MFEprimer

RRID:SCR_003066
Type: Tool

Proper Citation

MFEprimer (RRID:SCR_003066)

Resource Information

URL: https://github.com/quwubin/MFEprimer/

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Description: A fast thermodynamics-based software program for checking PCR primer specificity against genomic DNA and mRNA/cDNA sequence databases.

Synonyms: MFEprimer-2.0

Resource Type: software resource

Defining Citation: PMID:22689644

Keywords: standalone software, bio.tools

Funding:

Availability: Free for academic use, Free for non-profit use, Free for personal use, Commercial use requires license

Resource Name: MFEprimer

Resource ID: SCR_003066

Alternate IDs: biotools:mfeprimer-2.0, OMICS_02355

Alternate URLs: https://bio.tools/mfeprimer-2.0

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250420T014134+0000

Ratings and Alerts

No rating or validation information has been found for MFEprimer.

No alerts have been found for MFEprimer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Tang C, et al. (2024) High-throughput nanopore targeted sequencing for efficient drug resistance assay of Mycobacterium tuberculosis. Frontiers in microbiology, 15, 1331656.

Zhang Z, et al. (2024) MiPRIME: an integrated and intelligent platform for mining primer and probe sequences of microbial species. Bioinformatics (Oxford, England), 40(7).

Caballero Méndez A, et al. (2024) Development and performance evaluation of a qPCR-based assay for the fully automated detection of group B Streptococcus (GBS) on the Panther Fusion Open Access system. Microbiology spectrum, 12(6), e0005724.

Kandel S, et al. (2023) Genomic Surveillance of SARS-CoV-2 Using Long-Range PCR Primers. bioRxiv : the preprint server for biology.

Leal-Calvo T, et al. (2021) A new paradigm for leprosy diagnosis based on host gene expression. PLoS pathogens, 17(10), e1009972.

O'Callaghan JL, et al. (2021) Limitations of 16S rRNA Gene Sequencing to Characterize Lactobacillus Species in the Upper Genital Tract. Frontiers in cell and developmental biology, 9, 641921.

Dutra HLC, et al. (2021) The impact of artificial selection for Wolbachia-mediated dengue virus blocking on phage WO. PLoS neglected tropical diseases, 15(7), e0009637.

Carneiro Dutra HL, et al. (2020) Wolbachia and Sirtuin-4 interaction is associated with alterations in host glucose metabolism and bacterial titer. PLoS pathogens, 16(10), e1008996.

Kawahara Y, et al. (2020) Mikan Genome Database (MiGD): integrated database of genome annotation, genomic diversity, and CAPS marker information for mandarin molecular breeding. Breeding science, 70(2), 200.

Mahapatra S, et al. (2020) Character-based identification system of scombrids from Indian waters for authentication and conservation purposes. Mitochondrial DNA. Part B, Resources, 5(3), 3221.

Johnston AD, et al. (2019) PrimerROC: accurate condition-independent dimer prediction using ROC analysis. Scientific reports, 9(1), 209.

Descalsota GIL, et al. (2018) Genome-Wide Association Mapping in a Rice MAGIC Plus Population Detects QTLs and Genes Useful for Biofortification. Frontiers in plant science, 9, 1347.

Collins RA, et al. (2018) Persistence of environmental DNA in marine systems. Communications biology, 1, 185.

Youngblut ND, et al. (2018) SIPSim: A Modeling Toolkit to Predict Accuracy and Aid Design of DNA-SIP Experiments. Frontiers in microbiology, 9, 570.

Perron GG, et al. (2015) Functional characterization of bacteria isolated from ancient arctic soil exposes diverse resistance mechanisms to modern antibiotics. PloS one, 10(3), e0069533.