Clone Manager 10   *Professional Edition*

Cloning, graphic maps, primer design, sequence alignment -- Version 10 for Windows

Clone Manager Professional provides a comprehensive, fully integrated set of tools for enzyme operations, cloning simulation, graphic map drawing, primer design and analysis, global and local sequence alignments, similarity searches, and laboratory-sized sequence assembly projects.

You can also use Clone Manager as a quick and easy way to view or edit sequence files, find open reading frames, translate genes, find genes or text in files, or organize primer collections.

Simulate Cloning

- Cut, ligate DNA, modify molecule ends
- New multiple-molecule Ligate window
- Cloning Wizards for current PCR-based techniques
- Plan Cloning Wizard for restriction enzyme cloning

Clone Manager can cut DNA at enzyme cut sites or at user-specified basepair positions. Molecule features and enzyme sites are automatically recalculated after a cut operation. The program can ligate DNA, checking for compatible ends. You can modify molecule ends, if needed for ligation, and select the cloning orientation.

For fast simulated cloning, you can cut, ligate, and modify ends -- all from the same Ligate display window showing sticky ends and molecule icon maps.
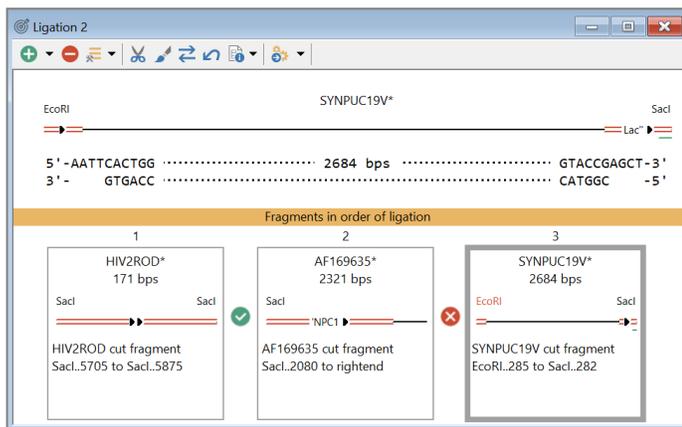
Use cloning wizards to help you to simulate cloning using a variety of current cloning techniques: Gateway® Recombination Cloning, Topo® Cloning, Gibson Assembly, In-Fusion Cloning, Ligation-Independent Cloning or related cloning techniques.

The wizards will help you select the appropriate components, show you the proposed result, and create the final recombinants. You can assemble a set of overlapping fragments, previously prepared, or use PCR to create amplified fragments with overlaps, then assemble the fragments. Save recombinant molecules, primers.
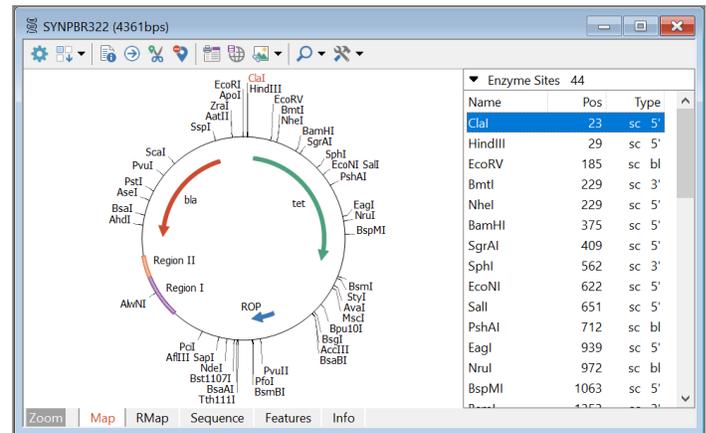
Draw Graphic Maps

- Prepare high-resolution graphic maps
- Print, copy to clipboard, export to file
- Enhanced Views of graphic map

Prepare high-resolution circular or linear graphic maps. Control styles and colors for feature types and enzyme sites; control map size and position. For your lab notebook, select to print the map with associated text (description and notes; map features and enzyme sites) .

For a publication or presentation, use an Enhanced View of the graphic map to customize a special molecule map. Set individual feature styles, colors, patterns, positions. Drag feature names to reposition, if needed. Remove enzyme sites or features from a map without modifying the original molecule data. Save enhanced views in the molecule file (maximum 6 views/file). Print, copy, export in vector or raster (Tif, Png, Gif, bitmap) formats.

Work with Enzymes

- Find enzyme sites, view enzyme information
- Do restriction enzyme analysis
- Create user enzyme lists, transient lists

Clone Manager scans the sequence and identifies enzyme recognition sites, drawing an accurate on-screen working map. Click tabs at the bottom of the molecule viewer window to see the map, restriction map data, sequence, features, or molecule information. Zoom to transiently view just a portion of a larger molecule.

Scrolling map sites list shows enzyme sites, primer sites, label sites or features. A fast and powerful restriction enzyme analysis module has five display styles, including a list of No-Cutters. Filter to see only the results you need. View enzyme properties, suppliers, isoschizomers, or compatible ends information. Update enzyme lists monthly using REBASE files.

