

MLPA[®] Designer

Designs Highly Specific MLPA[®] Assays



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

Supports MLPA[®] 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[™] import and checks their dimerization with probes for Bead-Coupled MLPA assays.

Exports results of designed MLPA[®] 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[®] oligos such as position, length, Tm, GC%, Hairpin ΔG, run length, and repeats.

MLPA[®] 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[®] Designer can be utilized to design oligos for both copy number detection and mutation studies.

MLPA[®] (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[®] oligos to check their specificity.

MLPA[®] Designer enables design of multiplex MLPA[®] 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 Mg²⁺ ion concentration, Total Na⁺ equivalent concentration and temperature for free energy calculation.

The screenshot shows the MLPA Designer 7.82 interface. The 'Sequence Information' tab is active, displaying a list of sequences and their search status. The 'MLPA@ Oligo Properties' tab is also visible, showing a table of 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

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