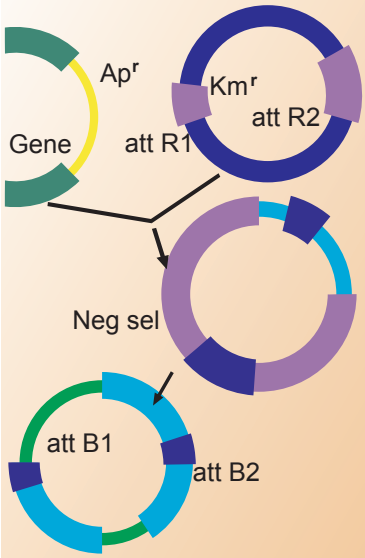
PREMIER Biosoft



Design thousands of primer pairs optimized for Gateway®, BD In-Fusion™, TOPO® Tools and epitope systems.

Add functionally useful tags for any expression system of your choice and design tagged primers.

Automatically maintain the reading frame of the ORF to be amplified when adding tags.

View primer secondary structures graphically.

Automatic check for in-frame termination.

Design sequencing primers for multiple sequences in a single search run.

Sequencing primers are designed across amplicons with a user defined interval between forward primers. Reverse primers stagger on the opposing strands.

Design primers for in vitro transcription-translation.

Primer Tm is calculated using highly accurate SantaLucia nearest neighbor thermodynamic values.

Optimizes all primers in a single search run for uniform PCR cycling conditions.

Primers are screened for thermodynamic properties and secondary structures.

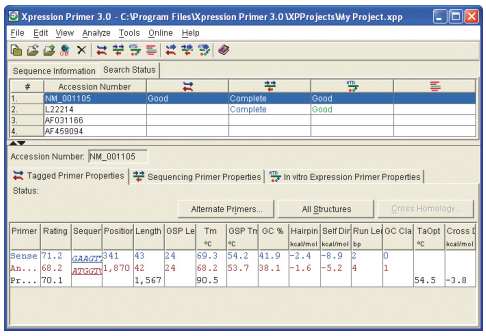
Retrieve batches of ORF sequences from Entrez using accession or GI numbers.

Comprehensive project management for easy and convenient storage and access of data from multiple experiments.

Xpression Primer

A revolutionary tagged primer design tool for designing expression cloning experiments

Extensive Assay Support for Tagged Primer design



Use the sophisticated algorithm of Xpression Primer to design thousands of tagged primers for expression cloning systems such as Gateway®, BD In-Fusion™, epitope and TOPO® Tools. You can choose to amplify an entire ORF or generate N terminal or C terminal fusion proteins. Xpression Primer ensures that the reading frame of the amplified ORF is conserved. To work with other expression systems, simply add functional tags of your choice and design tagged primers.

Successful Amplification with Nested PCR

To ensure the success of your PCR experiment, let Xpression Primer design nested tagged primers to amplify ORFs. You can locate the outer primers anywhere in the UTRs or in regions of no significant homology. Xpression Primer will BLAST your sequences, automatically interpret the results and design highly specific primers. The tagged inner primer pair amplifies the PCR product generated by the outer pair with little or no non-coding regions. You can also choose from a list of alternate primers to better meet specific experimental needs.

Sequencing for Product Verification Made Easy

The versatile algorithm of Xpression Primer can design optimal sequencing primers for multiple sequences in a single run. It picks forward primers across the amplicon at a specified interval and reverse primers staggered on the opposite strand. You can export the results for several popular well plate configurations.

Generate Precise Transcripts

Design primers to generate sense or antisense transcripts for *in vitro* expression studies.

Web Savvy

Xpression Primer searches Entrez and downloads batches of ORF sequences directly into the program.

To activate & evaluate, follow these steps
- Install Xpression Primer 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
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- Phone: 650-856-2703, Fax: 650-618-1773

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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.

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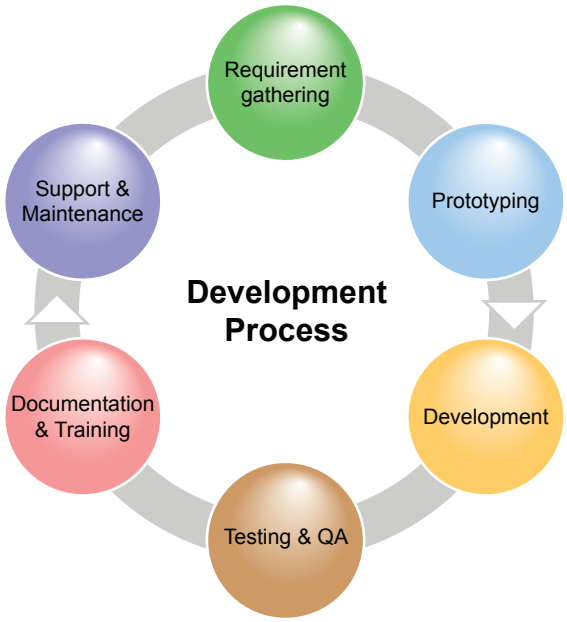

AlleleID®	A comprehensive tool designed to address the challenges of species identification & taxa discrimination using qPCR, xMAP® and microarrays. (for Win & Mac)
Array Designer	For fast and efficient design of specific oligos for whole genome arrays, tiling arrays and resequencing arrays. (for Win & 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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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)

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