


Graphic Maps


Standard Graphic Maps:

With a working map on screen, click Map, Format Map or use toolbar  button to set style and color options for printing the standard graphic maps. These settings are remembered and will provide consistent, standard high-resolution graphic maps until changed.


Click Format Map, Content tab to select a map style that adds descriptive text to the map page, a good choice for your notebook.

Enhanced Views:


With a working map on screen, click Map, Enhanced View, New View to create a special graphic map that you can customize to use for a presentation or publication. Drag lower right corner to increase size of map window. Delete non-essential enzyme sites or features in this view without removing them from your molecule file.

Features -- click on a feature to select. Then use toolbar buttons to change position, style, pattern, color for this one feature. Drag feature  name to reposition, if needed.

Enzyme Sites -- click Enz BP Num button to display or hide basepair numbers for all enzyme sites. Click Enz Italics to italicize the first 3 letters of all enzyme names.

Basics -- click the Basic Properties button to set basic options for the molecule map (format, size, basepair intervals, line widths), features  (font), or enzyme sites (font, tick lines).

Text -- click on text to select and then use toolbar controls to change font face, point size, color. All enzyme names use the same font and color; all feature names use the same font but can be in different colors.

Save Enhanced View -- click Save View button to save this enhanced view to the molecule file (maximum 6 per file). Remember to save  the modified molecule file to disk before exiting the program.

Print, Copy, Export Maps:

Click Map, Print or use toolbar Print button to send the standard or enhanced view graphic map to your printer.

Click Map, Copy to Clipboard or use toolbar button to copy the map for use in other applications. Use Edit, Paste Special to paste map into a word processing document.

Click Map, Export to prepare a Windows Metafile (emf or wmf) for use in other Windows applications.

Click Map, Save for Web to prepare a raster graphic file in png format for web page or on-screen presentations.

For enhanced views, click Copy/Export View button in enhanced view window to copy to the clipboard or export to file in vector (wmf, emf) or raster (GIF, TIF, PNG) formats at high or low resolution.

Quick Reference

Clone Manager 9 Professional Edition

Getting Started

for Windows

To install an individual or workgroup copy, insert the program CD in drive and allow disk to autorun or select Start, Settings, Control Panel, and then click Add/Remove Programs. Follow the instructions on your screen.



Double-click the Clone Manager icon to start the program.

Getting Help -- click Help, Help Topics to view complete application help. Click special Help with View toolbar buttons on complex display screens for help related to this display or the results presented.

Click File, Preferences to set author name, default save format, or features to import when loading files in GenBank or EMBL formats. Click Operations, Find in Files to locate molecule files containing specified feature or text.

Working with Molecules

Open Files -- Load Molecules:

Click File, Open or use Open toolbar button. Use Shift or Control keys in conjunction with mouse to open more than one file at the same time.

Information on the clipboard can be read as if it were a disk file using the Paste Molecule button found in the file open dialog box.

Click File, Retrieve from Entrez to find sequence files at the NCBI. With search results on screen, click to select file. Click button Show GenBank File to view or Get Molecule to import molecule for immediate use.


In the file open dialog box, use the Work Boxes button to open the folder containing the shortcuts to your favorite locations. Use the Add Work Box button to add a shortcut to the "Look in" location.

Creating new molecules:

Click File, New or use New toolbar button and then follow the wizard instructions. Save new molecule to disk when complete.

Selecting molecules:


Active molecule is in active window (dark title bar). Click on a different window to change the active molecule or select from Molecule List.

Click File, Molecule List or use Molecule List toolbar button to access list of loaded molecules. Click on column heading to sort.  Resize columns by dragging column heading join point. Diamond symbol marks unsaved new or modified molecules.

Molecule Viewer Window


Click tabs at the bottom of the window to see molecule Map, Restriction Map data, Sequence, Features or molecule Information. Click Zoom button in tab region (left) to temporarily view just a part of the molecule.

Map Tab -- Working Map display

Enzyme sites, primer sites and features (genes, regions, markers) appear on the working map. Click AutoScan button to scan for enzyme sites, click Find ORFs button to locate open reading frames, enter as genes. 


