

Supplemental Help - Clone Manager Professional Suite v 8

Updates to the Clone Manager Professional Suite include new functions that provide the capability to view multiple traces and edit the consensus sequence in the sequence assembly module, and to import primer collections from a tab-delimited text file. To help you get started with these new functions, the following help text is provided.

Sequence and Trace

When a sequence assembly operation has been performed, you can now view multiple traces in a new page of the results window. Traces can be viewed if the assembly was performed using sequence files from automated sequencing machines and these files contain trace data (ABI or SCF format files). You can view the aligned sequences with one trace chromatogram or multiple trace chromatograms shown below the sequences in a split pane.



Click the Sequence and Trace toolbar button to display one trace chromatogram.

Click on a base in one of the aligned sequences to view the trace data for this sequence at and around this base position. Vertical and horizontal highlighters mark the sequence and base in the upper panel that you have selected. The lower panel displays the trace data with the selected base marked with a vertical highlighter and centered in the display, if possible. Click on another base to view trace data at another position.



Click the Sequence and Multiple Traces toolbar button to display trace chromatograms for all sequences shown.

Click on a base in any line of aligned sequence data to view trace data for all sequences at this position in the alignment. A vertical highlighter marks the column of sequence bases you selected. The lower panel displays the trace data with the appropriate base marked in each sequence frame.

Use the mouse to pull on the assembly viewer window frame to make the entire data window larger, if needed. Use the mouse to move the split bar between the upper and lower panes to change the proportion of space available for the sequence or trace displays.

Navigation

You can use the horizontal scroll controls in the upper sequence panel or the keyboard arrow keys to move the contig to the left or right. As long as the selected base stays within the visible sequence, the vertical highlighter remains on this base and the trace data in the lower panel continues to show the trace for the selected base, centered within the display.

If, however, the vertical highlighter in the upper panel hits either the left or right window frame, the highlighter will begin to shift from one sequence base to the next, to remain within the visible display. At this point, the vertical highlighter in the lower panel will also begin to shift, synchronizing the trace data to the sequence data scrolling in the upper display.

To move the vertical highlighter to the left or right within the sequence, use Alt + arrow key or just click on another base with the mouse.



Click the View Sequence toolbar button to return to the plain sequence display and close the split pane view.

Special Note

If you are using this new feature to view traces from a sequence assembly previously saved to disk, you might find an incorrect positioning of the trace view if a sequence had non-aligned (clipped) bases at the left end. To correct your data, open your previously saved assembly results data file (*.aa4). Click the Redefine toolbar button (first button in the assembly results window toolbar). When the set up dialog box appears, just click Next to accept the same assembly type. When the next page in the dialog box appears, just click Finish to accept the same sequences and parameters. When the sequence assembly is complete, use File, Save to save the new results to disk, overwriting the previously saved data.

Edit Consensus Sequence

When viewing sequence assembly results, you can edit the consensus sequence if you believe there is an error in a base shown. You can replace one base with another or remove a base from the consensus sequence, if required. And you can quickly find ambiguous bases in the consensus sequence, where problems with base calling may be most likely.


You can edit the consensus sequence from any display screen that shows sequence data. You might find the Sequence and Trace (see above) display the most helpful in identifying miscalled bases.



Click the Go To Ambiguous toolbar button to move to the next position in the consensus sequence that has an ambiguous base.

To edit the consensus sequence:

1. Click on the base in the consensus sequence that you want to change.

2. Click the Edit Consensus  toolbar button.
3. Verify that the correct base is shown and the edit pointer (black arrowhead) marks the correct base in the sequence.
4. To replace a base, click the Replace Base option and enter the base you want to use as a replacement.
5. To remove a base, click the Remove Base option.
6. Click OK to make the requested change to the consensus sequence.

When replacing a base using this method, you can enter (type in) any valid base, including ambiguous bases. When removing a base, a gap will be shown in the consensus sequence on the screen. If this sequence is entered to the molecule list and later used or saved to disk, the gap will be closed up.

To move the edit pointer:

You can move the edit pointer (black arrowhead that marks the base to be changed in the sequence) without leaving the Edit Consensus dialog box, if needed. Click on the left or right sides of the spinner control to move the pointer one base position to the left or right within the consensus sequence. You can also use the keyboard combination of Alt key and plus (+) or minus (-) keys to move the edit pointer.

Remember changes:

If you have already saved the sequence assembly results to a disk file, you should save to disk again so that the changes made to the consensus sequence will be written to file. To save just the consensus sequence to a disk file, click the Enter Contig to Molecule List toolbar button and then click File, Save when the molecule viewer window shows the newly-entered molecule.



Hint -- simple base change

For a quick and easy base replacement, just right-click on the base you want to replace and then select Change to A, C, G or T from the drop-down menu. Or select Change to Gap to remove the base at this position.

Export / Import Primer Collections

You can use the Export option to prepare a tab-delimited text file containing the information in a primer collection file. Programs like Microsoft Excel or Microsoft Access can import this data allowing you to use this information in other applications.

Export a primer collection:

1. Open the Primer List and select (highlight) the primer collection you want to export.
2. Click the Folder Options button and select Export.
3. In the Export Primer Collection dialog box, select to export to a disk file or copy to the clipboard.
4. Use the checkbox to indicate if you want the exported file to contain headers at the top of each column of data.

You can use the Import option to read in primer data contained in a tab-delimited file prepared in another application in order to create a new primer collection.

Import a primer collection:

1. Open the Primer List and click My Collections.
2. Click the Folder Options button and select Import.
3. Select the tab-delimited text file containing your primer data.
4. In the Import Primer Collection dialog box, specify the first row that contains primer data to import. (If your file has column headers, the data usually starts at row 2.)
5. Use the small drop-down arrow keys above each column to pick the type of data in that column or indicate that the data should be skipped (not imported).
6. Enter the name for the new primer collection and click OK.

Preparing data for import:

If your primer data is in an Excel worksheet, for example, you can open the worksheet in Excel and use Save As... to save your file in Text (tab delimited) format.