

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

In-Silico PCR

RRID:SCR_003089

Type: Tool

Proper Citation

In-Silico PCR (RRID:SCR_003089)

Resource Information

URL: <http://genome.ucsc.edu/cgi-bin/hgPcr?command=start>

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Description: Tool that searches a sequence database with a pair of PCR primers, using an indexing strategy for fast performance. When successful, the search returns a sequence output file in fasta format containing all sequence in the database that lie between and include the primer pair. The fasta header describes the region in the database and the primers. The fasta body is capitalized in areas where the primer sequence matches the database sequence and in lower-case elsewhere. Sources and executables to run batch jobs on your own server are available free for academic, personal, and non-profit purposes. Non-exclusive commercial licenses are also available.

Abbreviations: In-Silico PCR

Synonyms: UCSC In-Silico PCR

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

Keywords: pcr primer, polymerase chain reaction, primer

Availability: Free, Available for download, Freely available

Resource Name: In-Silico PCR

Resource ID: SCR_003089

Alternate IDs: OMICS_02344

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132457+0000

Ratings and Alerts

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

No alerts have been found for In-Silico PCR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Siegl D, et al. (2023) A PCR protocol to establish standards for routine mycoplasma testing that by design detects over ninety percent of all known mycoplasma species. *iScience*, 26(5), 106724.

Ferreira de Oliveira JMP, et al. (2021) 3',4'-Dihydroxyflavonol Modulates the Cell Cycle in Cancer Cells: Implication as a Potential Combination Drug in Osteosarcoma. *Pharmaceuticals (Basel, Switzerland)*, 14(7).

Tsujita M, et al. (2020) Selective Correction of Genotype Yield by Probucol in HDL-Deficient Mice Propagation. *Journal of atherosclerosis and thrombosis*, 27(1), 25.

Valpione S, et al. (2019) Detection of circulating tumor DNA (ctDNA) by digital droplet polymerase chain reaction (dd-PCR) in liquid biopsies. *Methods in enzymology*, 629, 1.

Coutinho L, et al. (2017) Hesperetin-etoposide combinations induce cytotoxicity in U2OS cells: Implications on therapeutic developments for osteosarcoma. *DNA repair*, 50, 36.

Kalagara R, et al. (2016) Identification of stable reference genes for lipopolysaccharide-stimulated macrophage gene expression studies. *Biology methods & protocols*, 1(1), bpw005.

Mlynarski EE, et al. (2015) Copy-Number Variation of the Glucose Transporter Gene SLC2A3 and Congenital Heart Defects in the 22q11.2 Deletion Syndrome. *American journal of human genetics*, 96(5), 753.

Zhang JJ, et al. (2015) An Internal Reference Control Duplex Real-Time Polymerase Chain Reaction Assay for Detecting Bacterial Contamination in Blood Products. *PloS one*, 10(7), e0134743.

Lee W, et al. (2015) Genome-wide target site triplication of Alu elements in the human genome. *Gene*, 561(2), 283.

Ferreira de Oliveira JM, et al. (2014) Sulforaphane induces oxidative stress and death by p53-independent mechanism: implication of impaired glutathione recycling. *PloS one*, 9(3), e92980.

Dumas LJ, et al. (2012) DUF1220-domain copy number implicated in human brain-size pathology and evolution. *American journal of human genetics*, 91(3), 444.

Erlich RL, et al. (2011) Next-generation sequencing for HLA typing of class I loci. *BMC genomics*, 12, 42.

Xu X, et al. (2011) Next-generation DNA sequencing-based assay for measuring allelic expression imbalance (AEI) of candidate neuropsychiatric disorder genes in human brain. *BMC genomics*, 12, 518.

Lee SH, et al. (2011) Lack of association between response of OROS-methylphenidate and norepinephrine transporter (SLC6A2) polymorphism in Korean ADHD. *Psychiatry research*, 186(2-3), 338.

Pole JC, et al. (2011) Single-molecule analysis of genome rearrangements in cancer. *Nucleic acids research*, 39(13), e85.

Radeva MY, et al. (2010) Defensin alpha 6 (DEFA 6) overexpression threshold of over 60 fold can distinguish between adenoma and fully blown colon carcinoma in individual patients. *BMC cancer*, 10, 588.

Cui W, et al. (2007) qPrimerDepot: a primer database for quantitative real time PCR. *Nucleic acids research*, 35(Database issue), D805.