

Resource Summary Report

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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

Resource Name: Basic OligoNucleotide Design

Resource ID: SCR_004492

Alternate IDs: OMICS_00827

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260725T190551+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 17 mentions in open access literature.

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

Habib A, et al. (2025) Rapamycin rescues APC-mutated colon organoid differentiation. *Cancer gene therapy*, 32(9), 1008.

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.