

Resource Summary Report

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SqueezeMeta

RRID:SCR_021821

Type: Tool

Proper Citation

SqueezeMeta (RRID:SCR_021821)

Resource Information

URL: <https://github.com/jtamames/SqueezeMeta>

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Description: Software tool as fully automated pipeline for metagenomic analysis. Used for metagenomics covering all steps of analysis. Features several characteristics including co-assembly procedure or co-assembly of unlimited number of metagenomes via merging of individual assembled metagenomes, both with read mapping for estimation of abundances of genes in each metagenome. Includes binning and bin checking for retrieving individual genomes.

Resource Type: data processing software, data analysis software, software resource, software application

Defining Citation: [DOI:10.3389/fmicb.2018.03349](https://doi.org/10.3389/fmicb.2018.03349)

Keywords: automated metagenomics pipeline, metagenomics analysis steps, metagenomic analysis

Funding: Spanish Ministry of Economy and Competitiveness.

Availability: Free, Available for download, Freely available

Resource Name: SqueezeMeta

Resource ID: SCR_021821

License: GNU General Public License v3.0

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260813T055238+0000

Ratings and Alerts

No rating or validation information has been found for SqueezeMeta.

No alerts have been found for SqueezeMeta.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Pérez-Rocher B, et al. (2026) Topological and Functional Diversity of Gut Microbiota Metabolism Across the Human Lifespan. *Metabolites*, 16(2).

Brown JL, et al. (2026) Bacterial Community Composition and Functional Potential of the Kleptoplastic Sea Slug *Elysia papillosa*. *Biomolecules*, 16(6).

De Visscher J, et al. (2026) Functional genetic potential of benthic microbial mat communities in Arctic, Antarctic, and sub-Antarctic lakes. *FEMS microbiology ecology*, 102(7).

Flores-Gallegos FA, et al. (2025) Microbial diversity and metabolic potential in long-term Cr(VI) polluted soil during in situ biostimulation: a pilot effective assay. *Environmental science and pollution research international*, 32(33), 19885.

Laso-Pérez R, et al. (2025) Nitrogen cycling during an Arctic bloom: from chemolithotrophy to nitrogen assimilation. *mBio*, 16(6), e0074925.

Kiige JK, et al. (2025) Metagenomic characterization of bacterial abundance and diversity in potato cyst nematode suppressive and conducive potato rhizosphere. *PloS one*, 20(5), e0323382.

Lemieux É, et al. (2025) Effect of an antibiotic and a probiotic on phage communities in the swine gut microbiota. *BMC research notes*, 18(1), 402.

Redondo-Río Á, et al. (2024) Specialized Bacteroidetes dominate the Arctic Ocean during marine spring blooms. *Frontiers in microbiology*, 15, 1481702.

Wang FQ, et al. (2024) Particle-attached bacteria act as gatekeepers in the decomposition of complex phytoplankton polysaccharides. *Microbiome*, 12(1), 32.

Monger XC, et al. (2024) Resilience of Loin Meat Microbiota and of Resistance Genes to a Chlortetracycline Treatment in Weaned Piglets. *Antibiotics (Basel, Switzerland)*, 13(10).

Panyako PM, et al. (2024) Metagenomic Characterization of Poultry Cloacal and Oropharyngeal Swabs in Kenya Reveals Bacterial Pathogens and Their Antimicrobial Resistance Genes. *International journal of microbiology*, 2024, 8054338.

Omar KM, et al. (2024) Investigating antimicrobial resistance genes in Kenya, Uganda and Tanzania cattle using metagenomics. *PeerJ*, 12, e17181.

Bell CJ, et al. (2024) A root nodule microbiome sequencing data set from red alder (*Alnus rubra* Bong.). *Scientific data*, 11(1), 1343.

Sánchez C, et al. (2023) A Novel Dependoparvovirus Identified in Cloacal Swabs of Monk Parakeet (*Myiopsitta monachus*) from Urban Areas of Spain. *Viruses*, 15(4).

Lomakina A, et al. (2023) Microbial Communities in Ferromanganese Sediments from the Northern Basin of Lake Baikal (Russia). *Microorganisms*, 11(7).

von Arx JN, et al. (2023) Methylphosphonate-driven methane formation and its link to primary production in the oligotrophic North Atlantic. *Nature communications*, 14(1), 6529.

Calabrese FM, et al. (2022) Metabolic framework of spontaneous and synthetic sourdough metacommunities to reveal microbial players responsible for resilience and performance. *Microbiome*, 10(1), 148.

Fierer N, et al. (2022) A Metagenomic Investigation of Spatial and Temporal Changes in Sewage Microbiomes across a University Campus. *mSystems*, 7(5), e0065122.

Raj A, et al. (2021) Tapping the Role of Microbial Biosurfactants in Pesticide Remediation: An Eco-Friendly Approach for Environmental Sustainability. *Frontiers in microbiology*, 12, 791723.

Puente-Sánchez F, et al. (2020) SQMtools: automated processing and visual analysis of 'omics data with R and anvi'o. *BMC bioinformatics*, 21(1), 358.