Resource Summary Report

Generated by NIF on Apr 27, 2025

Basic OligoNucleotide Design

RRID:SCR_004492
Type: Tool

Proper Citation

Basic OligoNucleotide Design (RRID:SCR_004492)

Resource Information

URL: http://www.csd.uwo.ca/~ilie/BOND/

Proper Citation: Basic OligoNucleotide Design (RRID:SCR_004492)

Description: Software program to compute highly specific DNA oligonucleotides, for all the genes that admit unique probes, while running orders of magnitude faster than the existing programs.

Abbreviations: BOND

Synonyms: BOND: Basic OligoNucleotide Design

Resource Type: software resource

Defining Citation: PMID:23444904

Keywords: dna, oligonucleotide, design, oligonucleotide design

Funding:

Resource Name: Basic OligoNucleotide Design

Resource ID: SCR_004492

Alternate IDs: OMICS_00827

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250420T014224+0000

Ratings and Alerts

No rating or validation information has been found for Basic OligoNucleotide Design.

No alerts have been found for Basic OligoNucleotide Design.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Paczkowska J, et al. (2024) Cancer-specific innate and adaptive immune rewiring drives resistance to PD-1 blockade in classic Hodgkin lymphoma. Nature communications, 15(1), 10740.

Kumarasamy V, et al. (2024) The Extracellular Niche and Tumor Microenvironment Enhance KRAS Inhibitor Efficacy in Pancreatic Cancer. Cancer research, 84(7), 1115.

Ni J, et al. (2022) p16INK4A-deficiency predicts response to combined HER2 and CDK4/6 inhibition in HER2+ breast cancer brain metastases. Nature communications, 13(1), 1473.

Fix RL, et al. (2022) Improving Black adolescent daughter-single mother relationships during the COVID-19 pandemic in the U.S.: A brief exploration of participant experiences. Maternal and child health journal, 26(6), 1181.

Sabat-Po?piech D, et al. (2022) Aggressive uveal melanoma displays a high degree of centrosome amplification, opening the door to therapeutic intervention. The journal of pathology. Clinical research, 8(4), 383.

Gong G, et al. (2022) The regulation mechanism of different hair types in inner Mongolia cashmere goat based on PI3K-AKT pathway and FGF21. Journal of animal science, 100(11).

Javaid MK, et al. (2021) Patients' priorities and expectations on an EU registry for rare bone and mineral conditions. Orphanet journal of rare diseases, 16(1), 463.

Hatswell A, et al. (2020) Summarising salient information on historical controls: A structured assessment of validity and comparability across studies. Clinical trials (London, England), 17(6), 607.

Jin J, et al. (2017) Integrated transcriptomics and metabolomics analysis to characterize cold stress responses in Nicotiana tabacum. BMC genomics, 18(1), 496.

Zhong D, et al. (2014) Identification of Differentially Expressed Gene after Femoral Fracture via Microarray Profiling. International journal of genomics, 2014, 208751.

Ilie L, et al. (2013) BOND: Basic OligoNucleotide Design. BMC bioinformatics, 14, 69.

Peng CH, et al. (2012) Feature Identification of Compensatory Gene Pairs without Sequence Homology in Yeast. Comparative and functional genomics, 2012, 653174.

Kuo HC, et al. (2011) Discovering amino acid patterns on binding sites in protein complexes. Bioinformation, 6(1), 10.

Kim J, et al. (2009) Finding motif pairs in the interactions between heterogeneous proteins via bootstrapping and boosting. BMC bioinformatics, 10 Suppl 1(Suppl 1), S57.

Das A, et al. (2008) Cytoprotective effects of melatonin on C6 astroglial cells exposed to glutamate excitotoxicity and oxidative stress. Journal of pineal research, 45(2), 117.

Razick S, et al. (2008) iRefIndex: a consolidated protein interaction database with provenance. BMC bioinformatics, 9, 405.