

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/>

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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: software application, simulation software, software resource

Defining Citation: [PMID:32483366](#)

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

Funding: NSF IOS CAREER 1942647;
NIDDK U54DK102557;
NIDDK R24DK110499;
NSERC ;
GlaxoSmithKline

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: 20260728T043647+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 368 mentions in open access literature.

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

Ding W, et al. (2026) Impact of carbapenem-resistant *Klebsiella pneumoniae* infection on gut microbiota and host immunity: a case-control study. *Microbiology spectrum*, 14(1), e0297525.

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.

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

Schumacher SM, et al. (2025) PICRUST2 Analysis of Fecal Microbiome Associated With a Murine Model of Multiple Sclerosis. *FASEB bioAdvances*, 7(7), e70029.

Cui P, et al. (2025) Fungal community composition and function in different Chinese post-fermented teas. *Scientific reports*, 15(1), 8514.

Fan F, et al. (2025) Longitudinal dynamics of plasma bile acids and their associations with physiological parameters and fecal microbiome during the transition period in dairy cows. *Animal bioscience*, 38(6), 1194.

Li L, et al. (2025) Effects of supplementing bile acids on the production performance, fatty acid and bile acid composition, and gut microbiota in transition dairy cows. *Journal of animal science and biotechnology*, 16(1), 83.

Song J, et al. (2025) Efficiency, Microbial Communities, and Nitrogen Metabolism in Denitrification Biological Filter: Insights into Varied Pore Ceramsite Media. *Microorganisms*, 13(6).

- Wei Y, et al. (2025) Lipid metabolism and microbial regulation analyses provide insights into the energy-saving strategies of hibernating snakes. *Communications biology*, 8(1), 45.
- Sawada K, et al. (2025) Microbiome Landscape and Association with Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors: A SCRUM-Japan MONSTAR-SCREEN Study. *Cancer research communications*, 5(5), 857.
- Luo H, et al. (2025) Assessing the Risks of Potential Pathogens and Antibiotic Resistance Genes Among Heterogeneous Habitats in a Temperate Estuary Wetland: a Meta-analysis. *Microbial ecology*, 87(1), 172.
- Li S, et al. (2025) Microbial changing patterns across lateral and vertical horizons in recently formed permafrost after the outburst of Zonag Lake, Tibetan Plateau. *FEMS microbiology ecology*, 101(2).
- Miralles-Lorenzo J, et al. (2025) Environmental Gradients and Conservation Status Determine the Structure and Carbon-Related Metabolic Potential of the Prokaryotic Communities of Mediterranean Inland Saline Shallow Lakes. *Ecology and evolution*, 15(5), e71286.
- Yang N, et al. (2025) Bacterial colonization contributes to pathological scar formation via the regulation of inflammatory response. *Journal of translational medicine*, 23(1), 569.
- Choi Y, et al. (2025) Evaluation of kefir consumption on gut microbial diversity in a healthy young population using full-length 16S rRNA sequencing. *Frontiers in microbiology*, 16, 1587831.
- Yang H, et al. (2025) Diversity and Function of Strawberry Endophytic Bacterial Communities Associated with Host Genotype and Niche. *Current microbiology*, 82(6), 244.
- Li H, et al. (2025) The gut microbiota features and the application value in predicting recurrent risks for gallstone patients who underwent laparoscopic cholecystectomy. *mSystems*, 10(8), e0176024.
- Wagner S, et al. (2025) Absolute abundance calculation enhances the significance of microbiome data in antibiotic treatment studies. *Frontiers in microbiology*, 16, 1481197.
- Shin J, et al. (2025) Modulation of Gut Microbiota by Red Ginseng Extract Powder and Dietary Fiber in Obese Mice: Identification of Key Microbial Candidates. *Journal of microbiology and biotechnology*, 35, e2506016.
- Xu B, et al. (2025) Gut microbiota-derived short-chain fatty acids promote follicular maturation via gWAT-ovary axis in mammals. *Microbiome*, 13(1), 220.