Resource Summary Report

Generated by dkNET on May 21, 2025

MPprimer

RRID:SCR_003063
Type: Tool

Proper Citation

MPprimer (RRID:SCR_003063)

Resource Information

URL: https://code.google.com/p/mpprimer/

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Description: A software program for reliable multiplex PCR primer design. It employs the widely used primer design program Primer3 and the primer specificity evaluation program MFEprimer to design and evaluate the candidate primers based on genomic or transcript DNA database, followed by careful examination to avoid primer dimerization. The graph-expanding algorithm derived from the greedy algorithm was used to determine the optimal primer set combinations (PSCs) for multiplex PCR. In addition, it provides a virtual electrophotogram to help users choose the best PSC. It is a valuable tool for designing specific, no dimer formation and amplicons size constrained PSCs to improve the multiplex PCR experiments.

Synonyms: MPprimer: a program for reliable multiplex PCR primer design

Resource Type: data analysis service, service resource, software resource, analysis service resource, production service resource

Defining Citation: PMID:20298595

Keywords: standalone software, pcr, multiplexpcr, mfeprimer, primer3, specificity, dimer, primer design

Funding:

Availability: GNU General Public License, v3

Resource Name: MPprimer

Resource ID: SCR_003063

Alternate IDs: OMICS_02364

Alternate URLs: http://biocompute.bmi.ac.cn/MPprimer/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250521T060908+0000

Ratings and Alerts

No rating or validation information has been found for MPprimer.

No alerts have been found for MPprimer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Miringu G, et al. (2024) Development of two multiplex PCR assays for rapid detection of eleven Gram-negative bacteria in children with septicemia. Tropical medicine and health, 52(1), 40.

Gupta S, et al. (2022) RNA sequencing-based screen for reactivation of silenced alleles of autosomal genes. G3 (Bethesda, Md.), 12(2).

Amenga-Etego LN, et al. (2021) Temporal evolution of sulfadoxine-pyrimethamine resistance genotypes and genetic diversity in response to a decade of increased interventions against Plasmodium falciparum in northern Ghana. Malaria journal, 20(1), 152.

Klima CL, et al. (2020) Multidrug Resistance in Pasteurellaceae Associated With Bovine Respiratory Disease Mortalities in North America From 2011 to 2016. Frontiers in microbiology, 11, 606438.

?erenak A, et al. (2019) New Male Specific Markers for Hop and Application in Breeding Program. Scientific reports, 9(1), 14223.

Gulla S, et al. (2018) Multilocus Variable-Number Tandem-Repeat Analysis of Yersinia ruckeri Confirms the Existence of Host Specificity, Geographic Endemism, and

Anthropogenic Dissemination of Virulent Clones. Applied and environmental microbiology, 84(16).

Ghirardini E, et al. (2018) Expression of functional inhibitory neurotransmitter transporters GlyT1, GAT-1, and GAT-3 by astrocytes of inferior colliculus and hippocampus. Molecular brain, 11(1), 4.

Cardamone G, et al. (2018) Genetic Association and Altered Gene Expression of CYBB in Multiple Sclerosis Patients. Biomedicines, 6(4).

Lanikova L, et al. (2017) Evolutionary selected Tibetan variants of HIF pathway and risk of lung cancer. Oncotarget, 8(7), 11739.

Contreras R, et al. (2017) Neutral molecular markers support common origin of aluminium tolerance in three congeneric grass species growing in acidic soils. AoB PLANTS, 9(6), plx060.

Gremel G, et al. (2016) Distinct subclonal tumour responses to therapy revealed by circulating cell-free DNA. Annals of oncology : official journal of the European Society for Medical Oncology, 27(10), 1959.

Mercier R, et al. (2014) General principles for the formation and proliferation of a wall-free (L-form) state in bacteria. eLife, 3.