

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

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 [dkNET](#) .

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.

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

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.

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.

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.

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.

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.

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.

Gao W, et al. (2026) Rumen-protected betaine supplementation improves ileal function by affecting microbe and metabolite in Tibetan sheep. *AMB Express*, 16(1).

Liu L, et al. (2026) The function of Toll-like receptor 2 in control of transcriptome responses to the microbiome and microbiome composition. *Animal microbiome*, 8(1), 5.

Lee SM, et al. (2026) Early-onset Palmijihwang-hwan treatment modulates phospholipid metabolism and gut microbiota for healthy aging: reducing adipose inflammation and oxidative stress. *npj aging*, 12(1), 35.

Rong C, et al. (2026) Astaxanthin improve the intestinal microbiota and metabolism after ischemic stroke. *Scientific reports*, 16(1), 5848.

Choi H, et al. (2026) Antarctic moss fairy rings serve as reservoirs for plant growth-promoting bacteria. *BMC plant biology*, 26(1), 299.

Ma Y, et al. (2026) Characteristics comparative of gut microbiota in four small mammal species co-occurring in the Hengduan Mountains: differences in environmental adaptation strategies between alien and endemic species. *BMC microbiology*, 26(1).

Li J, et al. (2026) Oxytocin attenuates isolation-evoked emotional and social behavioral dysregulation through neural, immune, and microbiota mechanisms. *Translational psychiatry*, 16(1).

Frings DM, et al. (2026) Microbial Diversity Across Chemolithotrophic and Phototrophic Biofilms in Cold Sulfur Springs. *MicrobiologyOpen*, 15(1), e70223.