

Resource Summary Report

Generated by T1D on Aug 2, 2026

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/>

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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: data analysis service, service resource, production service resource, analysis service resource

Defining Citation: [PMID:15215361](#), [PMID:9149949](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260801T190909+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 [T1D](#) .

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.

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

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- κ B Activity Enhances Sensitivity to Anticancer Drugs in Cholangiocarcinoma Cells. *Oncology research*, 23(1-2), 21.

Kamphuis LG, et al. (2015) Transcriptome sequencing of different narrow-leaved 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.