# **Resource Summary Report**

Generated by <u>dkNET</u> on Apr 29, 2025

# **MetaVelvet**

RRID:SCR\_011915 Type: Tool

**Proper Citation** 

MetaVelvet (RRID:SCR\_011915)

#### **Resource Information**

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

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**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 assember for metagenomics

Resource Type: software resource

Keywords: bio.tools

Funding:

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: 20250420T014602+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

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 77 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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

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

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

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.

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.

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.

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

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

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

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.

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) Ruminal volatile fatty acid absorption is affected by elevated ambient temperature. Scientific reports, 10(1), 13092.

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

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

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.

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

Klimina KM, et al. (2019) Employing toxin-antitoxin genome markers for identification of Bifidobacterium and Lactobacillus strains in human metagenomes. PeerJ, 7, e6554.