

Resource Summary Report

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Metagenomes Used in The Statistical Analysis

RRID:SCR_008483

Type: Tool

Proper Citation

Metagenomes Used in The Statistical Analysis (RRID:SCR_008483)

Resource Information

URL: <http://www.theseed.org/DinsdaleSupplementalMaterial/>

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Description: his table shows the metadata and links to sources of the data and citations associated with the publicly available metagenome sequences used in the Dinsdale, Edwards, et al., analysis of 87 different metagenomes. The links will take you to the annotated sequences in the metagenomics SEED, CAMERA, and the NCBI Short Read Archive. Please note that all metagenomes are currently available to download via the ftp links, some are available in the meta-RAST, and other links will be added as soon as they become available. Citations for individual metagenomes will also be added as and when they become available. DNA sequences for all metagenomes are available via anonymous FTP. Sponsor. This project was supported by the Gordon and Betty Moore Foundation Marine Microbial Initiative, National Science Foundation grants (F.R. and D.L.V.), a Department of Commerce ATP grant (F.R.), a National Research Initiative Competitive Grant from the USDA Cooperative State Research, Education and Extension Service (B.W.), the National Institute of Allergy and Infectious Diseases, the National Institutes of Health and the Department of Health and Human Services (R.S.).

Synonyms: Metagenomes

Resource Type: software resource

Resource Name: Metagenomes Used in The Statistical Analysis

Resource ID: SCR_008483

Alternate IDs: nif-0000-30453

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260808T185910+0000

Ratings and Alerts

No rating or validation information has been found for Metagenomes Used in The Statistical Analysis.

No alerts have been found for Metagenomes Used in The Statistical Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1743 mentions in open access literature.

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

Pitt A, et al. (2025) *Aquirufa esocilacus* sp. nov., *Aquirufa originis* sp. nov., *Aquirufa avitistagni*, and *Aquirufa echingensis* sp. nov. discovered in small freshwater habitats in Austria during a citizen science project. *Archives of microbiology*, 207(4), 71.

Urrea V, et al. (2025) Metagenomic Analysis of Surface Waters and Wastewater in the Colombian Andean Highlands: Implications for Health and Disease. *Current microbiology*, 82(4), 162.

Bargheet A, et al. (2025) Dynamics of gut resistome and mobilome in early life: a meta-analysis. *EBioMedicine*, 114, 105630.

Kang X, et al. (2025) The Gut Microbiome of the Asiatic Toad (*Bufo gargarizans*) Reflects Environmental Changes and Human Activities. *Ecology and evolution*, 15(5), e71394.

Parra B, et al. (2024) Characterization and Abundance of Plasmid-Dependent Alphatectivirus Bacteriophages. *Microbial ecology*, 87(1), 85.

Hoetzing M, et al. (2024) Geographic population structure and distinct intra-population dynamics of globally abundant freshwater bacteria. *The ISME journal*, 18(1).

Reinsch S, et al. (2024) Co-located ecological data for exploring top- and subsoil carbon dynamics across grassland-woodland contrasts. *Scientific data*, 11(1), 478.

Valles-Colomer M, et al. (2023) The person-to-person transmission landscape of the gut and oral microbiomes. *Nature*, 614(7946), 125.

Giacomini JJ, et al. (2023) Site Specialization of Human Oral *Veillonella* Species. *Microbiology spectrum*, 11(1), e0404222.

Jeyanathan M, et al. (2022) Parenteral BCG vaccine induces lung-resident memory macrophages and trained immunity via the gut-lung axis. *Nature immunology*, 23(12), 1687.

Hedžet S, et al. (2021) Novel Siphoviridae Bacteriophages Infecting *Bacteroides uniformis* Contain Diversity Generating Retroelement. *Microorganisms*, 9(5).

Sabater C, et al. (2021) A Machine Learning Approach to Study Glycosidase Activities from Bifidobacterium. *Microorganisms*, 9(5).

Rapp JZ, et al. (2021) Divergent Genomic Adaptations in the Microbiomes of Arctic Subzero Sea-Ice and Cryopeg Brines. *Frontiers in microbiology*, 12, 701186.

Roux S, et al. (2021) Ecology and molecular targets of hypermutation in the global microbiome. *Nature communications*, 12(1), 3076.

Peterson D, et al. (2021) Comparative Analysis of 16S rRNA Gene and Metagenome Sequencing in Pediatric Gut Microbiomes. *Frontiers in microbiology*, 12, 670336.

Alcorta J, et al. (2020) Taxonomic Novelty and Distinctive Genomic Features of Hot Spring Cyanobacteria. *Frontiers in genetics*, 11, 568223.

Zhou Z, et al. (2020) Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. *The ISME journal*, 14(8), 2060.

Hendriksen RS, et al. (2019) Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. *Nature communications*, 10(1), 1124.

Engevik MA, et al. (2019) Microbial Metabolic Capacity for Intestinal Folate Production and Modulation of Host Folate Receptors. *Frontiers in microbiology*, 10, 2305.

Bergk Pinto B, et al. (2019) Do Organic Substrates Drive Microbial Community Interactions in Arctic Snow? *Frontiers in microbiology*, 10, 2492.