

Clone Manager File Viewer

for Windows mobile devices

Version 1.0 --- User Guide

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CM Viewer - Overview

In the Clone Manager File Viewer, you can look at molecule files, complete with features and enzyme and primer sites (data tree), as well as molecule sequence data. You can also view primer collection files and use a set of helpful tools.

Open Files

You can open molecule files and primer collection files in Clone Manager file formats (*.cm5, *.cx5, *.px5). You can only have one file open at a time. To open a file:

- Tap Open to display the list of available files.
- In Type, select molecule or primer collection files.
- Tap the name of the file you want to open.

Tap a column header to sort files by the data in that column.

Molecule Data Tree

In the Clone Manager File Viewer, you can view molecule data in a concise tree format. Click View > Tree if this page is not the current view.

View Features

Tap [+] beside Features node to expand the features list to show each feature as a one-line entry.

Tap [+] beside a feature to view the Feature Key or description data.

Info-only features -- If the number of features shows a partial listing (5 of 7 for example), you have two Info-only features that are not shown. Tap Format > Features to show this feature type.

Format Features

You can change the display style or sort order for the features list. To format the features list:

- Tap Format > Features.
- In Display Style, select to Show or Hide info features.
- In Sort by, select to sort by feature name or basepair position.

When information-only features are hidden, the feature count reports a partial listing, such as 5 of 7 (5 features shown out of a total of 7).

View Enzyme Sites

Tap [+] beside Enzyme Sites node to expand the enzyme sites list to show each enzyme or site as a one-line entry.

If enzyme sites are grouped by enzyme, tap [+] beside an enzyme to view the position of each site.

Tap Format > Enzyme Sites to change the display style.

Format Enzyme Sites

You can change the display style or sort order for the enzyme sites list. To format the enzyme sites list:

- Tap Format > Enzyme Sites.
- In Display Style, select to show one enzyme site per line or group sites by enzyme.
- In Sort by, select to sort by enzyme name or position/number of cuts.

Number of Cuts sorting replaces Position sorting when enzyme sites are grouped.

View Primer Sites

Tap [+] beside Primer Sites node to expand the primer sites list to show each primer site as a one-line entry.

Tap [+] beside a primer site to view the primer sequence, primer length or description data.

Tap Format > Primer Sites to change the display style.

Format Primer Sites

You can change the display style or sort order for the primer sites list. To format the primer sites list:

- Tap Format > Primer Sites.
- In Display Style, select one primer site per line.
- In Sort by, select to sort by primer name or position in molecule.

One primer site per line is the defined display style for this version.

View Notes

Tap [+] beside Notes node to expand the notes display to show all of the text in this entry.

Tap [-] beside Notes node to close the expanded notes display when finished.

The molecule name, size, description, filename and file date appear at the top of the molecule data tree and are always visible.

Molecule Sequence

In the Clone Manager File Viewer, you can view molecule sequence data in three different formats. Click View > Sequence if this page is not the current view.

Tap Tools > Go To to move to a specified basepair position in the sequence.

Tap Format > Font Style to change the font size, if needed.

Tap Format to select an alternate sequence style.

Annotated Sequence Format

Double-stranded sequence is shown (center), with enzyme and primer sites above and features below the sequence. Basepairs numbers appear at the upper left and right corners. Use horizontal scroll bar to move through sequence.

Translated Sequence Format

Double-stranded sequence is shown (center), with 3 frames of translation above (normal strand) and 3 below (complement strand). Basepairs numbers appear at the upper left and right corners. Use horizontal scroll bar to move through sequence.

Plain Sequence Format

Single-stranded sequence is shown with basepair numbers at left. Use vertical scroll bar (right) to move through sequence.

Format Font Style

You can change the font attributes for text in the sequence display. To format the font style:

- Tap Format > Font Style.
- In Font Size, select standard or slightly larger or smaller point sizes for sequence data.
- In Font Colors, select to use color for sequence annotations or to show all text in black.

If color option is selected, enzyme sites, primer sites, features and translation use pre-defined colors.

Primer Collection

In the Clone Manager File Viewer, you can view primer collection files.

Tap [+] beside a primer to view the primer sequence or descriptive data.

Tap Format > Collections to change display style or sort order.

Format Collection

You can change the display style or sort order for the primer collection data. To format the primer collection:

- Tap Format > Collections.
- In Display Style, select to show the primer name, length and type or to show the primer description.
- In Sort by, select to sort by primer name or description or to sort by primer type and then by primer length.

Use Tools

The Clone Manager File Viewer toolbox has options to let you export data to share with others, jump to specific positions in a molecule sequence, or search for a feature or text string.

Tap Tools to access the toolbox.

Help

Tap Tools > Help to access help for the Clone Manager Filer Viewer.

Tap the link for help you need now or tap CM Viewer Overview for the main contents page. To find a topic:

- In the help viewer, tap Search or Find.
- Enter a search string to find topics with this keyword.
- In Type, select Help.
- When results appear, tap on a help topic to open.

Find

You can search the molecule data tree text, the molecule sequence, or text in a primer collection file, looking for an exact match to a search string you enter. To find text:

- Tap Tools > Find.
- In Search for, enter text string.
- Matching text found will be marked and moved into view.
- Tap Tools > Find Next to continue the search, looking for another match.

Export GenBank

You can export essential molecule data to a file in a format that is consistent with the standard GenBank file format.

Tap Tools > Export GenBank and enter a name for the new file. Identify a folder or storage location, if appropriate.

Use this option to prepare a file to share with a colleague.

Export Primer

You can export the sequence of a primer to a plain ASCII (DOS) text file.

Tap Tools > Export Primer and enter a name for the new file. Identify a folder or storage location, if appropriate.

Use this option to prepare a file to share with a colleague or use in another program.

Go To (sequence)

Tree View

Tap and hold an enzyme site, primer site, or molecule feature and select Go To from the pop-up menu. The Sequence view will open at this position in the Annotated format. Tap View > Tree to return.

Sequence View

Tap Tools > Go To and enter the basepair position to bring this part of the sequence into view.