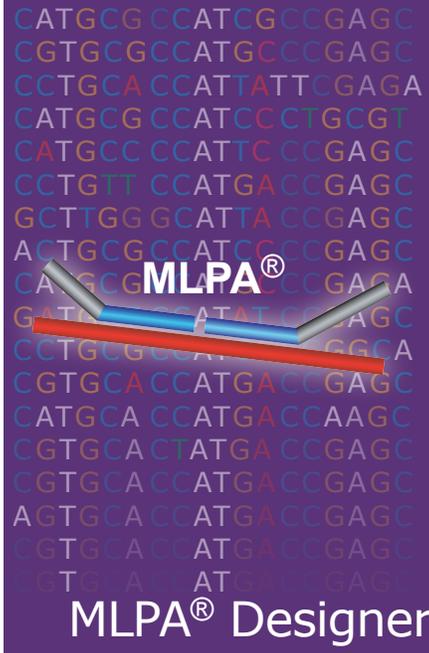


# MLPA<sup>®</sup> Designer

## Designs Highly Specific MLPA<sup>®</sup> Assays



Enables creation of new projects to manage the data of every new assay design.

Supports MLPA<sup>®</sup> probe design for copy number variation and SNP specific assays.

Imports exon and SNP information from GenBank annotations.

Supports BLAST search against all the genomic databases at the NCBI-BLAST to ensure high specificity.

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

Supports MagPlex-TAG<sup>™</sup> import and checks their dimerization with probes for Bead-Coupled MLPA assays.

Exports results of designed MLPA<sup>®</sup> oligos in .xls and other spreadsheet formats.

Displays the graphical view of all possible secondary structures such as hairpins, repeats and runs found in oligos.

Displays detailed properties of the designed MLPA<sup>®</sup> oligos such as position, length, Tm, GC%, Hairpin ΔG, run length, and repeats.

MLPA<sup>®</sup> Designer designs synthetic probes for MLPA (Multiplex Ligation dependent Probe Amplification) assays. The oligos are designed by avoiding regions of homologies making them highly specific. MLPA<sup>®</sup> Designer can be utilized to design oligos for both copy number detection and mutation studies.

MLPA<sup>®</sup> (Multiplex Ligation-dependent Probe Amplification) is a simple, high throughput and easy to perform method developed by MRC-Holland that allows detection of DNA copy number changes of up to 50 sequences in a single reaction.

The program allows importing sequences directly from Entrez, dbSNP, a local file (in GenBank or FASTA format), or from a UCSC file. It allows BLAST searching sequences to design highly specific oligos. The program automatically identifies regions of cross homology and avoids designing oligos in those regions. The program also enables BLAST search of the designed MLPA<sup>®</sup> oligos to check their specificity.

MLPA<sup>®</sup> Designer enables design of multiplex MLPA<sup>®</sup> experiments. The oligos designed for multiple sequences in a single search run are automatically checked for cross-dimers with each other and with all the designed oligos, preventing competition in multiplex reactions. The probes are designed based on standard reaction conditions such as Nucleic acid concentration, Monovalent concentration, Free Mg<sup>2+</sup> ion concentration, Total Na<sup>+</sup> equivalent concentration and temperature for free energy calculation.

The screenshot shows the MLPA Designer 7.82 software interface. The main window displays sequence information and search status. A table lists designed oligos with their properties:

	Rating	Sequence	Position	Length bp	Tm °C	GC %	Hairpin ΔG kcal/mol	Run Length bp	Rep... bp	BLAST Status
Exon 1										
Sense Left Probe Oligo (e...	82.4	GGGTCCTAAGGGTTGG	588	31	72.5	48.4	-0.4	2	0	
Sense Right Probe Oligo (...)	75.3	AGATCACGTGAGACGAA	619	31	71.9	48.4	-0.7	2	2	
Exon 2										
Sense Left Probe Oligo (e...	68.9	GGGTCCTAAGGGTTGG	1,165	28	73.6	50.0	-0.4	3	0	
Sense Right Probe Oligo (...)	37.6	GCCTCAGAACGAAGACC	1,193	22	71.8	59.1	-2.2	3	2	
Exon 3										
Sense Left Probe Oligo (e...	55.9	GGGTCCTAAGGGTTGG	1,255	31	71.4	41.9	-0.4	2	0	

Ready | Poor: 0-50 Good: 50-75 Best: 75-100 | Sequences: 1/96

# 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.

For more information, please write to us at [info@premierbiosoft.com](mailto:info@premierbiosoft.com) or call 650-856-2703 or visit the "Services" section of our website.



## AlleleID®

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

## Array Designer

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)

## MALDIVision

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)

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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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## SimVector

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## Xpression Primer

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