Point to a site or feature on the map to see basepair position information and suppressed enzyme sites, if present (++ notation indicates suppressed sites in crowded areas). Click on site or feature and then use toolbar buttons to view site properties, go to sequence at site, or take other action. Click Format Map button, Screen Basics tab to set working map display options.

RMap Tab -- Restriction Map data

Click column headers to sort by enzyme name or number of sites or to select display style. Click No Cutters button to view list of enzymes that do not cut this molecule. Click again to return to prior display.  Select a different enzyme list and regenerate restriction map data.

Click Format button to set display styles and remember settings. Click Filter button to set filter options to limit data displayed to just what you need. Click again to remove filter. Click on an enzyme and then use toolbar buttons to view enzyme properties, suppliers, isoschizomers or compatible ends information, add enzyme sites to the map, or cut with this enzyme.


Sequence Tab -- Sequence data

View, edit or format molecule sequence. Click Format button to set sequence display styles and colors and memorize settings. Click My Style button to format sequence using your memorized settings. 

Edit sequence -- click the Edit Sequence button to change the sequence by adding or removing bases. You can also use cut, copy and paste operations on sequence data. Sequence is stored in the program single-stranded and all operations work on the upper strand of sequence.

Features Tab -- Features table

Click Features tab to view features table and add or edit information about molecule features. Click Feature properties button to see codon usage, amino acid composition, molecular weight and pI for gene translation products. Click GB Location/Qualifiers button see join segment data.


Click Customize button to set custom feature styles for map or sequence. Click Info Features button to display or hide information-only features. Click Filter to limit by feature type or location. 

Info Tab -- Molecule information


Click Info tab to view or edit molecule name, description, translation table setting, notes, starting bp number, or view molecule composition.

Enzyme Operations

Find Enzyme sites:

Click Clone, Find Enzyme Sites or use toolbar button. Find sites for specific enzymes or all enzymes on a list that meet a specific requirement (like single cutters) or all enzymes on a user list. 

View or build enzyme lists:

To view, click Clone, Enzyme Lists. To edit a user list, click the Unlock List button and then add or delete enzymes. To build a new user list, click the Build User List button. Follow wizard instructions. 

REBASE updates:


Click Clone, Enzyme Lists and then click the REBASE Update button to update your master enzyme file using the latest REBASE data file (updated monthly). Each time you update, the Commercial (Main), All Enzymes, and Scanner enzyme lists will be regenerated. User enzyme lists and any special enzymes you entered will not be affected.

Instant enzyme information:


Click toolbar buttons on the Map, RMap or Enzyme List displays to view enzyme Properties, Suppliers, Isoschizomers or Compatible Ends. Enzyme information is updated when you do a REBASE update.

Cloning Operations

Cut molecules:

Click Clone, Cut or use toolbar button. Cut a molecule with specific enzymes, cut at a single map site, or cut at specified bp positions. 


Ligate molecules:

Click Clone, Ligate or use toolbar button. Join together two pieces of DNA or join the ends of the same molecule (self-ligate). Use the small buttons (right) to change the molecule, cut the DNA, or modify the molecule ends. After ligation, a circular recombinant will be rotated to restore the original reference frame of the vector (upper molecule window). 

Modify molecule ends:

Click Clone, Modify Ends or use small button on ligate display. Use Klenow Fill-In, 5'->3' or 3'->5' exonuclease, Partial Fill-In, or custom.

Use the Cloning Wizards:


Click Clone, Plan Cloning or use toolbar button. Identify insert and vector sequences and indicate your preferences for the cloning experiment (or use default settings). Examine results, recombinants.  Click Clone, PCR Cloning to design PCR primers to amplify region to clone, use enzymes to prepare vector, generate recombinant molecules. Click Clone, Gateway Cloning or Topoisomerase Cloning to simulate cloning using Gateway® Recombination Cloning or Topo® Cloning techniques. The wizards will help you select the appropriate components, show you the proposed result, and create the final recombinant molecule.


Viewing Alignment Results

Results are displayed in a comprehensive, tabbed viewing window and can be printed, copied to the Windows clipboard or exported to a disk file.

