

Resource Summary Report

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

Defining Citation: [PMID: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: 20260729T044421+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 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

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.

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.

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*.

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.

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.

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.

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.

Arikan M, et al. (2022) Axillary Microbiota Is Associated with Cognitive Impairment in Parkinson's Disease Patients. *Microbiology spectrum*, 10(1), e0235821.

Yildirim 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.

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

Babalola OO, et al. (2021) 16S rRNA gene amplicon sequence data from sunflower endosphere bacterial community. *Data in brief*, 39, 107636.

Tang B, et al. (2021) Pharmacological inhibition of MELK restricts ferroptosis and the inflammatory response in colitis and colitis-propelled carcinogenesis. *Free radical biology & medicine*, 172, 312.

Sultan M, et al. (2021) Endocannabinoid Anandamide Attenuates Acute Respiratory Distress Syndrome through Modulation of Microbiome in the Gut-Lung Axis. *Cells*, 10(12).

Alghetaa H, et al. (2021) Resveratrol-mediated attenuation of superantigen-driven acute respiratory distress syndrome is mediated by microbiota in the lungs and gut. *Pharmacological research*, 167, 105548.

Chaudhari SN, et al. (2021) A microbial metabolite remodels the gut-liver axis following bariatric surgery. *Cell host & microbe*, 29(3), 408.

Abdulla OA, et al. (2021) The Ability of AhR Ligands to Attenuate Delayed Type Hypersensitivity Reaction Is Associated With Alterations in the Gut Microbiota. *Frontiers in immunology*, 12, 684727.

Adeleke BS, et al. (2021) Bacterial community structure of the sunflower (*Helianthus annuus*) endosphere. *Plant signaling & behavior*, 16(12), 1974217.

Osgood RS, et al. (2020) Gut microbiota from androgen-altered donors alter pulmonary responses to ozone in female mice. *Physiological reports*, 8(19), e14584.