

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

Nephele

RRID:SCR_016595

Type: Tool

Proper Citation

Nephele (RRID:SCR_016595)

Resource Information

URL: <https://nephele.niaid.nih.gov>

Proper Citation: Nephele (RRID:SCR_016595)

Description: Cloud based platform for simplified, standardized and reproducible microbiome data analysis. Allows users to process microbiome datasets through pipelines of existing software tools.

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource, web application

Defining Citation: [PMID:29028892](https://pubmed.ncbi.nlm.nih.gov/29028892/)

Keywords: microbiome, datasets, process, analyze, metagenome, sequencing, data, bio.tools

Funding: NIH Department of Health and Human Services GS35F0373X

Availability: Free, Available for download, Freely available

Resource Name: Nephele

Resource ID: SCR_016595

Alternate IDs: biotools:nephele

Alternate URLs: <https://github.com/niaid/Nephele>, <https://bio.tools/nephele>

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260912T200019+0000

Ratings and Alerts

No rating or validation information has been found for Nephele.

No alerts have been found for Nephele.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Zhu A, et al. (2026) Household Food Insecurity Alters Gut Microbiome Composition and Enriches Sutterella in Ethiopian Schoolchildren. *Nutrients*, 18(4).

Yeo S, et al. (2026) Dereplication-assisted culturomics enables strain-level ecological analysis of the human gut microbiome. *Gut microbes*, 18(1), 2681840.

Mamun MAA, et al. (2026) VERU-111 Promotes an Anti-Tumor Response Through Restoration of Gut Microbial Homeostasis and Associated Metabolic Dysregulation. *Cells*, 15(2).

Hill K, et al. (2026) Impact of a GABA-Producing *Lactococcus lactis* on Microbiota and Mycobiota During CNS Inflammatory Demyelination. *FASEB bioAdvances*, 8(1), e70085.

Sumithra TG, et al. (2026) Egg disinfection improves larval survival and shapes the microbial community in snubnose pompano (*Trachinotus blochii*). *Scientific reports*, 16(1), 5761.

Tashiro H, et al. (2026) Distinct gut microbiome signatures associated with sedentary behavior improvement following rehabilitation in chronic obstructive pulmonary disease patients with higher functional exercise capacity. *Scientific reports*, 16(1).

Band VI, et al. (2025) Bismuth subsalicylate profoundly alters gut microbiome and immunity with increased susceptibility to infection. *medRxiv : the preprint server for health sciences*.

Chandrasekaran P, et al. (2025) The intestinal microbiome and metabolome discern disease severity in cytotoxic T-lymphocyte-associated protein 4 deficiency. *Microbiome*, 13(1), 51.

Shetty P, et al. (2025) Profiling of microbes associated with chronic irreversible pulpitis using metagenomic next-generation sequencing. *BMC oral health*, 26(1), 118.

Daddy Gaoh S, et al. (2025) A metagenomic analysis coupled with oligotrophic enrichment approach for detecting specified microorganisms in potable groundwater samples. *Frontiers in microbiology*, 16, 1645324.

Munyoki SK, et al. (2025) The microbiota extends the reproductive lifespan of mice by safeguarding the ovarian reserve. *Cell host & microbe*.

Valencia EM, et al. (2024) Mock community taxonomic classification performance of publicly available shotgun metagenomics pipelines. *Scientific data*, 11(1), 81.

Alt?n H, et al. (2024) Temporal microbiome changes in axolotl limb regeneration: Stage-specific restructuring of bacterial and fungal communities with a *Flavobacterium* bloom during blastema proliferation. *Wound repair and regeneration* : official publication of the Wound Healing Society [and] the European Tissue Repair Society, 32(6), 826.

Ar?kan M, et al. (2023) Metaproteogenomic analysis of saliva samples from Parkinson's disease patients with cognitive impairment. *NPJ biofilms and microbiomes*, 9(1), 86.

Cui W, et al. (2023) The gut microbiome changes in wild type and IL-18 knockout mice after 9.0 Gy total body irradiation. *Animal microbiome*, 5(1), 42.

Drummond RA, et al. (2022) Long-term antibiotic exposure promotes mortality after systemic fungal infection by driving lymphocyte dysfunction and systemic escape of commensal bacteria. *Cell host & microbe*, 30(7), 1020.

Piro VC, et al. (2022) Contamination detection and microbiome exploration with GRIMER. *GigaScience*, 12.

Gu W, et al. (2022) MiCloud: A unified web platform for comprehensive microbiome data analysis. *PloS one*, 17(8), e0272354.

Dhar GA, et al. (2022) First insights into the rhizospheric bacterial abundance data of *Cerriops tagal* (Perr.) C.B.Rob. from Indian Sundarbans. *Data in brief*, 43, 108468.

Y?ld?r?m S, et al. (2022) Stratification of the Gut Microbiota Composition Landscape across the Alzheimer's Disease Continuum in a Turkish Cohort. *mSystems*, 7(1), e0000422.