

Resource Summary Report

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BiSearch: Primer Design and Search Tool

RRID:SCR_002980

Type: Tool

Proper Citation

BiSearch: Primer Design and Search Tool (RRID:SCR_002980)

Resource Information

URL: <http://bisearch.enzim.hu>

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Description: BiSearch is a primer-design algorithm for DNA sequences. It may be used for both bisulfite converted as well as for original not modified sequences. You can search various genomes with the designed primers to avoid non-specific PCR products by our fast ePCR method. This is especially recommended when primers are designed to amplify the highly redundant bisulfite treated sequences. It has the unique property of analyzing the primer pairs for mispriming sites on the bisulfite-treated genome and determines potential non-specific amplification products with a new search algorithm. The options of primer-design and analysis for mispriming sites can be used sequentially or separately, both on bisulfite-treated and untreated sequences. In silico and in vitro tests of the software suggest that new PCR strategies may increase the efficiency of the amplification.

Abbreviations: BiSearch

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

Defining Citation: [PMID:17022803](#), [PMID:15653630](#)

Keywords: dna, sequence, primer, design, algorithm, analysis, priming, bisulfite, genome, amplification, in vitro, in silico, amplification, epcr, cytosines

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Resource Name: BiSearch: Primer Design and Search Tool

Resource ID: SCR_002980

Alternate IDs: nif-0000-30170

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260821T042559+0000

Ratings and Alerts

No rating or validation information has been found for BiSearch: Primer Design and Search Tool.

No alerts have been found for BiSearch: Primer Design and Search Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Yang SB, et al. (2025) Epigenetic aging signatures and age prediction in human skeletal muscle. Aging, 17(11), 2809.

Weber S, et al. (2025) Salivary oxytocin and amygdalar alterations in functional neurological disorders. Brain communications, 7(1), fcae455.

McGrail K, et al. (2025) Transcriptional reprogramming triggered by neonatal UV radiation or Lkb1 loss prevents BRAFV600E-induced growth arrest in melanocytes. Oncogene, 44(21), 1592.

Rahmani B, et al. (2025) Investigation methylation status of tumor suppressor gene NR4A1 and NR4A3 and frequency of rs1569686 polymorphism of DNMT3B gene in patients with acute myeloid leukemia. Molecular biology research communications, 14(2), 149.

Peng D, et al. (2025) Hormonal dynamics reveal a stimulatory role for secretoneurin in zebrafish ovulation. PNAS nexus, 4(4), pgaf097.

Abak N, et al. (2024) DNA Methylation Pattern and mRNA Expression Level of E-Cadherin and P16 Genes in Thrombotic Disorders. Clinical and applied thrombosis/hemostasis : official journal of the International Academy of Clinical and Applied Thrombosis/Hemostasis, 30, 10760296241300490.

Batdorj E, et al. (2023) Genetic variation in the Y chromosome and sex-biased DNA methylation in somatic cells in the mouse. Mammalian genome : official journal of the International Mammalian Genome Society, 34(1), 44.

Marie-Claire C, et al. (2023) Methylomic biomarkers of lithium response in bipolar disorder: a clinical utility study. *International journal of bipolar disorders*, 11(1), 16.

Kouter K, et al. (2023) Difference in Methylation and Expression of Brain-Derived Neurotrophic Factor in Alzheimer's Disease and Mild Cognitive Impairment. *Biomedicines*, 11(2).

Stepanyan A, et al. (2023) Long-term environmental metal exposure is associated with hypomethylation of CpG sites in NFKB1 and other genes related to oncogenesis. *Clinical epigenetics*, 15(1), 126.

Poppova L, et al. (2022) Memory B-cell like chronic lymphocytic leukaemia is associated with specific methylation profile of WNT5A promoter and undetectable expression of WNT5A gene. *Epigenetics*, 17(12), 1628.

Nguyen E, et al. (2022) hTERT DNA Methylation Analysis Identifies a Biomarker for Retinoic Acid-Induced hTERT Repression in Breast Cancer Cell Lines. *Biomedicines*, 10(3).

Vermeirssen V, et al. (2022) Whole transcriptome profiling of liquid biopsies from tumour xenografted mouse models enables specific monitoring of tumour-derived extracellular RNA. *NAR cancer*, 4(4), zcac037.

Woźniak A, et al. (2021) Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. *Aging*, 13(5), 6459.

Redlich R, et al. (2020) The role of BDNF methylation and Val66 Met in amygdala reactivity during emotion processing. *Human brain mapping*, 41(3), 594.

Armenta-Castro E, et al. (2020) Histone H3K9 and H3K14 acetylation at the promoter of the LGALS9 gene is associated with mRNA levels in cervical cancer cells. *FEBS open bio*, 10(11), 2305.

Jørgensen N, et al. (2020) Characterization of HLA-G Regulation and HLA Expression in Breast Cancer and Malignant Melanoma Cell Lines upon IFN- γ Stimulation and Inhibition of DNA Methylation. *International journal of molecular sciences*, 21(12).

Galamb O, et al. (2020) Promoter Hypomethylation and Increased Expression of the Long Non-coding RNA LINC00152 Support Colorectal Carcinogenesis. *Pathology oncology research : POR*, 26(4), 2209.

Klobužar T, et al. (2020) IMPLICON: an ultra-deep sequencing method to uncover DNA methylation at imprinted regions. *Nucleic acids research*, 48(16), e92.

Fullár A, et al. (2020) Two ways of epigenetic silencing of TFPI2 in cervical cancer. *PloS one*, 15(6), e0234873.