 104381.

van der Loos LM, et al. (2025) Low functional change despite high taxonomic turnover characterizes the Ulva microbiome across a 2000-km salinity gradient. Science advances, 11(3), eadr6070.

Zhang C, et al. (2025) Gut microbiota profiles of sympatric snub-nosed monkeys and macaques in Qinghai-Tibetan Plateau show influence of phylogeny over diet. Communications biology, 8(1), 95.

Liu Z, et al. (2025) Growth of microbes in competitive lifestyles promotes increased ARGs in soil microbiota: insights based on genetic traits. Microbiome, 13(1), 8.

Zeng S, et al. (2025) Warming-driven migration of enterotypes mediates host health and disease statuses in ectotherm Litopenaeus vannamei. Communications biology, 8(1), 126.