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Design Primers

- Search for primers and list results
- Position primer in molecule sequence and evaluate
- Use the Sequencing Primer Wizard

Search for PCR primers or pairs, sequencing primers, or probes. Sort results lists by rank (quality) or position, or view summary of search progress showing which criteria eliminated primers.

Design by positioning a primer in the molecule sequence at a target position or just select (highlight) sequence in the molecule viewer to initiate primer design at this position. View the primer evaluation, the sequence flanking the primer, genes that are nearby, and the location of neighboring primers that will meet the evaluation criteria you have set.

Use the Direct Entry wizard to enter sequence and other information for primers already in use or purchased commercially. Use the Sequencing Primer Wizard to design a set of primers for sequencing a molecule region.

Analyze Primers

- Evaluate using primer criteria
- Do in-depth analyses
- Use the Analyze Mix Wizard

To find or evaluate primers, the program analyzes GC content, melting temperature (Tm), dimers, stability, runs of bases and repeats, hairpins and false priming. Detailed analysis options display primer dimers, summarize cautions, and report homologies between the primer and template (false priming or other homologies).

The Analyze Mix Wizard will analyze primer binding and products formed in a mix of primers and molecules. Just identify the primers and molecules, set the parameters for the analysis, and view results.

The Primer Viewer Window puts all primer information in one convenient location. Click tabs at the bottom of the window to see primer information, edit the primer, or analyze the primer. Save to a file or a primer collection.

Primer Operations

- Find primers that bind to your molecule
- Find molecules with sites for your primer
- Primer Values, Mutagenesis Profiles

Scan the primers you have created to find which could bind effectively to a molecule of interest. Primer sites can be added to molecule files and displayed on the molecule map or formatted sequence. Or scan molecule files on your computer or local network to look for molecules that have binding sites for a primer of interest.

Use the Primer Values profile to analyze regions of the molecule to assist in identifying areas for primers in difficult situations. Calculate Tm, GC and stability for primers of a length specified and plot these profile values. Use the Mutagenesis Profile to help construct mutant primers, identify restriction enzyme sites that can be introduced, or to check for changes in translation.

Organize, Use Primers

- Store primers in Primer Collections
- Easy-to-use Create Product module
- Use primer sites on molecule map

Store essential information about many primers in one or more collection files for streamlined storage and access. Create new collection files, as needed, and create folders to organize your collection files.

Search in collection files to find a specific primer. Export collection file data in tab-delimited format for use in other applications.

Use the Create Product module to identify two primers and one molecule to produce an amplified product with a PCR-type reaction. Create a new DNA molecule or export the product sequence. Review product size, GC content, melting temperature, annealing temperature.

Select a primer site on your molecule map and export the primer sequence, rename the primer, create the primer from its sequence, or (with a second primer on this map) quickly create an amplified product.

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Align Multiple Sequences

- Align many sequences against a reference
- Align many sequences against each other
- Save, export, edit alignment data

Align a group of DNA or protein sequences against a reference sequence. View a summary table of results, aligned sequences in a variety of formats, or a graphic display of areas of significant similarity in each sequence. Enter name, description. Save alignment results.
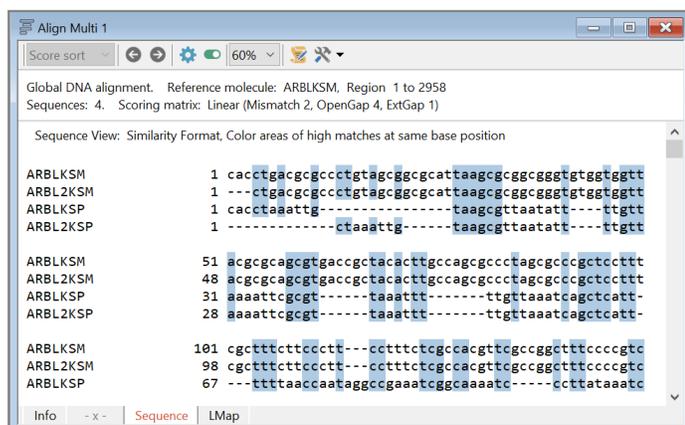
A multi-way alignment function lets you do exhaustive pairwise alignments of all sequences and progressive assembly of alignment using Neighbor-Joining phylogeny. Alignment results include a dendrogram which suggests the pattern of relatedness of all of the sequences aligned.

Edit alignment data — replace a base if you believe it is in error, or shift unaligned bases left or right. If the sequence files contain trace data, view the trace for a base in question before editing.

Export the consensus sequence derived from an alignment or export the aligned sequences in CLUSTAL W multiple sequence alignment format.

Compare Two Sequences

- Find regions of local similarity
- Progressively assemble an alignment

Search two DNA or protein molecules for regions of local similarity using the FastScan method, maximized for score or quality, or the Needleman-Wunsch method.

Results of local alignments include a sortable list or graphic view of similarities found, and aligned sequences or a detailed map for each homology block listed. Move easily to Next or Previous result in sequence/map views.

