

Resource Summary Report

Generated by [NIF](#) on Apr 20, 2025

PrimerProspector

RRID:SCR_012136

Type: Tool

Proper Citation

PrimerProspector (RRID:SCR_012136)

Resource Information

URL: <http://pprospector.sourceforge.net/>

Proper Citation: PrimerProspector (RRID:SCR_012136)

Description: A pipeline of software programs to design and analyze PCR primers. It is built in Python using the open-source PyCogent toolkit.

Resource Type: software resource

Defining Citation: [PMID:21349862](#)

Keywords: standalone software, python

Funding:

Resource Name: PrimerProspector

Resource ID: SCR_012136

Alternate IDs: OMICS_05884

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014607+0000

Ratings and Alerts

No rating or validation information has been found for PrimerProspector.

No alerts have been found for PrimerProspector.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Arnolds KL, et al. (2023) Disruption of Genes Encoding Putative Zwitterionic Capsular Polysaccharides of Diverse Intestinal Bacteroides Reduces the Induction of Host Anti-Inflammatory Factors. *Microbial ecology*, 85(4), 1620.

Yang W, et al. (2021) Tumor-Associated Microbiota in Esophageal Squamous Cell Carcinoma. *Frontiers in cell and developmental biology*, 9, 641270.

Singleton CM, et al. (2021) Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. *Nature communications*, 12(1), 2009.

Wasimuddin , et al. (2020) Evaluation of primer pairs for microbiome profiling from soils to humans within the One Health framework. *Molecular ecology resources*, 20(6), 1558.

Dueholm MS, et al. (2020) Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax). *mBio*, 11(5).

Grimshaw SG, et al. (2019) The diversity and abundance of fungi and bacteria on the healthy and dandruff affected human scalp. *PloS one*, 14(12), e0225796.

Ferreira RM, et al. (2018) Gastric microbial community profiling reveals a dysbiotic cancer-associated microbiota. *Gut*, 67(2), 226.

Nash AK, et al. (2017) The gut mycobiome of the Human Microbiome Project healthy cohort. *Microbiome*, 5(1), 153.

Thijs S, et al. (2017) Comparative Evaluation of Four Bacteria-Specific Primer Pairs for 16S rRNA Gene Surveys. *Frontiers in microbiology*, 8, 494.

Zou B, et al. (2017) MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. *PloS one*, 12(3), e0174609.

Adams SE, et al. (2017) A randomised clinical study to determine the effect of a toothpaste containing enzymes and proteins on plaque oral microbiome ecology. *Scientific reports*, 7, 43344.

Williamson CHD, et al. (2017) Differentiating Botulinum Neurotoxin-Producing Clostridia with

a Simple, Multiplex PCR Assay. *Applied and environmental microbiology*, 83(18).

Usyk M, et al. (2017) Novel ITS1 Fungal Primers for Characterization of the Mycobiome. *mSphere*, 2(6).

Belda E, et al. (2017) Preferential suppression of *Anopheles gambiae* host sequences allows detection of the mosquito eukaryotic microbiome. *Scientific reports*, 7(1), 3241.

Beckers B, et al. (2016) Performance of 16s rDNA Primer Pairs in the Study of Rhizosphere and Endosphere Bacterial Microbiomes in Metabarcoding Studies. *Frontiers in microbiology*, 7, 650.

Walker FM, et al. (2016) Species From Feces: Order-Wide Identification of Chiroptera From Guano and Other Non-Invasive Genetic Samples. *PloS one*, 11(9), e0162342.

Taylor DL, et al. (2016) Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. *Applied and environmental microbiology*, 82(24), 7217.

Kopylova E, et al. (2016) Open-Source Sequence Clustering Methods Improve the State Of the Art. *mSystems*, 1(1).

Ziesemer KA, et al. (2015) Intrinsic challenges in ancient microbiome reconstruction using 16S rRNA gene amplification. *Scientific reports*, 5, 16498.

Narrowe AB, et al. (2015) Perturbation and restoration of the fathead minnow gut microbiome after low-level triclosan exposure. *Microbiome*, 3, 6.