

Resource Summary Report

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AmpliconNoise

RRID:SCR_007814

Type: Tool

Proper Citation

AmpliconNoise (RRID:SCR_007814)

Resource Information

URL: <https://code.google.com/p/ampliconnoise/>

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Description: A collection of programs for the removal of noise from 454 sequenced PCR amplicons. This project also includes the Perseus algorithm for chimera removal.

Abbreviations: AmpliconNoise

Resource Type: software resource

Defining Citation: [DOI:10.1186/1471-2105-12-38](https://doi.org/10.1186/1471-2105-12-38)

Keywords: bio.tools

Funding:

Resource Name: AmpliconNoise

Resource ID: SCR_007814

Alternate IDs: biotools:pyronoise, OMICS_01112

Alternate URLs: <https://bio.tools/pyronoise>, <https://sources.debian.org/src/anfo/>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250420T014406+0000

Ratings and Alerts

No rating or validation information has been found for AmpliconNoise.

No alerts have been found for AmpliconNoise.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Eo J, et al. (2021) Shift of Dominant Species in Plant Community and Soil Chemical Properties Shape Soil Bacterial Community Characteristics and Putative Functions: A Case Study on Topographic Variation in a Mountain Pasture. *Microorganisms*, 9(5).

Wallis C, et al. (2021) Subgingival microbiota of dogs with healthy gingiva or early periodontal disease from different geographical locations. *BMC veterinary research*, 17(1), 7.

Javelle E, et al. (2021) Gut Microbiota in Military International Travelers with Doxycycline Malaria Prophylaxis: Towards the Risk of a Simpson Paradox in the Human Microbiome Field. *Pathogens* (Basel, Switzerland), 10(8).

Piwoz K, et al. (2020) Bacterial and Eukaryotic Small-Subunit Amplicon Data Do Not Provide a Quantitative Picture of Microbial Communities, but They Are Reliable in the Context of Ecological Interpretations. *mSphere*, 5(2).

Storesund JE, et al. (2020) Planctomycetes as a Vital Constituent of the Microbial Communities Inhabiting Different Layers of the Meromictic Lake Sælenvannet (Norway). *Microorganisms*, 8(8).

Bubier JA, et al. (2020) A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. *Genetics*, 214(3), 719.

Gran-Stadniczeňko S, et al. (2019) Seasonal Dynamics of Algae-Infecting Viruses and Their Inferred Interactions with Protists. *Viruses*, 11(11).

Wootton DG, et al. (2019) A *Haemophilus* sp. dominates the microbiota of sputum from UK adults with non-severe community acquired pneumonia and chronic lung disease. *Scientific reports*, 9(1), 2388.

Goel RM, et al. (2019) *Streptococcus Salivarius*: A Potential Salivary Biomarker for Orofacial Granulomatosis and Crohn's Disease? *Inflammatory bowel diseases*, 25(8), 1367.

Jung J, et al. (2019) Microbial Fe(III) reduction as a potential iron source from Holocene

sediments beneath Larsen Ice Shelf. *Nature communications*, 10(1), 5786.

Grimshaw SG, et al. (2019) The diversity and abundance of fungi and bacteria on the healthy and dandruff affected human scalp. *PloS one*, 14(12), e0225796.

Goebbels M, et al. (2019) Rapid Microbial Community Changes During Initial Stages of Pine Litter Decomposition. *Microbial ecology*, 77(1), 56.

Fyhrquist N, et al. (2019) Microbe-host interplay in atopic dermatitis and psoriasis. *Nature communications*, 10(1), 4703.

Bergelson J, et al. (2019) Characterizing both bacteria and fungi improves understanding of the *Arabidopsis* root microbiome. *Scientific reports*, 9(1), 24.

Kearl J, et al. (2019) Salt-Tolerant Halophyte Rhizosphere Bacteria Stimulate Growth of Alfalfa in Salty Soil. *Frontiers in microbiology*, 10, 1849.

Gran-Stadniczeňko S, et al. (2019) Protist Diversity and Seasonal Dynamics in Skagerrak Plankton Communities as Revealed by Metabarcoding and Microscopy. *The Journal of eukaryotic microbiology*, 66(3), 494.

Yoo K, et al. (2018) Classification and Regression Tree Approach for Prediction of Potential Hazards of Urban Airborne Bacteria during Asian Dust Events. *Scientific reports*, 8(1), 11823.

Aanderud ZT, et al. (2018) Stoichiometric Shifts in Soil C:N:P Promote Bacterial Taxa Dominance, Maintain Biodiversity, and Deconstruct Community Assemblages. *Frontiers in microbiology*, 9, 1401.

Liu B, et al. (2018) Rapid Succession of Actively Transcribing Denitrifier Populations in Agricultural Soil During an Anoxic Spell. *Frontiers in microbiology*, 9, 3208.

Pedersen C, et al. (2018) Fecal Enterobacteriales enrichment is associated with increased in vivo intestinal permeability in humans. *Physiological reports*, 6(7), e13649.