

# Resource Summary Report

Generated by [dkNET](#) on Aug 7, 2026

## MicrobiomeUtilities

RRID:SCR\_014611

Type: Tool

### Proper Citation

MicrobiomeUtilities (RRID:SCR\_014611)

### Resource Information

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

**Proper Citation:** MicrobiomeUtilities (RRID:SCR\_014611)

**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:** sequence analysis software, software resource, data analysis software, data processing software, software application

**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:** 20260807T042824+0000

### Ratings and Alerts

No rating or validation information has been found for MicrobiomeUtilities.

No alerts have been found for MicrobiomeUtilities.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

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

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.