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Design SYBR Green primers, TaqMan® probes, FRET probes and Molecular Beacons for real time QPCR

Highly Efficient Dual Labeled Probes

ATCGTATCA CONTING NGAGTCTCGA GATC

The built-in sophisticated algorithm designs optimal TagMan® probes, FRET probes or molecular beacons. It analyzes every possible oligo within the specified length range at every position of the entire template and, using statistical techniques, selects the best probe. Properties considered include all possible secondary structures, runs, repeats and Tm, calculated using nearest neighbor theory with SantaLucia values. Probes can be designed for predesigned SYBR Green primers, making it possible to upgrade from SYBR Green to any of the supported chemistries. You can even analyze properties of pre-designed assays. To check the specificity of the design, we have included the ability to BLAST search the probes.

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oth wild and mutant probes for SNP ng assays. The program identifies the

ations from GenBank annotations, or you r them manually. Control the design ers for specific experimental needs, or let Designer choose the best primer-probe the default parameters we have set

after considerable research. You can even choose probes from a list of alternate probes to meet specific experimental needs. The primers and probes are checked for cross homologies to prevent competition and to ensure high signal strength in a multiplex reaction. TaqMan® probes and molecular beacons can be designed for multiplex reactions as well.

Template Secondary

at the Mfold server. The

results are automatically

secondary structures. A

graphical depiction of the

template structures is made

available for your reference.

analyzed and primers are

designed avoiding significant

Beacon Designer automatically avoids secondary structures in

the template found by folding it

Structures

1.22214 Sequence Range Z Launch result page after search Cancel

Graphical Interface

Graphically display the location of the designed primers and probes on the sequence. Display all possible dimers, cross dimers, repeats and runs graphically.

Primer Secondary Structures				
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f Dimer Haimin Cross Dimer Run		Primer Secondary Structures		
Sense Self Dimer	Acc	ession Number: AF185802		
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3 GGACTGTACTCACA	#	Sense Runs	Loca	# of Bases
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1 111 111 1	2.	TACC AA TAACACTCATGTCAGG	5	2
31 GGACTGTACTCACAATAA	3.	TACCAAT <mark>AA</mark> CACTCATGTCAGG	8	2
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Anti-sense Self Dime	100		4	
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3' GGTACGTCCTCCAC	2.	CCTTCACCTCCTGCATGG	3	2
	3.	CCTTCACC TCCTGCATGG	7	2
	4.	CCTTCACCTCCTGCATGG	10	2
	5.	CCTTCACCTCCTGCATGG	17	2

Optimal Primer Design

Design PCR primers optimized for SYBR Green, TaqMan®, FRET or molecular beacon assays. Highly specific primers are designed to avoid significant h Beacon Designer BLAST sea sequences using private local public databases at NCBL It a

interprets the search results and then designs primers avoiding identified homologie The specificity of the design can be verified by BLAST searching the primers against any genomic database or the redundant sequence nr database available at NCBI. To enhance primer efficiency, template secondary structure identified by Mfold are

rch da	mologies. nes the atabases or omatically	F Search Range Begures length range From To 1/1965 239 2500 Lypole60 1000 2100							
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automatically avoided during primer design.

The primers designed for SYBR Green assay can be exported to TaqMan®, FRET or molecular beacon design modes to design compatible dual labeled probes.

Search type		
· Hyman Genome BLAST C Eukaryotic Genome	Open Sequence From Entrez	2
C Local Database BLAST C Microbial Genome Server Name/IP Address:	Accession(s) numbers AF363013 AB036365 X12528	
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genome I Launch II Ref RNA Build RNA	Advanced	
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Generate Attractive Reports

You can create an attractively formatted report for your assay design. The report helps visualize the positions of the primers and probes on the sequence. It shows the design parameters, the recommended primers and probes, with displays of their sequences and their properties. It is intended for use in record keeping and for sharing information with colleagues.

retrieve sequences from public databases. Just enter the accession or GI numbers and retrieve batches of sequences from Entrez directly into the program. Integrated BLAST search helps identify regions of significant homologies for choosing the best possible primer-probe set. X

Strong Web Integration Beacon Designer lets you

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Other bioinformatics tools from PREMIER Biosoft International

PGFD-N

publication

Macintosh

For fast. efficient design of specific oligos foi designing Whole genome arrays and Tiling arrays for SNP genotyping and expression studies for Windows and I inux

Arrav Designer designs efficient specific oligos for SNP genotyping, and expression microarrays, starting with a list of sequences or the whole genome sequence to study entire organisms effortlessly. The program interprets BLAST results to design specific oligos, and verifies them by reBLASTing against local or NCBI databases, including nr. Designing tiling arrays has never been so easy Avoiding repetitive regions, spot every base of a genomic sequence, to characterize regulatory elements, or to study epigenetic modifications, methylation patterns and protein binding sites.

PREMIER

Biosoft International ere for the mole

primer 5 ININ Δ comprehensive er design for Windows and Macintosh

Primer Premier 5 is a comprehensive primer design tool for PCR and multiplex experiments. Primer Premier is a multifunctional oligo design program for PCR and multiplex experiments with additional facilities like sequence translation and enzyme and motif analysis included. It is one of the most comprehensive primer design programs available and includes a multiple sequence alignment module to design primers for cross species, allele specific and pathogen detection.

SimVector is a web savvv Windows mVector 3 and Mac program for cloning simulation, drawing and sequence analysis. It transforms sequence An exceptional An exception tool for designing cloning experiments and drawing header annotations in GenBank or local files into fully illustrated vector maps. An intuitive cloning wizard steps you through protocols such as Gateway®, TA and restriction cloning to create fully annotated quality graphics for Windows and recombinant maps. Exceptional quality graphics help customize circular or linear maps and write curved text for publication via Adobe Illustrator or Microsoft Power Point. or as ready-to-host web pages.

Xpression Primer is a web sav 40 X Primer 3 Designing expression cloning experiments for Windows and Macintosh

Windows and Mac program with a Windows artu mac program besigning expression ORFs for expression cloning systems. It provides comprehensive support for popular systems such as Gateway®, BD In-Fusion™, epitope and TOPO® tools. The program is flexible enough to work with virtually any expression system of researcher's choice. Xpression Primer also designs optimal sequencing primers to verify the transcripts

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