

Resource Summary Report

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PICRUSt2

RRID:SCR_022647

Type: Tool

Proper Citation

PICRUSt2 (RRID:SCR_022647)

Resource Information

URL: <https://huttenhower.sph.harvard.edu/picrust/>

Proper Citation: PICRUSt2 (RRID:SCR_022647)

Description: Software for predicting functional abundances based only on marker gene sequences. Used for prediction of metagenome functions. Contains updated and larger database of gene families and reference genomes, provides interoperability with any operational taxonomic unit (OTU)-picking or denoising algorithm, and enables phenotype predictions. Allows addition of custom reference databases.

Synonyms: Phylogenetic Investigation of Communities by Reconstruction of Unobserved States

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:32483366](#)

Keywords: predicting functional abundances, marker gene sequences, metagenome functions prediction

Funding: GlaxoSmithKline ;
NIDDK R24DK110499;
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NSERC ;
NSF IOS CAREER 1942647

Availability: Free, Available for download, Freely available

Resource Name: PICRUSt2

Resource ID: SCR_022647

Alternate URLs: <https://github.com/picrust/picrust2>

License: GNU GPL v3

Record Creation Time: 20220805T050153+0000

Record Last Update: 20260903T004306+0000

Ratings and Alerts

No rating or validation information has been found for PICRUST2.

No alerts have been found for PICRUST2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 583 mentions in open access literature.

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

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.

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.

Ko H, et al. (2026) Commensal microbe-derived butyrate enhances T follicular helper cell function to boost mucosal vaccine efficacy. Microbiome, 14(1), 37.

Wang J, et al. (2026) Tuber Inoculation Drives Rhizosphere Microbiome Assembly and Metabolic Reprogramming in Corylus. International journal of molecular sciences, 27(2).

Chen K, et al. (2026) Bifidobacterium animalis subsp. lactis BLa80 for preventing allergic, respiratory, and gastrointestinal diseases in young children in China: a randomized double-blind placebo-controlled trial. Clinical and experimental pediatrics, 69(2), 150.

Zhao H, et al. (2026) Early life fecal microbiota transplantation enhances fermentation potential by changing the microbial profiles in broiler chickens. Poultry science, 105(1), 106189.

Li RJ, et al. (2026) Host immune constraints delineate the window of microbial colonization during early development of Larimichthys crocea. Zoological research, 47(1), 17.

Ye WY, et al. (2026) Akkermansia muciniphila alleviates antibiotic- and LPS-induced oxidative stress via the p38?? MAPK-Nrf2 signaling axis. *Frontiers in microbiology*, 17, 1753421.

Costa-Santos M, et al. (2026) Seasonal dynamics and core stability of the bacterial microbiome of a *Drosophila suzukii* wild population. *Scientific reports*, 16(1), 6569.

Emmanouil C, et al. (2026) Rapid Remodeling of the Human Gut Microbiome in Response to Short-Term Animal Product Restriction and Associations with Host Molecular Phenotypes. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(30), e15575.

Ichimura R, et al. (2026) Association between bone marrow donor origin and gut microbiota composition following fecal microbiota transplantation in mice. *Scientific reports*, 16(1).

Silva L, et al. (2026) Macrophyte Extracts Promote the Growth of the Microbial Community Associated With *Microcystis aeruginosa* Alleviating Allelopathic Effects. *Water environment research : a research publication of the Water Environment Federation*, 98(2), e70297.

King Z, et al. (2026) Comparative Amplicon and Shotgun Metagenome Profiling of Soil Microbial Communities in Kauri Forests Affected by *Phytophthora agathidicida*. *Environmental microbiology reports*, 18(2), e70324.

Menezes GA, et al. (2026) Gut Microbiota and Dyslipidemia in Type 2 Diabetes: A Pilot Study of 16S rRNA Profiles and Predicted Functional Shifts. *Journal of diabetes research*, 2026(1), e9317962.

Qhanya LB, et al. (2026) Monitoring endocrine-disrupting chemicals and microbial diversity of wastewater treatment maturation ponds. *Applied and environmental microbiology*, 92(5), e0134225.

Hou P, et al. (2026) Characterization of Gut Bacteria in *Blepharipa tibialis* (Diptera: Tachinidae) Larvae Parasitizing Different Developmental Stages of *Antheraea pernyi*. *Insects*, 17(5).

Adeleke RA, et al. (2026) Diversity and functional potential of bacterial and fungal endophytes in traditional food wrapping leaves reveal implications for artisanal food safety and quality. *Frontiers in microbiology*, 17, 1641069.

Diakoumopoulou D, et al. (2026) Subgingival Microbiota Shifts Following Diode Laser-Activated Indocyanine Green Treatment in Periodontitis: A Pilot 16S rDNA Study. *Microorganisms*, 14(6).

Pan X, et al. (2026) Comparative Insights into Digestion and Gut Microbiota Modulation of Polysaccharides from Ginseng, *Ganoderma lucidum*, and *Dendrobium officinale*. *Foods* (Basel, Switzerland), 15(11).