Info tab -- contains alignment summary information table (multiple sequence alignments) or list of homologies found (local homology searches or scans for similarity). Sort list by score, percent matches, length or start position.

Picture tab -- shows phylogeny dendrogram (multi-way alignment) or picture view of list of homologies found (local homology searches).

Sequence tab -- shows aligned sequences for entire alignment of multiple sequences. Click Switch Format button to toggle between formats emphasizing the similarities or differences between the sequences. Click Format button to access full set of sequence formats and page style options. 

For local homology search results, sequence tab shows aligned sequences for the selected homology block. Click Next Result or Previous Result button to move through results list. 

Map tab -- shows similarity maps for multiple sequence alignments. Click Compress View to fit more data in the results window. Point with mouse and click to see basepair position number for area of interest on map.

For local homology search results, map tab shows a detailed location map for the selected homology block.

Sequence Assembly

Click Align, Assemble Sequences. Set Simple or Complex sequence assembly option and click Next to specify location of sequence files and set assembly parameters. Or set Subclones option to locate clones on a reference sequence.

Sequence assembly results are shown in a data window with multiple views. Resize display areas using mouse. If more than one contig results, use the combo box in the toolbar to select contig data to view. Click toolbar buttons to:

View Info -- review a table of results information.

View Picture -- display graphic picture of alignment locations. Blue bars align 5' to 3', light red bars align in reverse direction (3' to 5'). For Subclone results, black bars indicate gaps in coverage in normal or complement strands.


View Sequence -- view aligned sequences with optional accessory data in a split pane. Non-matching bases shown in red, ambiguous bases in consensus shown in light blue. Click toolbar button to color bases or background.

Sequence and Overview -- add assembly overview to sequence view. Brackets mark position and extent of sequence display. Click to set new location.


Sequence and Coverage -- add coverage histogram below sequences.

Sequence and Trace -- add trace data below sequence (if available). Click on base to show trace. Use sequence scroll bars to scroll sequence and trace data.


Designing Primers

Click Primer, Design or use toolbar button. Set option to Search for Primers or Create from Molecule, set primer type, enter primer length, click Next. Change molecule, if necessary and then follow instructions below. 

Search for Primers:

Enter target region or position and set search option. Primers found are listed. Sort by rank (quality) or position. Click Primer Report button to open primer viewer for information or analyses. 

Click Search Results/Search Stats button to review search summary.

Click Auto Adjust Length or Auto Adjust Criteria to find more primers by repeating search with adjusted length or criteria settings. 

Create from Molecule (display in sequence):

Enter target position for initial placement. Primer viewer window opens and shows primer and molecule sequence. Map appears above sequence.

Ticks on top line mark locations of neighboring primers that will meet criteria. Evaluation bar appears below primer. Click on value to see details on page in Analyze tab. Click Edit tab to return. Move primer or adjust length using toolbar buttons until primer meets criteria set.

Direct Entry of primer:


Click Primer, Direct Entry to start wizard. Enter primer name, type, primer sequence. When complete, view primer report in primer viewer window.

With primer open in primer viewer window, click File, Save to save new primer to disk or click File, Add to Collection to save to a primer collection file. Click Primer, Find Molecule Sites to scan your molecule collection to see if this new primer will bind effectively to any of the scanned molecules.


Use Sequencing Primer Wizard:

Click Primer, Sequencing Wizard to design a set of primers. Specify primer type, optimal primer length, preferred primer spacing. When set of primers designed, export all primer sequences or create a new primer collection.

Primer Collections

Click on Primer List to open. In left panel, click My Collections then select a collection file. Primers in file shown in right panel. Sort using column headers, resize columns or window by dragging with mouse. 

With highlight bar on primer, use toolbar buttons to view/edit this primer entry or export the primer sequence. Click Select button (lower right) to use this primer in a current operation or to open in primer viewer window. Click Add New Entry toolbar button to create new primer entry in place in the collection.

Click Folder Options toolbar button to add new folders or new empty collection files or to rename or delete collection files or folders. 

