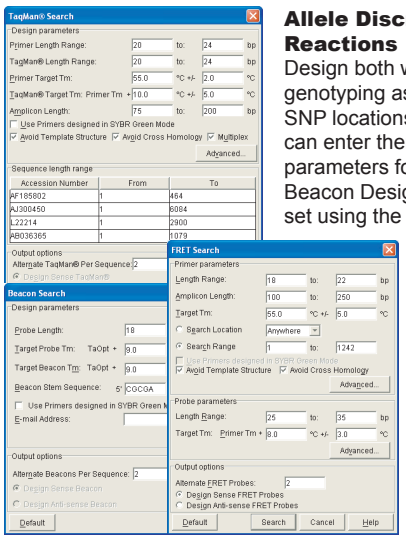
Beacon Designer 4

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

Highly Efficient Dual Labeled Probes

The built-in sophisticated algorithm designs optimal TaqMan® 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 pre-designed 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.

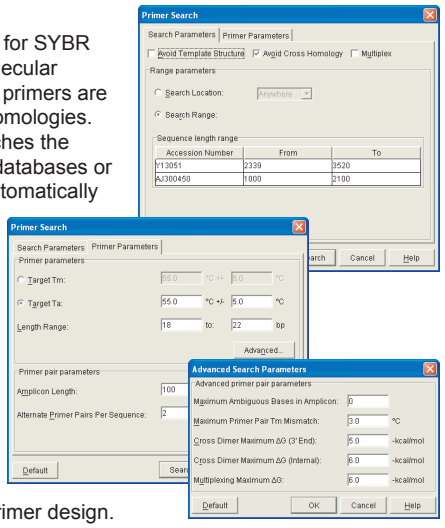


Allele Discrimination and Multiplex Reactions

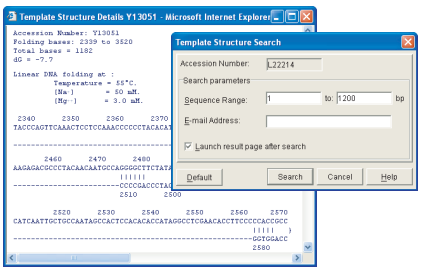
Design both wild and mutant probes for SNP genotyping assays. The program identifies the SNP locations from GenBank annotations, or you can enter them manually. Control the design parameters for specific experimental needs, or let Beacon Designer choose the best primer-probe set using the default parameters 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.

Optimal Primer Design

Design PCR primers optimized for SYBR Green, TaqMan®, FRET or molecular beacon assays. Highly specific primers are designed to avoid significant homologies. Beacon Designer BLAST searches the sequences using private local databases or public databases at NCBI. It automatically interprets the search results and then designs primers avoiding identified homologies. 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 structures identified by Mfold are automatically avoided during primer design.

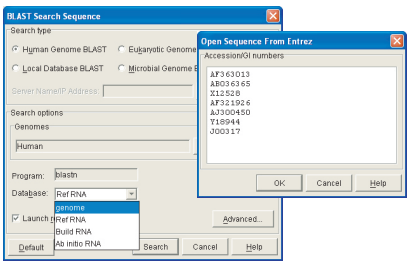


The primers designed for SYBR Green assay can be exported to TaqMan®, FRET or molecular beacon design modes to design compatible dual labeled probes.



Template Secondary Structures

Beacon Designer automatically avoids secondary structures in the template found by folding it at the Mfold server. The results are automatically analyzed and primers are designed avoiding significant secondary structures. A graphical depiction of the template structures is made available for your reference.

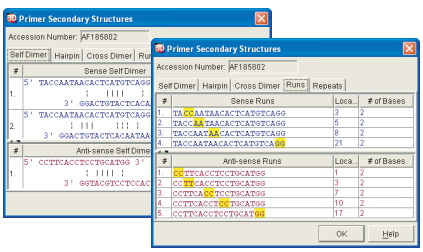


Strong Web Integration

Beacon Designer lets you 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.

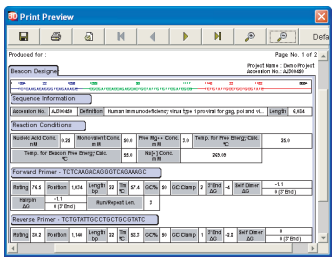
Graphical Interface

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



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.



Other bioinformatics tools from PREMIER Biosoft International

Array Designer 4

For fast, efficient design of specific oligos for designing Whole genome arrays and Tiling arrays for SNP genotyping and expression studies
for Windows and Linux

Array 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.

primer 5

A comprehensive primer design tool
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 3

An exceptional tool for designing cloning experiments and drawing publication quality graphics
for Windows and Macintosh

SimVector is a web savvy Windows and Mac program for cloning simulation, drawing and sequence analysis. It transforms sequence 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 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 3

Designing expression cloning experiments
for Windows and Macintosh

Xpression Primer is a web savvy Windows and Mac program with a sophisticated algorithm for designing optimal tagged primers to amplify 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.

PREMIER Biosoft International
Intuitive software for the molecular biologist

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