

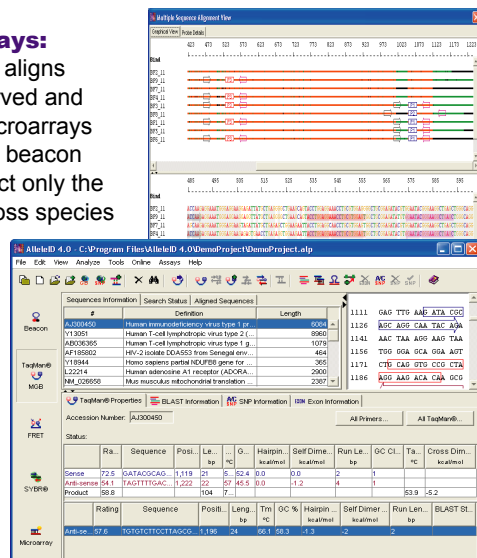
AlleleID

Design qPCR and Microarrays for Related Organisms

AlleleID is a comprehensive desktop tool designed to address the challenges of pathogen detection, bacterial identification or taxa/species discrimination using microarrays and qPCR assays.

Species Specific or Cross Species Assays:

To design species identification assays, AlleleID aligns sequences using ClustalW and analyzes conserved and species specific regions to design probes for microarrays and primers and probes for TaqMan®/molecular beacon qPCR assays. The assays are designed to detect only the strain or species of interest from the mix. For cross species assays, AlleleID identifies the conserved regions to design a universal probe. For related organisms, AlleleID can be used to study gene expression when genome draft of the organism under study is not available. This powerful functionality is sure to be helpful for many challenging tasks such as detection, identification, quantification or monitoring of contaminants, environments...



Designs SYBR® Green, TaqMan® TaqMan® MGB, and molecular beacon assays for taxa discrimination /species identification

Designs microarrays for species identification and cross species arrays for related organisms

Designs splice variant arrays

Enables the design of compatible TaqMan® probes, TaqMan® MGB probes, FRET probes and beacons for proven SYBR® Green assays, saving costs

Designs primers and probes for gene expression and SNP genotyping

Designs allele specific primers and probes

Designs primers across exon boundary for selectively amplifying cDNA to avoid gDNA

Loads exon and SNP information from GenBank annotations

Automatically interprets and displays BLAST search results. Uses BLAST search to assure specificity

Calculates Tm using nearest neighbor thermo-dynamic theory and highly accurate SantaLucia values

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

Available for Windows and Macintosh

Sophisticated Algorithms for Assay

Success: Highly specific oligos are designed by avoiding regions of significant homologies found by automatically interpreting BLAST results. Primer efficiency is enhanced by avoiding template secondary structures. "Minimal Set", one of the most innovative features in the program, helps design the fewest number of oligos that uniquely identify each species/strain/taxa from the mix, lowering assay costs. For taxa or cross species assays, this feature is especially useful when the group or taxa is highly dissimilar. For a partial set of pre-designed, proven primers and probes, AlleleID can design compatible oligos.

Splice Variant Microarrays: To detect alternative splicing events, AlleleID designs two types of probes called junction probes and intra-exon probes. Junction probes span exon-exon boundaries while intra-exon probes lie entirely within a single exon, making AlleleID an effective tool in designing microarrays to test novel splice forms.

Extensive support for qPCR Assays & SNP/Expression Microarrays: AlleleID designs optimal SYBR® Green primers, TaqMan® probes, TaqMan® Minor Groove Binding (MGB) probes, FRET probes or molecular beacons for real time qPCR differential gene expression and SNP genotyping assays. You can also design primers or probes for up to ten thousand sequences in a single run for making SNP detection or expression microarrays.

MLPA® Assays

AlleleID is the only program that designs synthetic probes for MLPA (Multiplex Ligation-dependent Probe Amplification). It designs specific and efficient probes by avoiding regions of homologies and template secondary structures for both copy number detection and mutation studies.

Activate the program following these steps:

- Install and launch AlleleID from the CD
- Click **Evaluate** on the first window that opens.
- Enter the evaluation key requested from us

Learn to use AlleleID

- Multimedia tutorial is included on the CD

Order on-line

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

Other bioinformatics tools from PREMIER Biosoft International

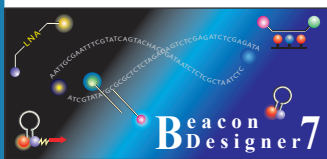
Array Designer Beacon Designer Primer Premier SimGlycan SimVector TMA Foresight Xpression Primer

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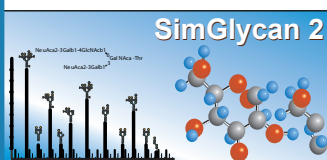
For fast and efficient design of specific oligos for whole genome arrays, tiling arrays and resequencing arrays (for Win & Linux)



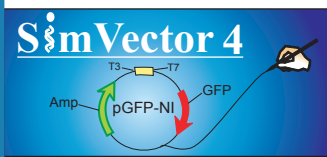
Design SYBR® Green primers, TaqMan® probes, MethyLight TaqMan® probes, LNA spiked TaqMan® probes, FRET probes, Scorpions® or molecular beacons for robust amplification and fluorescence in real time PCR (for Win & Mac)



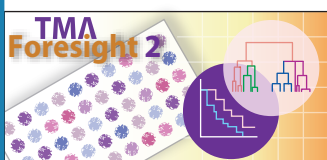
A comprehensive primer design tool (for Win)



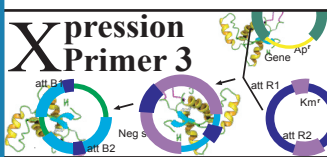
A glycan mass fingerprinting tool (for Win)



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



A statistical tool for tissue microarray data analysis (for Win)



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.

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.

TMA Foresight is a tissue microarray data analysis tool for performing multivariate statistical techniques such as Cox proportional hazard model to identify prognostic markers, Principal Component Analysis, hierarchical clustering and Kaplan-Meier survival plots to identify prognostically significant clusters and biomarkers and their impact on the outcome, and correlation analysis to measure the strength of association between variables. TMA Foresight not only analyzes the data but interprets it too, making it a useful tool for pathologists, clinicians and researchers.

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.

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