

Resource Summary Report

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MicrobiomeUtilities

RRID:SCR_014611

Type: Tool

Proper Citation

MicrobiomeUtilities (RRID:SCR_014611)

Resource Information

URL: <https://sourceforge.net/projects/microbiomeutil/files/>

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Description: A set of software utilities for processing and analyzing 16S rRNA genes including generating NAST alignments, chimera checking, and assembling paired 16S rRNA reads according to reference sequence homology.

Synonyms: Microbiome Utilities Portal of the Broad Institute

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [DOI:10.1101/gr.112730.110](https://doi.org/10.1101/gr.112730.110)

Keywords: microbiome, utilities, srna, 16s, nast alignment, chimera checking

Availability: Available for download

Resource Name: MicrobiomeUtilities

Resource ID: SCR_014611

Alternate IDs: OMICS_16932

Alternate URLs: <http://microbiomeutil.sourceforge.net>,
<https://sources.debian.org/src/microbiomeutil/>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260821T194005+0000

Ratings and Alerts

No rating or validation information has been found for MicrobiomeUtilities.

No alerts have been found for MicrobiomeUtilities.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Bharathan G, et al. (2025) Temperature abuse and Salmonella Typhimurium colonization disrupt the indigenous bacterial communities of pasteurized bovine milk over time. Scientific reports, 15(1), 22567.

Paul SS, et al. (2025) Rumen Microbiota in Cattle and Buffaloes: Insights into Host-Specific Bacterial Diversity. Biology, 14(9).

Zulkifli S, et al. (2024) Distinct gut flora profile induced by postnatal trans-fat diet in gestationally bisphenol A-exposed rats. PloS one, 19(7), e0306741.

Steg PB, et al. (2023) Gut Colonization by ESBL-Producing Escherichia coli in Dogs Is Associated with a Distinct Microbiome and Resistome Composition. Microbiology spectrum, 11(4), e0006323.

Fusi M, et al. (2023) Gill-associated bacteria are homogeneously selected in amphibious mangrove crabs to sustain host intertidal adaptation. Microbiome, 11(1), 189.

Collard MK, et al. (2023) The Appendix Orchestrates T-Cell Mediated Immunosurveillance in Colitis-Associated Cancer. Cellular and molecular gastroenterology and hepatology, 15(3), 665.

Henares D, et al. (2021) Differential nasopharyngeal microbiota composition in children according to respiratory health status. Microbial genomics, 7(10).

Song Y, et al. (2013) Microbiota dynamics in patients treated with fecal microbiota transplantation for recurrent Clostridium difficile infection. PloS one, 8(11), e81330.