Resource Summary Report

Generated by NIF on May 19, 2025

COnsensus-DEgenerate Hybride Oligonucleotide Primers

RRID:SCR_002875
Type: Tool

Proper Citation

COnsensus-DEgenerate Hybride Oligonucleotide Primers (RRID:SCR_002875)

Resource Information

URL: http://blocks.fhcrc.org/blocks/codehop.html

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Description: This COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy has been implemented as a computer program that is accessible over the World-Wide Web and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences. This is a new primer design strategy for PCR amplification of unknown targets that are related to multiply-aligned protein sequences. Each primer consists of a short 3' degenerate core region and a longer 5' consensus clamp region. Only 3-4 highly conserved amino acid residues are necessary for design of the core, which is stabilized by the clamp during annealing to template molecules. During later rounds of amplification, the non-degenerate clamp permits stable annealing to product molecules. The researchers demonstrate the practical utility of this hybrid primer method by detection of diverse reverse transcriptase-like genes in a human genome, and by detection of C5 DNA methyltransferase homologs in various plant DNAs. In each case, amplified products were sufficiently pure to be cloned without gel fractionation. Sponsors: This work was supported in part by a grant from the M. J. Murdock Charitable Trust and by a grant from NIH. S. P. is a Howard Hughes Medical Institute Fellow of the Life Sciences Research Foundation.

Synonyms: CODEHOP

Resource Type: software application, service resource, production service resource, data analysis service, data analysis software, data processing software, analysis service resource, software resource

Keywords: fractionation, gel, 3', amplification, clone, dna, genome, homolog, human, hybrid, molecule, oligonucleotide, pcr, plant, primer, protein, sequence, transcriptase-methyltransferase

Funding:

Resource Name: COnsensus-DEgenerate Hybride Oligonucleotide Primers

Resource ID: SCR_002875

Alternate IDs: nif-0000-25557

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250519T204315+0000

Ratings and Alerts

No rating or validation information has been found for COnsensus-DEgenerate Hybride Oligonucleotide Primers.

No alerts have been found for COnsensus-DEgenerate Hybride Oligonucleotide Primers.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Wang X, et al. (2016) Differential regulation of taurine biosynthesis in rainbow trout and Japanese flounder. Scientific reports, 6, 21231.

Orell A, et al. (2013) Molecular characterization of copper and cadmium resistance determinants in the biomining thermoacidophilic archaeon Sulfolobus metallicus. Archaea (Vancouver, B.C.), 2013, 289236.

Zhu L, et al. (2012) Cloning and characterization of genes involved in nostoxanthin biosynthesis of Sphingomonas elodea ATCC 31461. PloS one, 7(4), e35099.

Lu B, et al. (2009) Expression and evolutionary divergence of the non-conventional olfactory receptor in four species of fig wasp associated with one species of fig. BMC evolutionary biology, 9, 43.

Harbott LK, et al. (2007) Androgen receptors in a cichlid fish, Astatotilapia burtoni: structure, localization, and expression levels. The Journal of comparative neurology, 504(1), 57.

Buckner FS, et al. (2003) Cloning and analysis of Trypanosoma cruzi lanosterol 14alpha-demethylase. Molecular and biochemical parasitology, 132(2), 75.

Sanchez D, et al. (2002) Molecular identification of Kvalpha subunits that contribute to the oxygen-sensitive K+ current of chemoreceptor cells of the rabbit carotid body. The Journal of physiology, 542(Pt 2), 369.

Buckner FS, et al. (2002) Cloning, heterologous expression, and substrate specificities of protein farnesyltransferases from Trypanosoma cruzi and Leishmania major. Molecular and biochemical parasitology, 122(2), 181.