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## 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** Basic Edition

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### 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.

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### 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 file open on screen, click Get Molecule button on browser  window toolbar 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.

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## 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 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. 

Click on Map Site list header control to select what to display. Click on column headers to sort by name or position. 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).


Select (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 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, notes, change starting bp number or view molecule composition.


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## 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.


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## 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 to the right of each molecule in the ligate display 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 (in 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. Define what you want to clone, define the vector use, specify your cloning preferences (or use default settings). Use toolbar buttons to examine results, construct the recombinant of choice, or redefine the procedure. 

Click Clone, Gateway Cloning to simulate cloning using Gateway® Recombination Cloning techniques. The wizard will help you select the appropriate components, show you the proposed result, and create the final recombinant molecule.