



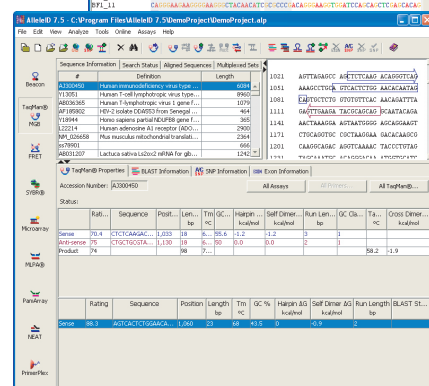
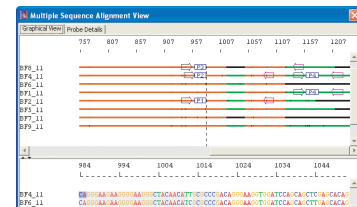
AlleleID®

Design qPCR and Microarray Assays for Related Organisms

AlleleID® is a comprehensive desktop tool designed to address the challenges of taxa/species discrimination using qPCR and microarrays.

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 oligos for TaqMan®/ molecular beacon assays & microarrays. 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 help in many challenging tasks such as detection, identification, quantification of pathogens, bacteria, contaminants...



Designs SYBR® Green, TaqMan® and xMAP® 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.

Supports the NEAT technology from DxTery Diagnostics.

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 thermodynamic 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.

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. AlleleID® also designs primers or probes for up to ten thousand sequences in a single run for making SNP detection or expression microarrays.

MLPA® Assays

AlleleID® designs synthetic probes for MLPA (Multiplex Ligation dependent Probe Amplification) assays and custom oligos for PamGene's PamChip® microarrays. It designs these specific and efficient probes by avoiding regions of homologies and template secondary structures for both copy number detection and mutation studies.

xMAP® Assays

AlleleID® can design strain differentiation multiplex assays for Suspension Array systems based on Luminex's xMAP® technology. For users working with closely related organisms, this functionality enables running experiments in a single reaction vessel. Support for single template xMAP® assays is also available wherein oligos are designed for rapid and high-throughput detection of nucleic acid sequences. Pre-designed proven oligos can be used to design compatible oligos for rest of the sequences to form a multiplex set.

To activate & evaluate, follow these steps

- Install AlleleID® 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.

For more information, please write to us at 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)

SimGlycan®

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

SimLipid®

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

SimMet®

A robust high throughput informatics software for qualitative and quantitative analysis of mass spectrometry metabolite data. (for Win)

SimVector

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

Xpression Primer

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