

Resource Summary Report

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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

Resource Name: PrimerProspector

Resource ID: SCR_012136

Alternate IDs: OMICS_05884

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260801T190434+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 25 mentions in open access literature.

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

Abdelkader A, et al. (2025) metaGEENOME: an integrated framework for differential abundance analysis of microbiome data in cross-sectional and longitudinal studies. BMC bioinformatics, 26(1), 189.

Furuta Y, et al. (2025) MitoCOMON: whole mitochondrial DNA sequencing by primer design and long overlapping amplicon assembly. BMC genomics, 26(1), 787.

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.

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

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

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

Williamson CHD, et al. (2017) Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. Applied and environmental microbiology, 83(18).

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.

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).