

Resource Summary Report

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MetaVelvet

RRID:SCR_011915

Type: Tool

Proper Citation

MetaVelvet (RRID:SCR_011915)

Resource Information

URL: <http://metavelvet.dna.bio.keio.ac.jp/>

Proper Citation: MetaVelvet (RRID:SCR_011915)

Description: Software for a short read de novo metagenome assembly created by modifying and extending a single-genome and de Bruijn-graph based assembler, Velvet.

Abbreviations: MetaVelvet

Synonyms: MetaVelvet: a short read assembler for metagenomics

Resource Type: software resource

Keywords: bio.tools

Resource Name: MetaVelvet

Resource ID: SCR_011915

Alternate IDs: OMICS_01427, biotools:metavelvet

Alternate URLs: <https://bio.tools/metavelvet>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T132715+0000

Ratings and Alerts

No rating or validation information has been found for MetaVelvet.

No alerts have been found for MetaVelvet.

Data and Source Information

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Kim JW, et al. (2025) Standardizing the approach to clinical-based human microbiome research: from clinical information collection to microbiome profiling and human resource utilization. *Osong public health and research perspectives*, 16(3), 300.

Banerjee G, et al. (2024) Protocol for the construction and functional profiling of metagenome-assembled genomes for microbiome analyses. *STAR protocols*, 5(3), 103167.

Espinal RBA, et al. (2023) Uncovering a Complex Virome Associated with the Cacao Pathogens *Ceratocystis cacaofunesta* and *Ceratocystis fimbriata*. *Pathogens (Basel, Switzerland)*, 12(2).

Martin S, et al. (2023) Capturing variation in metagenomic assembly graphs with MetaCortex. *Bioinformatics (Oxford, England)*, 39(1).

Song Y, et al. (2022) Metagenomic analysis provides bases on individualized shift of colon microbiome affected by delaying colostrum feeding in neonatal calves. *Frontiers in microbiology*, 13, 1035331.

Yang C, et al. (2021) A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. *Computational and structural biotechnology journal*, 19, 6301.

Stelzer CP, et al. (2021) Comparative analysis reveals within-population genome size variation in a rotifer is driven by large genomic elements with highly abundant satellite DNA repeat elements. *BMC biology*, 19(1), 206.

Liang KC, et al. (2021) MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenome assembly. *BMC bioinformatics*, 22(Suppl 6), 427.

Kayani MUR, et al. (2021) Genome-resolved metagenomics using environmental and clinical samples. *Briefings in bioinformatics*, 22(5).

McDaniel EA, et al. (2021) Metabolic Differentiation of Co-occurring *Accumulibacter* Clades Revealed through Genome-Resolved Metatranscriptomics. *mSystems*, 6(4), e0047421.

de Oliveira Ribeiro G, et al. (2021) Guapiaçu virus, a new insect-specific flavivirus isolated from two species of *Aedes* mosquitoes from Brazil. *Scientific reports*, 11(1), 4674.

James GL, et al. (2021) Metagenomic datasets of air samples collected during episodes of severe smoke-haze in Malaysia. *Data in brief*, 36, 107124.

Xiao Y, et al. (2020) Fecal, oral, blood and skin virome of laboratory rabbits. Archives of virology, 165(12), 2847.

Kim HR, et al. (2020) Viral metagenomic analysis of chickens with runting-stunting syndrome in the Republic of Korea. Virology journal, 17(1), 53.

Santiago-Rodriguez TM, et al. (2020) Potential Applications of Human Viral Metagenomics and Reference Materials: Considerations for Current and Future Viruses. Applied and environmental microbiology, 86(22).

Bedford A, et al. (2020) Ruminant volatile fatty acid absorption is affected by elevated ambient temperature. Scientific reports, 10(1), 13092.

D'Amico F, et al. (2019) Gut resistome plasticity in pediatric patients undergoing hematopoietic stem cell transplantation. Scientific reports, 9(1), 5649.

Ulloa R, et al. (2019) Domestication of Local Microbial Consortia for Efficient Recovery of Gold Through Top-Down Selection in Airlift Bioreactors. Frontiers in microbiology, 10, 60.

Cui J, et al. (2019) Metagenomic Insights Into a Cellulose-Rich Niche Reveal Microbial Cooperation in Cellulose Degradation. Frontiers in microbiology, 10, 618.

Mittal P, et al. (2019) Metagenome of a polluted river reveals a reservoir of metabolic and antibiotic resistance genes. Environmental microbiome, 14(1), 5.