

Resource Summary Report

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PICRUSt

RRID:SCR_016855

Type: Tool

Proper Citation

PICRUSt (RRID:SCR_016855)

Resource Information

URL: <https://picrust.github.io/picrust/>

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Description: Software package to predict metagenome functional content from marker gene (e.g., 16S rRNA) surveys and full genomes. Used to predict which gene families are present and then combines gene families to estimate the composite metagenome.

Abbreviations: PICRUSt

Synonyms: Phylogenetic Investigation of Communities by Reconstruction of Unobserved States, PICRUSt

Resource Type: software application, simulation software, software resource

Defining Citation: [PMID:23975157](#)

Keywords: predict, metagenome, functional, content, DNA, sample, marker, gene, sequence, data, microbiome, 16S, RNA

Funding: Canadian Institutes of Health Research ;
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Availability: Free, Available for download, Freely available

Resource Name: PICRUST

Resource ID: SCR_016855

Alternate IDs: SCR_016856

License: GNU GPL v3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260728T043522+0000

Ratings and Alerts

No rating or validation information has been found for PICRUST.

No alerts have been found for PICRUST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Yang YT, et al. (2025) Optimization, application effects and improved microecology of a composite microbial agent containing oyster shells. Scientific reports, 15(1), 6922.

Pascual-García A, et al. (2025) Replicating community dynamics reveals how initial composition shapes the functional outcomes of bacterial communities. Nature communications, 16(1), 3002.

Dendooven L, et al. (2025) Young maize plants impact the bacterial community in Australian cotton-sown vertisol more than agricultural practices. Environmental microbiology reports, 17(3), e13322.

Kim CW, et al. (2025) Gut dysbiosis from high-salt diet promotes glioma via propionate-mediated TGF- β activation. The Journal of experimental medicine, 222(8).

Yan Y, et al. (2024) Gut microbiota-derived cholic acid mediates neonatal brain immaturity and white matter injury under chronic hypoxia. iScience, 27(5), 109633.

Kumari A, et al. (2024) Substantially altered bacterial diversity associated with developmental stages of litchi stink bug, Tessaratomia javanica (Thunberg) (Hemiptera: Tessaratomidae). Heliyon, 10(11), e32384.

Ling Z, et al. (2024) Altered gut microbiota and systemic immunity in Chinese patients with schizophrenia comorbid with metabolic syndrome. Journal of translational medicine, 22(1),

Qi D, et al. (2024) Unveiling the gut microbiota blueprint of schizophrenia: a multilevel omics approach. *Frontiers in psychiatry*, 15, 1452604.

Wang Y, et al. (2024) Perturbations in gut microbiota composition in schizophrenia. *PLoS one*, 19(7), e0306582.

Lovecchio N, et al. (2024) Hydrocarbonoclastic Biofilm-Based Microbial Fuel Cells: Exploiting Biofilms at Water-Oil Interface for Renewable Energy and Wastewater Remediation. *Biosensors*, 14(10).

Zhen J, et al. (2024) Shaoyao Decoction reduced T lymphocyte activation by regulating of intestinal flora and 5-hydroxytryptamine metabolism in ulcerative colitis. *Chinese medicine*, 19(1), 87.

Sun C, et al. (2024) Harnessing biosynthesized selenium nanoparticles for recruitment of beneficial soil microbes to plant roots. *Cell host & microbe*, 32(12), 2148.

Deng F, et al. (2023) Gut microbe-derived milnacipran enhances tolerance to gut ischemia/reperfusion injury. *Cell reports. Medicine*, 4(3), 100979.

Ling Z, et al. (2023) Altered oral microbiota and immune dysfunction in Chinese elderly patients with schizophrenia: a cross-sectional study. *Translational psychiatry*, 13(1), 383.

Maji UJ, et al. (2022) Exploring the gut microbiota composition of Indian major carp, rohu (*Labeo rohita*), under diverse culture conditions. *Genomics*, 114(3), 110354.

Pettersen VK, et al. (2022) Inferring early-life host and microbiome functions by mass spectrometry-based metaproteomics and metabolomics. *Computational and structural biotechnology journal*, 20, 274.

Hall NC, et al. (2022) The Presence of Denitrifiers In Bacterial Communities of Urban Stormwater Best Management Practices (BMPs). *Environmental management*, 69(1), 89.

Mondal HK, et al. (2022) Alteration of gut microbiota composition and function of Indian major carp, rohu (*Labeo rohita*) infected with *Argulus siamensis*. *Microbial pathogenesis*, 164, 105420.

Yan L, et al. (2022) Effects of corn particle size on growth performance, gastrointestinal development, carcass indices and intestinal microbiota of broilers. *Poultry science*, 101(12), 102205.

Liu X, et al. (2022) Comparative Study of the Gut Microbiota Community between the Farmed and Wild *Mastacembelus armatus* (Zig-Zag Eel). *Metabolites*, 12(12).