

Beacon Designer™

Design SYBR® Green primers, primers for HRMA, TaqMan® probes, MethyLight TaqMan® probes, LNA spiked TaqMan® probes, Scorpions®, FRET probes or molecular beacons for robust amplification and fluorescence in real time PCR

Optimal SYBR® Green Primer Design

Use Beacon Designer™ to design highly specific and efficient SYBR® Green primers. Specificity is assured by avoiding significant cross homologies identified by automatically interpreting BLAST search results. To assure efficient hybridization and high yield, the program avoids template secondary structures for locating primers.

High Resolution Melt Analysis (HRMA) Primer Design

Beacon Designer™ offers a comprehensive solution for mutation detection. High Resolution Melt Analysis (HRMA) is a more cost-effective method than probe-based genotyping analysis. The program employs proprietary algorithms that enable designing the best primers for detecting SNPs, MNPs, DIPs and Mixed type mutations.

Design Multiplex Assays

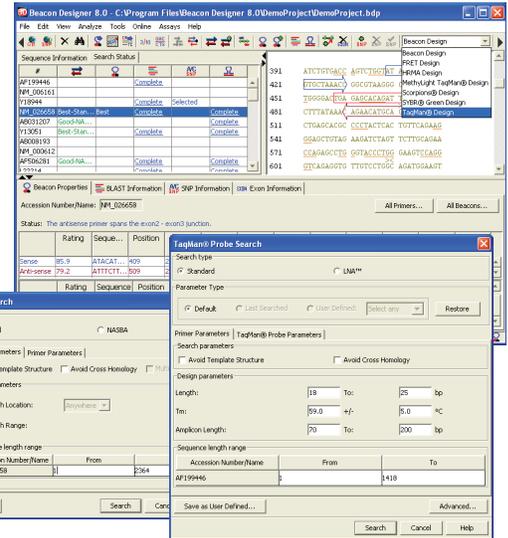
Beacon Designer™ uses innovative proprietary algorithms to design optimal primer-probe sets for single tube multiplex assays. You can choose the set best suited for your experimental needs from a list of alternates presented in variously sortable order. If you want to incorporate well-proven sets for some of the templates, or include reference or housekeeping genes for normalization purposes in the assay, Beacon Designer™ is equipped to fully support your needs.

Dual Labeled Probe Design

Beacon Designer™ offers comprehensive support for designing TaqMan®, molecular beacon, Scorpions® and FRET assays for studying differential gene expression or detecting SNPs using single template or multiplex reactions. You can even confirm SYBR® Green assay results by designing probes compatible with previously designed primer pairs for any of these techniques. Or simply evaluate partially or fully pre-designed assays using instant analysis capabilities of Beacon Designer™.

LNA™, MethyLight, NASBA® & Scorpions® Assays

Design the increasingly popular Locked Nucleic Acid (LNA™) substituted TaqMan® probes, which are more stable than standard probes. TaqMan® probes can also be designed for MethyLight assays. MethyLight is a high throughput assay used to discriminate between methylated and unmethylated DNA. Nucleic acid sequence-based amplification (NASBA®) is a primer-dependent technology that can be used for the continuous amplification of nucleic acids in a single mixture at one temperature. You can now design molecular beacons for NASBA® assays for single template or multiplex reactions. Design Scorpions® to achieve sequence-specific priming and PCR product detection using a single oligonucleotide.



Design SYBR® Green primers, TaqMan® probes, MethyLight TaqMan® probes, LNA™ spiked TaqMan® probes, Scorpions®, FRET probes & molecular beacons free of secondary structures for increased signal strength.

Evaluate pre-designed probes, primer pairs and beacon or TaqMan® probes.

Tm calculated using nearest neighbor thermodynamic theory and highly accurate SantaLucia values.

Design primers across an exon-exon or exon-intron junctions to selectively amplify cDNA.

Design compatible primers for other targets in multiplex reactions.

View the location of primers, probes, regions of BLAST homology and template structures on the sequence and check for all possible secondary structures.

Retrieve sequence from Entrez and dbSNP and perform BLAST search.

Load SNP using GenBank or add your own SNP information.

Export results in a tab delimited format for easy ordering or for importing into central databases like Oracle.

Ability to generate an attractive report of the designed assays.

Local built-in database maintains sequence information, search results and BLAST result summaries.

Strong web integration.

Available for Windows and Mac.

To activate & evaluate, follow these steps

- Install Beacon Designer™ from our website or the CD
- Launch the program and click 'Activate' on the first window
- Enter the 'Registration Number' requested from us and your e-mail address. Click 'Next'
- Update the registration information following the on-screen prompts and click 'Submit'

For a quick start

- Check the Multimedia Tutorial

Order on-line

- E-mail: sales@premierbiosoft.com
- Phone: 650-856-2703, Fax: 650-618-1773

Bioinformatics Services

PREMIER Biosoft has a successful record of software development in bioinformatics molecular biology since 1994. Our software products have been well received by the life science community over these years. We specialize in software development, design, testing and maintenance. If you have a new requirement or need the upkeep of a current database/software system, our team of bioinformatics scientists and computer professionals can assist.

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AlleleID®

A comprehensive tool designed to address the challenges of species identification & taxa discrimination using qPCR, xMAP® and microarrays. (for Win & Mac)

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For fast and efficient design of specific oligos for whole genome arrays, tiling arrays and resequencing arrays. (for Win & Linux)

Beacon Designer™

Design specific and efficient oligos for all major qPCR assays. (for Win & Mac)

LAMP Designer

Design primers for Loop-mediated Isothermal Amplification. (for Win)

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A comprehensive data processing & visualization tool for MALDI IMS data. (for Win)

MLPA® Designer

A comprehensive tool co-developed with MRC-Holland to design highly specific oligos for MLPA assays. (for Win & Mac)

PrimerPlex

A multiplex PCR primer design tool. (for Win & Mac)

Primer Premier

A comprehensive primer design tool for standard PCR assays. (for Win and Mac)

PROTEOIQ

Right from validation to quantification, a powerful software that supports the entire proteomic data analysis pipeline. (for Win & Mac)

SimGlycan®

High throughput glycan & glycopeptide identification tool for data from TripleTOF, MALDI TOF/TOF, LC-MS/MS systems. (for Win)

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High throughput lipid characterization tool for data from Triple TOF, MALDI TOF/TOF, LC-MS, LC-MS/MS systems. (for Win)

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A novel tagged primer design tool for expression cloning and for designing sequencing primers to verify transcripts. (for Win & Mac)