

Resource Summary Report

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QIIME2

RRID:SCR_021258

Type: Tool

Proper Citation

QIIME2 (RRID:SCR_021258)

Resource Information

URL: <https://qiime2.org/>

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Description: Software tool as next generation microbiome bioinformatics platform that is extensible, free, open source, and community developed. Enables researchers to start analysis with raw DNA sequence data and finish with publication quality figures and statistical results. Used to analyze and interpret nucleic acid sequence data from fungal, viral, bacterial, and archaeal communities.

Synonyms: Quantitative Insights Into Microbial Ecology 2

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

Keywords: Nucleic acid sequence data, nucleic acid sequence, fungal data, viral data, bacterial data, archaeal data, data analysis

Availability: Free, Available for download, Freely available

Resource Name: QIIME2

Resource ID: SCR_021258

Alternate URLs: <https://github.com/qiime2/qiime2>, <https://sources.debian.org/src/q2-sample-classifier/>

License: BSD 3-Clause "New" or "Revised" License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194204+0000

Ratings and Alerts

No rating or validation information has been found for QIIME2.

No alerts have been found for QIIME2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1929 mentions in open access literature.

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

Liu YY, et al. (2026) Assessing whether rectal swabs reflect appendiceal microbiota profiles in acute appendicitis: a 16S rRNA-based comparative study. Gut pathogens, 18(1), 10.

Apgar M, et al. (2026) Dietary fiber reduces mortality from secondary sepsis in a murine model of Clostridioides difficile infection. iScience, 29(4), 115258.

Kim S, et al. (2026) Gut microbiota transfer from autoimmune dry eye mice imprints stereotypic B cell receptor repertoires in the lacrimal gland and induces disease. Frontiers in immunology, 17, 1827057.

Takahashi H, et al. (2026) Testosterone deficiency synergistically exacerbates fructose-induced hepatic steatosis through gut microbiota and pyruvate in mice. American journal of physiology. Endocrinology and metabolism, 330(2), E233.

Huang W, et al. (2026) Core gastric microbiota linked to pathogenesis and preserved across age-stratified cohorts. Cell reports. Medicine, 7(7), 102905.

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.

Song SJ, et al. (2026) Arid1a deficiency promotes metabolic dysfunction-associated steatohepatitis and hepatocellular carcinoma by disrupting the FXR-gut microbiota-bile acid axis. Cancer letters, 652, 218567.

Parween S, et al. (2026) Host genome and bacterial taxa shape the Arabidopsis seed microbiome. EMBO reports, 27(1), 122.

Kong JY, et al. (2026) Cross-site oral and esophageal microbiome signatures define diagnostic patterns and reveal mechanistic drivers of ESCC. iScience, 29(8), 116667.

Howells AEG, et al. (2026) Pushing the upper temperature limit of methanotrophy in continental hydrothermal ecosystems, active biological methane oxidation in hot springs of Yellowstone National Park. Frontiers in microbiology, 17, 1736896.

Shah UA, et al. (2026) A High-Fiber, Plant-Based Diet in Myeloma Precursor Disorders: Results from the NUTRIVENTION Clinical Trial and Preclinical Vk*MYC Model. *Cancer discovery*, 16(4), 697.

Huang W, et al. (2026) Gut microbiota-derived xanthohumol protects against heatstroke by inhibiting macrophage pyroptosis in mice. *Journal of advanced research*, 82, 967.

Fang S, et al. (2026) Colored Plastic Pollution Reshapes Aquatic Microbial Community and Resistance Profile via Divergent Pseudonatural Dissolved Organic Matter. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(3), e14529.

Maimaitimin B, et al. (2026) Effects of Feeding High-Moisture Corn on Meat Performance, Meat Quality, Muscle Metabolism, and Gut Microbiota in Kazakh Rams. *Animals : an open access journal from MDPI*, 16(9).

Wei D, et al. (2026) The crayfish-rice coculture model contributes to regulating the soil fertility of rice fields and maintaining the stability of soil microbial community composition and function. *Advanced biotechnology*, 4(2).

Zhao W, et al. (2026) Engineered probiotics constitutively expressing SOD alleviate inflammatory bowel disease by targeting ROS. *iScience*, 29(6), 115930.

Zhang J, et al. (2026) Terracing influences soil microbial assembly in citrus orchards: stochastic processes dominate community dynamics in a karst sloping land. *BMC microbiology*, 26(1).

Almela P, et al. (2026) Enhancing DNA recovery in low-biomass snow algae samples: a comparative study of extraction methods and their effect on community composition. *Applied and environmental microbiology*, 92(4), e0003126.

Li Y, et al. (2026) Integrated multi-omics implicates the gut microbiota and bilirubin in abdominal fat deposition in Huainan yellow chickens. *Poultry science*, 105(6), 106769.

Guo Y, et al. (2026) Carbon monoxide oxidation expands the known metabolic capacity in anaerobic methanotrophic consortia. *Nature communications*, 17(1).