



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



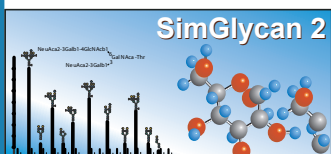
A comprehensive tool designed to address the challenges of pathogen detection, bacterial identification, species identification and taxa discrimination using TaqMan®, molecular beacon assays and microarrays (for Win & Mac)



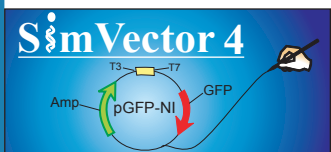
Design SYBR® Green primers, TaqMan® probes, MethyLight TaqMan® probes, LNA spiked TaqMan® probes, FRET probes, Scorpions® or molecular beacons for robust amplification and fluorescence in real time PCR (for Win & Mac)



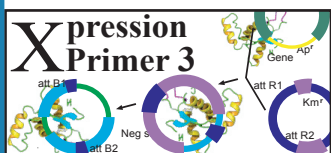
A comprehensive primer design tool (for Win)



A glycan mass fingerprinting tool (for Win)



A tool for drawing publication, vector catalog quality maps and designing cloning experiments (for Win & Mac)



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

Array Designer is a comprehensive desktop tool to efficiently design hundreds of specific oligos for SNP detection or expression studies or hundreds of PCR primer pairs for cDNA microarrays in seconds. It can automatically design whole genome, tiling, and resequencing arrays. All probes are checked for specificity by using BLAST to identify regions of cross homology and automatically avoiding these areas.

AlleleID designs probes and primers for pathogen detection, bacterial identification, species identification and taxa discrimination using qPCR assays and microarrays. It aligns sequences to locate differences in DNA and to find conserved regions. It then proceeds to design oligos to amplify and detect only the species or strains of interest from the mix. To design taxa/cross species assays, AlleleID designs the fewest number of oligos possible, resulting in cost savings. AlleleID supports assays for selectively amplifying cDNA from gDNA and designs oligos to detect splice variants by designing across intron/exon junctions. In addition, it designs MLPA® assays to detect mutations and copy number changes.

Beacon Designer designs oligos for SYBR® Green, TaqMan®, LNA spiked TaqMan®, MethyLight, molecular beacon, NASBA®, Scorpions® and FRET assays. Highly specific primers are designed by avoiding cross homologies found by automatically interpreting BLAST search results. The program ensures efficient hybridization and high yield by avoiding template secondary structures. Beacon Designer evaluates pre-designed assays and designs compatible oligos to extend the designs. It also designs beacons and TaqMan® for single tube multiplex experiments.

Primer Premier is a program for PCR, hybridization, sequencing, nested and multiplex primer design. It uses ClustalW multiple sequence alignment to design cross species primers automatically in regions of low degeneracy. Primer Premier reverse translates amino acid sequences to design degenerate primers. Designing allele specific primers and primers for site-directed mutagenesis is made easy. Sequences can be analyzed for restriction enzymes and motifs using extensive built-in databases.

SimGlycan predicts the structure of a glycan from the MS/MS data acquired by mass spectrometry, facilitating glycosylation and post translational modification studies. SimGlycan accepts the experimental MS profiles generated by a mass spectrometer, matches them with its own database of theoretical fragmentation of over 7,000 glycans and generates a list of probable glycan structures. Each structure is scored to reflect how closely it matches your experimental data. Other biological information for the probable glycan structures such as the glycan class, reaction, pathway and enzyme are also made available for easy reference.

SimVector is a web savvy program equipped with all the drawing tools necessary to publish engineered plasmid catalogs, as well as to simulate and draw plasmid constructs for Gateway®, TA, restriction or other popular cloning techniques. Export images in vector graphic format to produce the highest quality images for presentations in MS PowerPoint or publication in journals or vector catalogs using Adobe Illustrator. Alternatively, choose popular bitmap formats or export in ready-to-host web pages. With its powerful drawing features, it is easy to enhance vector maps with patterns, colors, fills, curved text and annotations.

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.