Resource Summary Report

Generated by RRID on Apr 18, 2025

e-PCR

RRID:SCR_003082
Type: Tool

Proper Citation

e-PCR (RRID:SCR_003082)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/tools/epcr/

Proper Citation: e-PCR (RRID:SCR_003082)

Description: Web tool that identifies sequence tagged sites (STSs) within DNA sequences. Using e-PCR, you can search for sub-sequences that closely match the PCR primers and have the correct order, orientation, and spacing. The software may also be downloaded to run locally.

Abbreviations: e-PCR

Synonyms: Electronic PCR, Electronic PCR (e-PCR)

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

Defining Citation: PMID:15215361, PMID:9149949

Keywords: sequence tagged site, dna sequence, reverse, forward

Funding:

Resource Name: e-PCR

Resource ID: SCR_003082

Alternate IDs: OMICS_02345

Alternate URLs: https://sources.debian.org/src/ncbi-epcr/

Old URLs: http://www.ncbi.nlm.nih.gov/sutils/e-pcr

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250418T055011+0000

Ratings and Alerts

No rating or validation information has been found for e-PCR.

No alerts have been found for e-PCR.

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 RRID.

Zhao C, et al. (2017) Genome-Wide Discovery of Microsatellite Markers from Diploid Progenitor Species, Arachis duranensis and A. ipaensis, and Their Application in Cultivated Peanut (A. hypogaea). Frontiers in plant science, 8, 1209.

Landínez-García RM, et al. (2016) Development and characterization of 24 polymorphic microsatellite loci for the freshwater fish Ichthyoelephas longirostris (Characiformes: Prochilodontidae). PeerJ, 4, e2419.

Seubwai W, et al. (2016) Inhibition of NF-?B Activity Enhances Sensitivity to Anticancer Drugs in Cholangiocarcinoma Cells. Oncology research, 23(1-2), 21.

Xiao Y, et al. (2016) Genome-Wide Identification and Transferability of Microsatellite Markers between Palmae Species. Frontiers in plant science, 7, 1578.

Kamphuis LG, et al. (2015) Transcriptome sequencing of different narrow-leafed lupin tissue types provides a comprehensive uni-gene assembly and extensive gene-based molecular markers. Plant biotechnology journal, 13(1), 14.

Niihama M, et al. (2015) PCR-based INDEL markers co-dominant between Oryza sativa, japonica cultivars and closely-related wild Oryza species. Breeding science, 65(4), 357.

Han B, et al. (2015) Genome-Wide Analysis of Microsatellite Markers Based on Sequenced Database in Chinese Spring Wheat (Triticum aestivum L.). PloS one, 10(11), e0141540.

Yao J, et al. (2014) Efficient bi-allelic gene knockout and site-specific knock-in mediated by TALENs in pigs. Scientific reports, 4, 6926.

Song Q, et al. (2013) Development and evaluation of SoySNP50K, a high-density genotyping array for soybean. PloS one, 8(1), e54985.

Hyten DL, et al. (2010) High-throughput SNP discovery and assay development in common bean. BMC genomics, 11, 475.

O'Dushlaine CT, et al. (2008) Marked variation in predicted and observed variability of tandem repeat loci across the human genome. BMC genomics, 9, 175.

Wright FA, et al. (2001) A draft annotation and overview of the human genome. Genome biology, 2(7), RESEARCH0025.