

Resource Summary Report

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MetAMOS

RRID:SCR_011914

Type: Tool

Proper Citation

MetAMOS (RRID:SCR_011914)

Resource Information

URL: <http://cbcb.umd.edu/software/metAMOS>

Proper Citation: MetAMOS (RRID:SCR_011914)

Description: A modular and open source metagenomic assembly and analysis pipeline.

Abbreviations: MetAMOS

Resource Type: software application, workflow software, software resource, data processing software

Keywords: microbiome, pipeline, microbiome, workflow software, metagenomic assembly, metagenomic assembly, bio.tools

Availability: Open source, Available for download

Resource Name: MetAMOS

Resource ID: SCR_011914

Alternate IDs: OMICS_01426, biotools:metamos

Alternate URLs: <https://github.com/marbl/metAMOS>, <https://bio.tools/metamos>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260728T043359+0000

Ratings and Alerts

No rating or validation information has been found for MetAMOS.

No alerts have been found for MetAMOS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Yang J, et al. (2023) A distinct microbiota signature precedes the clinical diagnosis of hepatocellular carcinoma. *Gut microbes*, 15(1), 2201159.

Lewin GR, et al. (2022) Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods. *mSystems*, 7(2), e0151921.

Pallikkuth S, et al. (2021) Age Associated Microbiome and Microbial Metabolites Modulation and Its Association With Systemic Inflammation in a Rhesus Macaque Model. *Frontiers in immunology*, 12, 748397.

Kesh K, et al. (2020) Type 2 diabetes induced microbiome dysbiosis is associated with therapy resistance in pancreatic adenocarcinoma. *Microbial cell factories*, 19(1), 75.

Devault AM, et al. (2017) A molecular portrait of maternal sepsis from Byzantine Troy. *eLife*, 6.

Salaheen S, et al. (2017) Alternative Growth Promoters Modulate Broiler Gut Microbiome and Enhance Body Weight Gain. *Frontiers in microbiology*, 8, 2088.

Samuelsen Ø, et al. (2017) Molecular and epidemiological characterization of carbapenemase-producing Enterobacteriaceae in Norway, 2007 to 2014. *PloS one*, 12(11), e0187832.

Thomson E, et al. (2016) Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. *Journal of clinical microbiology*, 54(10), 2470.

Treangen TJ, et al. (2016) Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. *PLoS neglected tropical diseases*, 10(4), e0004440.

Narayanasamy S, et al. (2016) IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. *Genome biology*, 17(1), 260.

Salman-Carvalho V, et al. (2016) How Clonal Is Clonal? Genome Plasticity across Multicellular Segments of a "Candidatus Marithrix sp." Filament from Sulfidic, Briny Seafloor Sediments in the Gulf of Mexico. *Frontiers in microbiology*, 7, 1173.

Hollister EB, et al. (2015) Structure and function of the healthy pre-adolescent pediatric gut microbiome. *Microbiome*, 3, 36.

Johnson SS, et al. (2015) Insights from the metagenome of an acid salt lake: the role of biology in an extreme depositional environment. PloS one, 10(4), e0122869.

Gevers D, et al. (2012) Bioinformatics for the Human Microbiome Project. PLoS computational biology, 8(11), e1002779.