

Resource Summary Report

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Pplacer

RRID:SCR_004737

Type: Tool

Proper Citation

Pplacer (RRID:SCR_004737)

Resource Information

URL: <http://matsen.fhcrc.org/pplacer/>

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Description: Software that places query sequences on a fixed reference phylogenetic tree to maximize phylogenetic likelihood or posterior probability according to a reference alignment. Pplacer is designed to be fast, to give useful information about uncertainty, and to offer advanced visualization and downstream analysis.

Abbreviations: Pplacer

Synonyms: pplacer: phylogenetic placement and downstream analysis

Resource Type: software resource

Defining Citation: [PMID:21034504](#)

Keywords: classification, phylogenetic classification

Resource Name: Pplacer

Resource ID: SCR_004737

Alternate IDs: OMICS_01462

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260815T182252+0000

Ratings and Alerts

No rating or validation information has been found for Pplacer.

No alerts have been found for Pplacer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Hsouna J, et al. (2025) Bradyrhizobium tunisiense sp. nov., a novel rhizobial species isolated from Acacia saligna nodules. International journal of systematic and evolutionary microbiology, 75(6).

Ramírez-Arenas PJ, et al. (2024) Highly diverse-Low abundance methanogenic communities in hypersaline microbial mats of Guerrero Negro B.C.S., assessed through microcosm experiments. PloS one, 19(10), e0303004.

Salgado JFM, et al. (2024) Unveiling lignocellulolytic potential: a genomic exploration of bacterial lineages within the termite gut. Microbiome, 12(1), 201.

Tandon K, et al. (2022) Genomic view of the diversity and functional role of archaea and bacteria in the skeleton of the reef-building corals Porites lutea and Isopora palifera. GigaScience, 12.

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. eLife, 11.

Lee JA, et al. (2022) Aerobic Methoxydotrophy: Growth on Methoxylated Aromatic Compounds by Methylobacteriaceae. Frontiers in microbiology, 13, 849573.

Martin K, et al. (2021) The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature communications, 12(1), 5483.

Kurth D, et al. (2021) Carbon fixation and rhodopsin systems in microbial mats from hypersaline lakes Brava and Tebenquiche, Salar de Atacama, Chile. PloS one, 16(2), e0246656.

Neal AL, et al. (2021) Microbiome Aggregated Traits and Assembly Are More Sensitive to Soil Management than Diversity. mSystems, 6(3), e0105620.

Atherton S, et al. (2020) Biodiversity between sand grains: Meiofauna composition across southern and western Sweden assessed by metabarcoding. Biodiversity data journal, 8, e51813.

Bremges A, et al. (2020) CAMITAX: Taxon labels for microbial genomes. GigaScience, 9(1).

Philips A, et al. (2020) Analysis of oral microbiome from fossil human remains revealed the significant differences in virulence factors of modern and ancient Tannerella forsythia. BMC genomics, 21(1), 402.

Prodinger F, et al. (2020) An Optimized Metabarcoding Method for Mimiviridae. *Microorganisms*, 8(4).

Abdel-Gadir A, et al. (2019) Microbiota therapy acts via a regulatory T cell MyD88/ROR γ t pathway to suppress food allergy. *Nature medicine*, 25(7), 1164.

van der Veer C, et al. (2019) Effects of an over-the-counter lactic-acid containing intra-vaginal douching product on the vaginal microbiota. *BMC microbiology*, 19(1), 168.

Xu J, et al. (2019) Mercury methylating microbial communities of boreal forest soils. *Scientific reports*, 9(1), 518.

Barbera P, et al. (2019) EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. *Systematic biology*, 68(2), 365.

Krausfeldt LE, et al. (2019) Insight Into the Molecular Mechanisms for Microcystin Biodegradation in Lake Erie and Lake Taihu. *Frontiers in microbiology*, 10, 2741.

Beinart RA, et al. (2019) The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. *Frontiers in microbiology*, 10, 1818.

Mihara T, et al. (2018) Taxon Richness of "Megaviridae" Exceeds those of Bacteria and Archaea in the Ocean. *Microbes and environments*, 33(2), 162.