

Resource Summary Report

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HYDEN

RRID:SCR_003126

Type: Tool

Proper Citation

HYDEN (RRID:SCR_003126)

Resource Information

URL: <http://acgt.cs.tau.ac.il/hyden/>

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Description: Software program for designing pairs of degenerate primers for a given set of DNA sequences. It works well for large input sets of genomic sequences (e.g., hundreds of sequences of length 1Kbp). It is a batch (i.e., command-line, as opposed to graphical interface) program, available for Windows XP (downloadable version) and Linux (upon request).

Abbreviations: HYDEN

Synonyms: HYDEN - A Software for Designing Degenerate Primers, Highly DEgeNerate primers

Resource Type: software resource

Defining Citation: [PMID:17951798](#)

Keywords: degenerate, primer, dna sequence, primer design, degenerate primer, windows, linux, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: HYDEN

Resource ID: SCR_003126

Alternate IDs: OMICS_02338, biotools:hyden

Alternate URLs: <https://bio.tools/hyden>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260815T182224+0000

Ratings and Alerts

No rating or validation information has been found for HYDEN.

No alerts have been found for HYDEN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Ibrahim Osman A, et al. (2025) Development of a highly degenerate primer-based molecular tool for detecting and classifying the four major classes of polyhydroxyalkanoate synthase (phaC) genes in bacteria. *Microbial cell factories*, 24(1), 205.

Rihtman B, et al. (2024) Coordinated transcriptional response to environmental stress by a *Synechococcus* virus. *The ISME journal*, 18(1).

Fang Y, et al. (2022) Chemokine CXCL10 regulates pain behaviors via PI3K-AKT signaling pathway in mice. *Neuropeptides*, 93, 102243.

Chukwuemeka PO, et al. (2020) In silico design and validation of a highly degenerate primer pair: a systematic approach. *Journal, genetic engineering & biotechnology*, 18(1), 72.

Takada T, et al. (2020) Dynamic analysis of human small intestinal microbiota after an ingestion of fermented milk by small-intestinal fluid perfusion using an endoscopic retrograde bowel insertion technique. *Gut microbes*, 11(6), 1662.

Nemoto W, et al. (2020) Effect of spinal angiotensin-converting enzyme 2 activation on the formalin-induced nociceptive response in mice. *European journal of pharmacology*, 872, 172950.

Berglund AK, et al. (2017) Nucleotide pools dictate the identity and frequency of ribonucleotide incorporation in mitochondrial DNA. *PLoS genetics*, 13(2), e1006628.

Lavezzo E, et al. (2016) Characterization of Intra-Type Variants of Oncogenic Human Papillomaviruses by Next-Generation Deep Sequencing of the E6/E7 Region. *Viruses*, 8(3), 79.

Lee SA, et al. (2016) Epigenetic profiling of human brain differential DNA methylation networks in schizophrenia. *BMC medical genomics*, 9(Suppl 3), 68.

Sauvage T, et al. (2016) A metabarcoding framework for facilitated survey of endolithic phototrophs with tufA. *BMC ecology*, 16, 8.

Bonilla-Rosso G, et al. (2016) Design and evaluation of primers targeting genes encoding NO-forming nitrite reductases: implications for ecological inference of denitrifying communities. *Scientific reports*, 6, 39208.

Olender T, et al. (2004) The canine olfactory subgenome. *Genomics*, 83(3), 361.