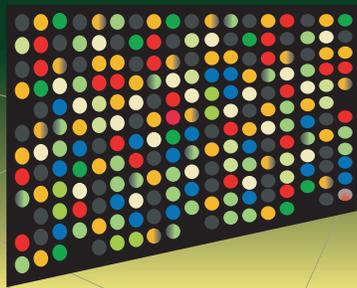


Array Designer

**For fast and efficient design of specific oligos
for whole genome arrays, tiling arrays and resequencing arrays**



*Designs oligos for genotyping microarrays.
Designs oligos or primer pairs for cDNA
microarray expression studies.*

*Designs multiple specific probes on each of
numerous templates in a single search run.*

*Avoids cross homologies among designed
probes and primers to ensure robust
signals in single tube multiplex reactions.*

*Adapted to most widely used SNP
detection methods including primer
extension assays and tiling arrays.*

*Displays probe properties including
graphical views of secondary structures.*

*Directly loads SNP information from
GenBank annotations.*

Conveniently add unpublished SNPs.

*Designs both wild and mutant probes for
the selected strand.*

*Designs the best primer pair for specificity
and amplification efficiency.*

*Automatically interprets and displays
BLAST search results.*

*BLAST searches against all the genomic
databases available at NCBI.*

*BLAST searches against your own local
database.*

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

Available for Windows and Linux.

Comprehensive Tool

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. You can efficiently retrieve, analyze and store data.

Arrays for the Post-sequencing Era

Whole Genome Arrays: With Array Designer you can study entire organisms effortlessly by detecting every gene or exon in the whole genome, characterizing transcriptomes, discovering differentially and alternatively spliced transcripts, SNP discovery and genotyping, DNA sequence variation in individuals or populations and comparative genome hybridization (CGH).

Tiling Arrays: You can even design tiling arrays to spot every base of a long genomic sequence, avoiding repetitive regions. Designing arrays to characterize regulatory elements, or to study epigenetic modifications, methylation patterns and protein binding sites has never been so easy.

Resequencing Arrays: Array Designer designs resequencing arrays with which you can detect SNP and other sequence variations in a large number of samples for applications such as biowarfare pathogen studies, predisposition and resistance to disease or discovering the genetic basis of phenotypic traits. With a unique feature which we call "Project BLAST", you can identify and avoid the homologous regions that create false positives.

Design Highly Specific Oligos

To ensure specific amplification and exact detection, Array Designer designs highly specific PCR primers and oligos by automatically avoiding regions of significant cross homologies identified during a BLAST search against a private local database or the genomic public databases available at NCBI. For a whole genome sequence, Array Designer automatically creates a local custom database of the input sequence and BLAST searches every fragment against it. To verify the specificity of design, you can BLAST the designed oligos.

Beyond NCBI Database Support

When working with confidential or publicly unavailable sequences, you can set up a local database either on a Unix based server for institution-wide access or on a PC for your own convenience.

To activate & evaluate, follow these steps

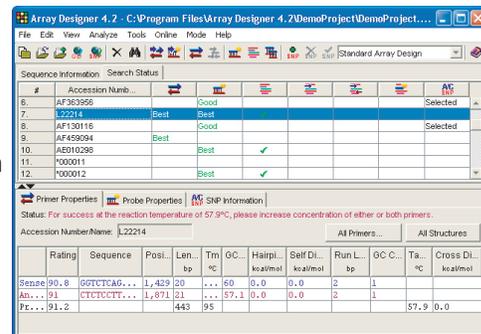
- Install Array Designer from our website or the CD
- Launch the program and click 'Activate' on the first window
- Enter the 'Registration Number' requested from us and your e-mail address. Click 'Next'
- Update the registration information following the on-screen prompts and click 'Submit'

For a quick start

- Check the Multimedia Tutorial

Order on-line

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



#	Accession Num.	Search	Status	Rating	Sequence	Posi.	Len.	Tm	GC	Hairp.	Self D.	Run L.	GC C.	Ta.	Cross D.
6	AF363956		Good												
7	U22214	Best	Best												
8	AF120115		Good												Selected
9	AF450294	Best													
10	AE010288	Best													
11	U000911														
12	U000912	Best													

Rating	Sequence	Posi.	Len.	Tm	GC	Hairp.	Self D.	Run L.	GC C.	Ta.	Cross D.
99.8	GGTCTCAAG...	1,429	20	...	60	0.0	0.0	2	1		
91	CTCTCTCTT...	1,871	21	...	57.1	0.0	0.0	2	1		
91.2		443	95							57.9	0.0

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)

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

SimVector

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