Search collection -- type in text to search for in Find edit box (lower left) and click Go button. New, transient folder Search Results will list primers found.

Analyzing Primers

To analyze one primer, select primer from Primer List to open primer viewer window and click Analyze tab. Or click Primer Report button from search list, or click Primer, Analyze and select one or two primers to analyze. Click toolbar buttons on Analyze tab for:

- Primer Reports — general analysis information summary
- Dimers — homologies between primers (primer dimers)
- Cautions — summary of Stability, GC Clamp, Runs of bases, Repeats, Hairpins analyses
- False Priming or Any Homologies — 3'-end homologies or any significant homologies between primer and template

Analyze Mix Wizard:

Found on Primer menu. Use wizard to identify list of primers and molecules and set parameters for analysis. Analyze possible products formed, binding sites found, and analysis cautions noted (primer dimers that might affect results or molecules or primers not used.)

Primer Values Profile:


Click Operations, Primer Values profile. Calculates T_m, GC content and stability for primers of specified length and plots values.

Mutagenesis Profile:


Click Operations, Mutagenesis profile. View sequence, enzyme recognition sites, translation and effect of mutation. Find 'almost' enzyme sites, construct mutants, create primers with mutation.

Primer Operations


Create Product:

Found on Primer menu. Create a new DNA molecule that is the amplified product of a PCR-type reaction using two primers and a molecule that you specify. Or use toolbar button where available. 

Find Primer Sites:


Found on Primer menu or use toolbar button. Find sites where your primers could bind effectively to the active molecule. Add primer sites to molecule for display on map or sequence. 

Display and Use Primer Sites:

On map, click Enzyme Sites/Primer Sites toolbar button to switch to primer sites. Select primer site and then use toolbar buttons to export primer sequence, create primer or product, change primer name. 

To display in sequence, click sequence Format button, check Primer Sites on Style tab and select display style. Select primer site colors on Color tab.


Link to Molecule:

Found on Info or Details tab in primer viewer window. Click Link to Molecule button to link a primer copy to the specified molecule or to add the primer site to the molecule map. 

Aligning Sequences

Use Align menu or toolbar buttons shown below to align multiple sequences, compare two sequences, scan for sequence similarity, or initiate remote (BLAST) searches using the NCBI BLAST server.


Align Multiple Sequences:

Click Align Multiple Sequences. Select type of alignment, set sequence type (DNA or amino acid) and select scoring matrix. 

Align sequences against a reference sequence or do a multi-way alignment of all sequences and progressive assembly of alignments.

Click Next to identify sequences to align. Click molecule list button at right and select sequences or group. Use small up or down arrowhead buttons to move sequences within list. Click Edit Item button to identify region to align, if less than full molecule. Click Finish to start the alignment.


Compare Two Sequences:

Click Compare Two Sequences. Select type of comparison, sequence type (DNA or amino acid), and set method or scoring matrix. 

FastScan uses rapid search lookup table method. MaxScore favors finding high scoring regions. MaxQual favors finding shorter regions of higher homology. Needleman-Wunsch uses exhaustive base-by-base comparisons to find long regions of homology, even if they have numerous mismatches.


Click Next to identify sequences to compare. For Sequence box 1, click Change... button at right and select sequence from molecule list. Repeat for Sequence box 2.

Scan for Similarity:


Click Scan for Similarity. Click New Search and identify the query sequence (search molecule name and region). Set translation option and click Next to identify files or folders to scan. 

Click Add Folder button to select a folder location to add to the search list. (Subfolders are included.) Click Add File button to select a library file to add to the search list. Click Save List button if you want to use the same search locations for later scans.

Set scan options -- Set Speed to make the search more or less sensitive. Set lower Cutoff to accept results of lower significance.

Use the Scan Results Wizard to select molecules to load for use now, extract molecules from a database file for use later, or set up a multiple sequence alignment, using the scan results as a starting point. 

Remote Searches:

Click BLAST Internet Search. Select the BLAST program to use and the BLAST database to search. You need an internet connection to send search requests to the NCBI BLAST server. 

A built-in web browser shows search results. Click Get Molecule button to import molecule in GenBank format for use now.