Assembled alignments begin with a FastScan local similarity search, lock in significant regions of homology found, and then complete the alignment of the remaining sequence. Export merged/spliced consensus sequence.

Scan for Similarities

- Scan sequence files in folders on your computer
- Scan databank library files on your computer

Search for similarities to a sequence by scanning folders of sequence files or databank library files on your personal computer or local network. The program will open each file, scan the sequences found, and record significant regions of similarity encountered. Set the speed and cutoff value to alter the sensitivity of the search.

Results include a sortable list or graphic view of regions of similarity found, and aligned sequences or a detailed map for each homology block listed. From the results list, use the Scan Results Wizard to identify molecules to load for use now, save to a disk file for later use, or set up as an assembled multiple sequence alignment.

Sequence Assembly

- Simple or complex assembly projects
- Locate subclones on reference sequence

Handles laboratory-sized assembly projects. Identify sequence files to assemble and set assembly parameters, if applicable. Sequence assembly results are shown in a data window with multiple views -- review a table of results information, a picture view of alignment locations, or the aligned sequences with optional accessory data in a split pane. Accessory data includes an assembly overview with a position locator, a histogram of coverage and errors, and trace data, if available in the sequence files.
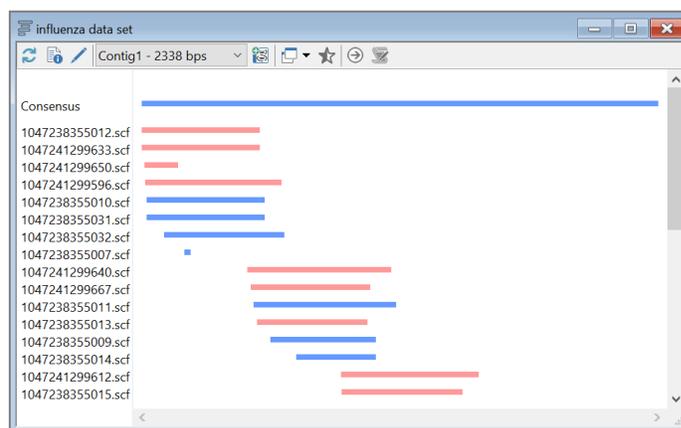
Public Domain Database Searches

Initiate remote searches of public domain databases, including NCBI BLAST databases, and display results in a built-in web browser. The program helps you set up a BLAST search by handling query sequence formatting, in-frame translation, or excision of a subsequence. Pick the BLAST program and database to use and your request is sent to the NCBI server over the internet. View BLAST results, access molecules of interest and save molecule files to disk or load a molecule for immediate use.

Other Features

- Integrated sequence editor and file handler
- Extensive sequence formatting options
- Use sequence phrase collections

Clone Manager reads files in GenBank, EMBL, FASTA or Clone Manager file formats, or sequence data in simple ASCII text files. You can also import (paste) files from the clipboard or retrieve files from Entrez (NCBI).

The sequence editor can display full or partial sequences in a variety of formats. Display any combination of sequence, enzyme sites, sequence labels, translation, annotations and memorize your favorite style settings.

You can also edit sequences, join sequences, rotate circular molecules, invert or translate sequences, find Open Reading Frames, or find regions in the sequence that match or nearly match a search string.

DataBook is a simple, built-in database to store and organize information about your molecules. Automatic data entry makes it really easy to use. Another module stores sequence phrases in collection files and lets you find matching sites in your molecules.

Analysis Functions

- Open Reading Frame analysis
- DNA Repeats, Dyad Symmetries analyses
- Hydrophilicity, Protein structure analyses
- Mutagenesis Profile module

Open Reading Frame analysis maps start and stop codons in 6 reading frames and calculates Fickett's TESTCODE scores to help identify coding regions.

Analyze direct or inverted repeats and dyad symmetries to identify regions that might be associated with biologically active sites such as control regions, transcription terminator regions, or RNA processing sites.

Analyze protein or translated DNA for hydrophilicity and surface exposure. Analyze protein structure for alpha-helix, beta-sheet (extended), beta-turn, random coil states.

Mutagenesis Profile shows a portion of molecule sequence with one frame of translation and enzyme sites. View possible silent changes, find 'almost' enzyme sites, or view base changes required to change from one amino acid to another. Introduce a mutation and create a new molecule.

Sample Pricing and System Requirements

Recommended configuration: Windows 10 or Windows 8. Minimum configuration: Windows 7. 20 Mb hard disk space required for program installation. Internet connection required for license activation. Concurrent user license installation supports most standard Windows network systems or TCP/IP networks. Upgrades from version 9 available.

Selected Pricing and License Type Examples	Price *	Catalog No
Clone Manager Professional 10, single Seat License	$750 USD	10-2503 Qty 1
Clone Manager Professional 10, 4 Seat Licenses	$1960 USD	10-2503 Qty 4
Clone Manager Professional 10, 8 Seat Licenses	$3440 USD	10-2503 Qty 8
Clone Manager Professional 10, Concurrent 5-User License	$3800 USD	10-2504-5

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