Main Toolbar Changes

New easier access with toolbar buttons on main toolbar:

Find in Files:

Use this feature to scan molecule files to look for certain genes or specific text in the molecule name or description, or search the Notes field in Clone Manager files (*.cm5).



Use this option to send the data in the active window to a file. Text data will be sent to file in html format, graphic data in wmf format. (For additional export options, use File, Export.)

Enzyme Lists:

View enzyme list information (recognition sequence, cut position, ends produced, overhang bases), build/edit user enzyme lists for enzymes routinely used, construct on-the-fly lists for a specific task.



Q

No longer accessed with buttons on main toolbar:

| | Now found on menu: | Keyboard access: |
|---------------------------|-----------------------|---------------------|
| Find Enzyme Sites | Clone menu | Alt + C, F |
| Cut | Clone menu | Alt + C, C |
| Ligate | Clone menu | Alt + C, L |
| Plan Cloning | Clone menu | Alt + C, P |
| Design primer | Primer menu | Alt + P, D |
| Analyze primer | Primer menu | Alt + P, A |
| Find primers that bind | Discover menu | Alt + D, P |
| Align Multiple Sequences | Align menu | Alt + A, A |
| Compare Two | Align menu | Alt + A, C |
| Scan for Similarity | Align menu | Alt + A, S |
| Sequence Assembly | Align menu | Alt + A, E |
| NCBI Blast search | Align menu | Alt + A, B |
| New (create new molecule) | File menu | Ctrl + N |

Upgrade Information Clone Manager 10 for Windows

Getting Started

Once the new version of Clone Manager has been installed on your computer (or you have set up your computer to run the new Clone Manager under a network concurrent license), you are ready to get started.

All of the files previously prepared using Clone Manager can be used with the new version.

If you assign the same home directory, you will have immediate access to your primer collections, sequence phrases, DataBook files, and your latest enzyme list. (This folder was called CMHome and was usually found in your Documents folder in the last version.)

Click File, Preferences to set your home directory.

User Interface Updates

Clone Manager 10 is now DPI-aware and can take advantage of your highresolution screen display. This means clearer text and better map drawing. In addition, new fonts are being used and a new color palette has been implemented.

To accommodate those with smaller displays (smaller laptops and 2-in-1s in tablet mode), menus are now shorter, toolbars are shorter, and individual toolbar buttons are larger.

The new main toolbar has some familiar buttons, some new buttons, and some buttons that have been removed and the functions accessed through the appropriate menu (see last page).

A new toolbar section gives easy access to places you may want to visit often:



Molecule List Primer List Enzyme Lists Sequence Phrases Data Book Add Entry View list of loaded or newly-created molecules View active/loaded primers and primer collections View lists of enzymes or create new user lists View or manage your sequence phrase collection Simple built-in database for molecule information Add an entry to DataBook or to a primer collection

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Ligation Update

The ligation module now supports joining together two or more pieces of DNA. The new ligate display window shows you the molecules or fragments as they are being prepared for ligation.

In the upper half of the new window, an icon map of the active molecule is shown, with features (if any). If enzymes were used to create the molecule's ends, these enzyme names appear above the respective end. The actual sequence of each end is shown below the map. The molecule in this window can be modified (see below).

Use the Fragment Information button to view the features table for this molecule or to find enzymes that could prepare ends that would be compatible to the fragment to the left or right (in lower window).

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|-----|---|
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| | |

In the lower half of the window, all of the molecules or fragments are shown in boxes. Click the Add Molecule button to select additional molecules to add to this window. You should arrange these fragments in the order in which they should be joined. Click on a molecule and drag to move to the right or left, as needed, or use the Move or Select Fragment button.

Small icons appear between each fragment box to indicate if ligation is possible. If changes are needed to a fragment, click to select the fragment, causing it to appear in the upper box, where modifications can be made.

Possible modifications to fragments:

Cut molecule

Use the Cut Fragment button to access the cut molecule operations for the selected molecule. You can cut a circular molecule to make it linear, cut out a region to be cloned, or cut with an enzyme to make a compatible end.

Modify Ends

Use the Modify Ends button to access the modify ends operations for the selected molecule. You can use standard or custom end modifications to prepare molecule ends for ligation.

Invert sequence

Use the Invert Fragment button to reverse (invert) the sequence of the selected molecule.

Undo last action

Use the Undo button to undo the last modification to the selected molecule.

Click the Ligate button to join all compatible ends of the fragments in the order shown. If you do not want the ligate operation to circularize the molecule, click on the drop-down arrow to the right on the Ligate button and select Do not circularize.



Once ligation is complete, you can enter the molecule to the molecule list for further use or save it to disk.

New Cloning Wizards Implemented

The assembly cloning wizards now support Gibson Assembly, In-Fusion cloning and Ligation-Independent cloning techniques. The wizards will help you to select the appropriate components, show you the proposed result, and create the resulting recombinant molecule.

Select one of the assembly cloning wizards from the Clone menu to get started. Use the Ligation-Independent Cloning wizard to join fragments previously prepared with correct overlaps.

Use the Gibson Cloning or In-Fusion cloning wizards to use PCR to create amplified fragments with overlaps, and then assemble the fragments, using the assembly procedure selected. Set the procedure and primer design options, if applicable.

Click the Create Molecule button to have the program automatically do the required steps to simulate the cloning experiment, produce the recombinant molecule, and enter to the Molecule List.



Working Map updates

Working (on-screen) maps now show features in the style and color selected. Features with joins use a narrow line to connect joined segments.

The updated color palette produces well-balanced map figures in contemporary colors. Updated fonts improve feature name and enzyme site text.

Easy, right-click access to customization now includes the ability to select your three default styles. New toolbar button in map window to create an Enhanced View map.



Features Table updates

New user settings support displaying feature basepair positions as left-toright or start-to-end. And you can now elect to show an iconic map of the molecule with selected feature highlighted above the table, and the selected feature map style/color and sequence color below the table.

The option to show information-only features on the features table is now included in Settings.

New custom style settings dialog box for features makes it easy to use the three default styles, as well as the individual feature custom settings. You may find it helpful to use style 1 (solids) for important features, and style 2 (shaded) or style 3 (open) for less-important features.

Molecule List update

The molecule list now has the ability to show more information about the selected molecule. You can see the number of features, primers and enhanced maps contained within the molecule file, as well as the start of the Notes field. Use the More Info/Less Info button to show or hide this additional information.

