

# Resource Summary Report

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## MOCAT

RRID:SCR\_011943

Type: Tool

### Proper Citation

MOCAT (RRID:SCR\_011943)

### Resource Information

**URL:** <http://vm-lux.embl.de/~kultima/MOCAT//>

**Proper Citation:** MOCAT (RRID:SCR\_011943)

**Description:** Software package for analyzing metagenomics datasets.

**Abbreviations:** MOCAT

**Resource Type:** software resource

**Resource Name:** MOCAT

**Resource ID:** SCR\_011943

**Alternate IDs:** OMICS\_01517

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260801T190426+0000

### Ratings and Alerts

No rating or validation information has been found for MOCAT.

No alerts have been found for MOCAT.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 41 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

Wang B, et al. (2025) Correlation with viruses enhances network complexity and stability of co-occurrence prokaryotes across the oceans. *mSystems*, 10(7), e0053925.

Lee S, et al. (2024) Global compositional and functional states of the human gut microbiome in health and disease. *Genome research*, 34(6), 967.

Yao X, et al. (2024) MOCAT: multi-omics integration with auxiliary classifiers enhanced autoencoder. *BioData mining*, 17(1), 9.

Bar-Shalom R, et al. (2023) Rhodopsin-mediated nutrient uptake by cultivated photoheterotrophic Verrucomicrobiota. *The ISME journal*, 17(7), 1063.

Cheng K, et al. (2023) MetaLab-MAG: A Metaproteomic Data Analysis Platform for Genome-Level Characterization of Microbiomes from the Metagenome-Assembled Genomes Database. *Journal of proteome research*, 22(2), 387.

Li L, et al. (2023) Revealing proteome-level functional redundancy in the human gut microbiome using ultra-deep metaproteomics. *Nature communications*, 14(1), 3428.

Chen J, et al. (2022) Osteopontin Exacerbates High-Fat Diet-Induced Metabolic Disorders in a Microbiome-Dependent Manner. *mBio*, 13(6), e0253122.

Davies M, et al. (2022) Enterobacteriaceae and Bacteroidaceae provide resistance to travel-associated intestinal colonization by multi-drug resistant *Escherichia coli*. *Gut microbes*, 14(1), 2060676.

Ye X, et al. (2021) Effect of host breeds on gut microbiome and serum metabolome in meat rabbits. *BMC veterinary research*, 17(1), 24.

Simonet C, et al. (2021) Kin selection explains the evolution of cooperation in the gut microbiota. *Proceedings of the National Academy of Sciences of the United States of America*, 118(6).

Chevalier G, et al. (2021) Blockage of bacterial FimH prevents mucosal inflammation associated with Crohn's disease. *Microbiome*, 9(1), 176.

Ye F, et al. (2021) Comparison of gut microbiota in autism spectrum disorders and neurotypical boys in China: A case-control study. *Synthetic and systems biotechnology*, 6(2), 120.

Lyu X, et al. (2021) Oral Microbiota Composition and Function Changes During Chronic Erythematous Candidiasis. *Frontiers in cellular and infection microbiology*, 11, 691092.

Mikan MP, et al. (2020) Metaproteomics reveal that rapid perturbations in organic matter prioritize functional restructuring over taxonomy in western Arctic Ocean microbiomes. *The ISME journal*, 14(1), 39.

Sun J, et al. (2020) Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. *Nature communications*, 11(1), 1427.

Fang S, et al. (2020) Effects of Gut Microbiome and Short-Chain Fatty Acids (SCFAs) on Finishing Weight of Meat Rabbits. *Frontiers in microbiology*, 11, 1835.

Li J, et al. (2020) A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. *GigaScience*, 9(6).

Cao J, et al. (2020) Metagenomic analysis reveals the microbiome and resistome in migratory birds. *Microbiome*, 8(1), 26.

Norouzi-Beirami MH, et al. (2019) Beyond Taxonomic Analysis of Microbiomes: A Functional Approach for Revisiting Microbiome Changes in Colorectal Cancer. *Frontiers in microbiology*, 10, 3117.

Salazar G, et al. (2019) Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. *Cell*, 179(5), 1068.