

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

DADA

RRID:SCR_008205

Type: Tool

Proper Citation

DADA (RRID:SCR_008205)

Resource Information

URL: <https://sites.google.com/site/dadadenoiser/>

Proper Citation: DADA (RRID:SCR_008205)

Description: Infers both the sample genotypes and error parameters that produced a metagenome data set.

Abbreviations: DADA

Synonyms: Divisive Amplicon Denoising Algorithm

Resource Type: software resource

Defining Citation: [PMID:23113967](#)

Resource Name: DADA

Resource ID: SCR_008205

Alternate IDs: OMICS_01117

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260919T195136+0000

Ratings and Alerts

No rating or validation information has been found for DADA.

No alerts have been found for DADA.

Data and Source Information

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Sun Z, et al. (2026) Intrapartum caesarean delivery and childhood BMI trajectories in relation to the infant gut microbiome in the VDAART prospective birth cohort. EBioMedicine, 129, 106347.

Howick J, et al. (2026) Therapeutic empathy in remote consultations in general practice: a realist review protocol. BMJ open, 16(5), e119075.

McNichol J, et al. (2025) Characterizing organisms from three domains of life with universal primers from throughout the global ocean. Scientific data, 12(1), 1078.

Driuchina A, et al. (2025) Unveiling the impact of competition weight loss on gut microbiota: alterations in diversity, composition, and predicted metabolic functions. Journal of the International Society of Sports Nutrition, 22(1), 2474561.

Zhang Y, et al. (2025) Activation of gut metabolite ACSL4/LPCAT3 by microplastics in drinking water mediates ferroptosis via gut-kidney axis. Communications biology, 8(1), 211.

McNamara KB, et al. (2024) Microbial biomarkers as indicators of sperm viability in an insect. Royal Society open science, 11(9), 240734.

Perry WB, et al. (2024) An integrated spatio-temporal view of riverine biodiversity using environmental DNA metabarcoding. Nature communications, 15(1), 4372.

Oaikhena AO, et al. (2024) The phyllosphere of Nigerian medicinal plants, Euphorbia lateriflora and Ficus thonningii is inhabited by a specific microbiota. Scientific reports, 14(1), 22806.

Ngqwala B, et al. (2024) Distribution of SARS-CoV-2 Genomes in Wastewaters and the Associated Potential Infection Risk for Plant Workers in Typical Urban and Peri-Urban Communities of the Buffalo City Region, South Africa. Viruses, 16(6).

Geraldi NR, et al. (2024) Environmental drivers of Arctic communities based on metabarcoding of marine sediment eDNA. Proceedings. Biological sciences, 291(2015), 20231614.

Carmichael MJ, et al. (2024) Microbial Communities in Standing Dead Trees in Ghost Forests are Largely Aerobic, Saprophytic, and Methanotrophic. Current microbiology, 81(8), 229.

Wei M, et al. (2024) The antitumor effect of diisopropylamine dichloroacetate on non-small cell lung cancer and its influence on the tumor immune microenvironment. Frontiers in oncology, 14, 1447828.

Cho G, et al. (2024) Role of microbial communities and nitrogen sources in suppressing root rot disease during ginseng cultivation. *Frontiers in microbiology*, 15, 1396686.

Li Y, et al. (2024) Increased stability of a subtropic bamboo forest soil bacterial communities through integration of water and fertilizer management compared to conventional management. *BMC plant biology*, 24(1), 1072.

Loo EP, et al. (2024) Sugar transporters spatially organize microbiota colonization along the longitudinal root axis of *Arabidopsis*. *Cell host & microbe*.

Collart L, et al. (2023) The volatilome reveals microcystin concentration, microbial composition, and oxidative stress in a critical Oregon freshwater lake. *mSystems*, 8(5), e0037923.

Steinrücken P, et al. (2023) A closer look into the microbiome of microalgal cultures. *Frontiers in microbiology*, 14, 1108018.

Hasper J, et al. (2023) Turnover and replication analysis by isotope labeling (TRAIL) reveals the influence of tissue context on protein and organelle lifetimes. *Molecular systems biology*, 19(4), e11393.

Williams A, et al. (2023) Peeling back the layers of coral holobiont multi-omics data. *iScience*, 26(9), 107623.

Goraj W, et al. (2023) Dynamics of Methane-Consuming Biomes from Wieliczka Formation: Environmental and Enrichment Studies. *Biology*, 12(11).