

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, software application, software resource, sequence analysis software, data processing software

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: 20260801T190715+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 1232 mentions in open access literature.

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

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

Serbanescu M, et al. (2026) Effects of Perioperative Exposure on the Microbiome and Outcomes From an Immune Challenge in C57Bl/6 Adult Mice. Anesthesia and analgesia, 142(1), 171.

Han R, et al. (2026) Gut microbiota Lactobacillus johnsonii alleviates hyperuricemia by modulating intestinal urate and gut microbiota-derived butyrate. Chinese medical journal, 139(1), 118.

Peng Y, et al. (2026) Halophyte-Derived Kushneria Strains Enhance Salt Tolerance and Rhizosphere Dynamics in Cabbage. Plant, cell & environment, 49(1), 531.

Favela A, et al. (2026) Lost and found: Rediscovering microbiome-associated phenotypes that reshape agricultural sustainability. Science advances, 12(1), eaed3360.

Pan Q, et al. (2026) Effects of Phthalate Exposure on Oral Microbiome Diversity and Enrichment of Gemella and Streptococcus. International dental journal, 76(1), 109292.

Peng Z, et al. (2026) Association between weaning stress and rumen microbiota in goat kids: evidence from granger causality and randomized controlled trial validation. Animal bioscience, 39(1), 250092.

Bai X, et al. (2026) Microbial Characteristics of the Extrinsic Black Stain in Primary Dentition. International dental journal, 76(1), 103988.

Hong S, et al. (2026) Clinical efficacy and multi-omics analysis of Si-Ni-San for depression treatment in breast cancer patients: a randomized, double-blind, placebo-controlled, crossover trial. Chinese medicine, 21(1), 9.

Gudi RR, et al. (2026) Human Gut Commensal Bacteroides fragilis Suppresses Mucin Production and Alters Microbiota Composition Resulting in Accelerated Type 1 Diabetes in Mice. Immunology, 177(1), 119.

Chen Z, et al. (2026) Ryegrass improves carcass trait of meat geese effects of dietary ryegrass supplementation on growth performance, carcass traits, and gut microbiota in meat geese. *Poultry science*, 105(1), 106035.

Sugimoto T, et al. (2026) Association of Preoperative Gut Microbiota Disturbances with Postoperative Infectious Complications in Major Gastrointestinal Cancer Surgery: A Large-Scale Exploratory Study. *Annals of surgical oncology*, 33(1), 224.

Han P, et al. (2026) Integrated multi-omics reveals microbial and metabolic mechanisms driving enhanced fermentation quality in cigar tobacco leaves with exogenous additives. *Bioresources and bioprocessing*, 13(1), 2.

Yang Z, et al. (2025) *Veillonella* intestinal colonization promotes *C. difficile* infection in Crohn's disease. *Cell host & microbe*, 33(9), 1518.

Zhang X, et al. (2025) Common mycorrhizal networks facilitate plant disease resistance by altering rhizosphere microbiome assembly. *Cell host & microbe*.

Bethune E, et al. (2025) Harnessing cosmic carbon: anaerobic microbial responses to fullerenes under early Earth conditions. *Frontiers in microbiology*, 16, 1511842.

Zhang Y, et al. (2025) Immune Dysregulation and Endometrial Receptivity Impairment in Women with Repeated Implantation Failure and Dyslipidemia. *The Journal of clinical endocrinology and metabolism*.

Abdill RJ, et al. (2025) Integration of 168,000 samples reveals global patterns of the human gut microbiome. *Cell*, 188(4), 1100.

Jiao X, et al. (2025) Progressive gut microbiota shifts and functional alterations across aging stages and frailty in mice. *iScience*, 28(7), 112985.

Jin S, et al. (2025) Disruption of the transsulfuration pathway by acute kidney injury causes intestinal damage. *iScience*, 28(10), 113511.