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, production service resource, data analysis service, 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: 20250426T055605+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 48 mentions in open access literature.

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

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

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.

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.

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.

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.

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.

Wo?niak 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-? Stimulation and Inhibition of DNA Methylation. International journal of molecular sciences, 21(12).

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Moon Y, et al. (2020) Hypoxia regulates allele-specific histone modification of the imprinted H19 gene. Biochimica et biophysica acta. Gene regulatory mechanisms, 1863(11), 194643.

Klobu?ar 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.

Šestáková Š, et al. (2019) DNA Methylation Validation Methods: a Coherent Review with Practical Comparison. Biological procedures online, 21, 19.

Roeh S, et al. (2018) HAM-TBS: high-accuracy methylation measurements via targeted bisulfite sequencing. Epigenetics & chromatin, 11(1), 39.

Kamstra JH, et al. (2018) Ionizing radiation induces transgenerational effects of DNA methylation in zebrafish. Scientific reports, 8(1), 15373.

Vidaki A, et al. (2018) Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. Genes, 9(5).

Renard M, et al. (2018) Expressed repetitive elements are broadly applicable reference targets for normalization of reverse transcription-qPCR data in mice. Scientific reports, 8(1), 7642.