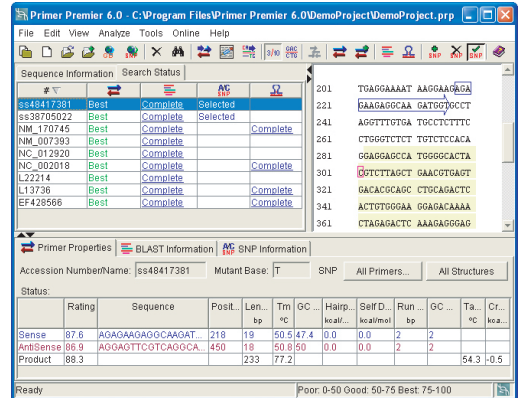


Primer Premier

A comprehensive PCR primer design software

Comprehensive Design Support

Primer Premier's search algorithm finds optimal PCR, multiplex and SNP genotyping primers with the most accurate melting temperature using the nearest neighbor algorithm. Primers are screened for secondary structures, dimers, hairpins, homologies and physical properties before reporting the best ones for your sequence, in a ranked order. Load the gene of interest from NCBI, select a search range, sit back and let Primer Premier pick the best possible primers for you.



Retrieves batches of sequences directly into the program from GenBank and dbSNP using accession /GI numbers and assay IDs.

Performs BLAST and template structure search and avoids cross homologies and secondary structures while designing primers. Supports Local and Desktop BLAST options for using local custom/unpublished databases.

Includes a sequence view with primers marked and homologies and template structures highlighted.

Evaluates a primer pair or a forward/reverse primer, designs a compatible primer and exports a complete analysis in an HTML or csv file format.

Edits Template sequences to add new bases or delete unwanted regions.

Exports a publication quality report for the assays designed for sharing with colleagues.

Includes a built-in calculator for computing the GC%, the base count and to obtain the complement and the reverse complement.

Organizes data in project format and maintains a local database of sequence information and search results.

Supported on latest operating systems Windows 7 and Mac Snow Leopard.

Automatic Homology & Template Structure Avoidance

Primer Premier automatically interprets the BLAST search results and utilizes a proprietary algorithm to check for possible secondary structures. Homologies and structures are avoided for designing highly specific and efficient primers.

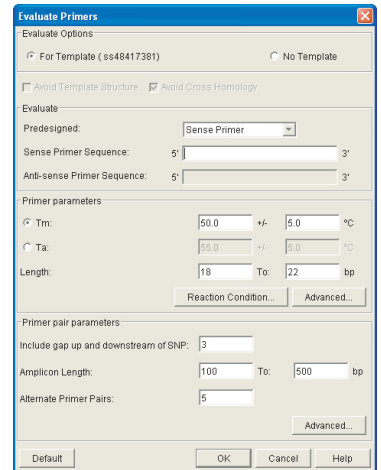
Accession Nu...	Type	Most Stable Cross Dimer	Cross Dimer ΔG
NM_007393	Primer	5' CTCACCTTCGACCTTCCA 3' 11: 1'	-7.3
NC_002918	Primer	3' CAGACAGAGGAGGTAATCC 5'	
NC_002918	Primer	5' CCTAATGGATGGACAGAGC 3' 7: 11:	-7.1
L22214	Primer	3' CTCCTGCTACTCTCTCT 5'	
L13736	Primer	5' GCTTCTCTGAGACTTATG 3' 11: 11:	-7.0
EF428566	Primer	3' TGGAGACGAGAGCATG 5'	
L13736	Primer	5' GCTGCTCTGATACTAG... 11:	-6.9
EF428566	Primer	3' AAGTAGGTCAGAGGCTGT 5'	
NM_170745	Primer	5' TCTGCTGAGATCTCTAAC 3' 11: 11:	-5.9
EF428566	Primer	3' TGGAGACGAGAGCATG 5'	
NM_170745	Primer	5' TCTGCTGAGATCTCTAAC 3' 11: 11:	-5.4
L22214	Primer	3' CTCCTGCTACTCTCTCT 5'	
NM_170745	Primer	5' TATGGAGAGATCTCT 3'	

Versatile Primer Design & Analysis

Using the manual primer search option, a user can click any nucleotide on the template sequence to get primers at the location of their choice. Primer Premier instantly analyzes the primer properties. The program also evaluates the properties of pre-designed primers and ranks them for you to adjudge how far the primers are from their desired target values. This feature is especially useful if you are working with published or pre-designed well proven primers. For any given primer, it even designs a compatible forward or reverse primer.

Multiplex Assays & SNP Genotyping

For a multiplex experiment, Primer Premier enables you to launch a primer search in batch mode and then checks the cross reactivity of the primers designed, thereby reducing false priming. For SNP genotyping assays, SNP flanking primers are designed.



To activate & evaluate, follow these steps

- Install Primer Premier 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

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A comprehensive tool designed to address the challenges of species identification & taxa discrimination using qPCR, xMAP® and microarrays. (for Win & Mac)

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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)

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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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