

Scientific & Educational Software

Clone Manager

User Configuration Settings

User configuration settings can be preset for Clone Manager users by the network administrator by adding user configuration settings to the Clone Manager configuration (.ini) file or by using Group Policy. You can select which method to use (but do not make user configuration settings with both methods). Instructions for adding settings to the configuration file are provided below. Please see the document CM_SetupPrefs.pdf for information about setting Group Policy.

Configuration file instructions:

Start the utility User Configuration File Editor (UserConfig.exe), found in the SciEdLicense folder of Program Files.

Next, identify the installation directory (folder) for the Clone Manager program. If not shown, use the Browse button to locate this folder. (The configuration (.ini) file will be found in this folder.)

Set the check box for each user configuration setting you want to enable and then select the option or enter the location required, based on the descriptions that follow. If you do not want individual users' preference settings to override your values, set the Lock checkbox to the right of the item.

Configuration Setting Descriptions

User's Home Directory

The user's home directory is the location where the Clone Manager program will look for personal configuration data and user-specific files and folders (databooks, work boxes, enzyme lists, primer collections). You can use macros to define the path: <UserName> can be used to specify the logon name of the current user. <UserDocs> can be used to specify the personal data folder of the user (MyDocuments under XP, Documents under Vista).

Sample value: <UserDocs>\CMHome

Default File Format

Sets the file save format the program should use when saving molecule files for the first time. You can save molecule files in the standard Clone Manager molecule format (*.cm5) or in a new xml format (*.cx5). The *.cm5 format is preferred and has a file association set (you can double-click on a *.cm5 file in File Explorer and open Clone Manager with this file loaded). The xml format is a human readable format that can make data portability easier. Although this file format is readable, it should not be edited outside Clone Manager.

Sample value: Sci Ed Molecule (*.cm5), standard

Shared Resource Location

Sets the location where shared resources are located. Enzyme lists and DataBook database files can be shared with others in the group. If you are using the Clone Manager Professional suite, you can also share primer collection files. Note that shared resources are read-only. Please refer to the Clone Manager help file topic Shared Resources, Set Up for instructions on how to set up this shared location. (The text of this help topic is included at the end of this document.)

Sample value: \\server\shared resource location

Prompt for Author Stamp

Select Yes to set the program to prompt for author information when a file is saved for the first time. Users can enter an author name, date, and notebook reference. This information is sent to the Notes field in Clone Manager molecule (*.cm5) files and can be printed on the page with a molecule map or written to a DataBook entry. Author stamping can help you to identify the source of a file or the location of needed documentation.

Author Name

This is the name that will be automatically entered in the Author Name field when the Author Stamp function is used. The macro <UserName> can be used to specify the logon name of the current user.

Sample value: <UserName>

Repository Location

Users can use Submit to Repository to instruct the Clone Manager program to send molecule data to a central shared folder (location) you specify. This location may be a central repository for molecule files shared by a group, or a back-up location where you have decided to keep an extra copy of critical files. You can use the Repository Data Format to set the data file format. Note: the path you enter must be accessible from the client computers. It is recommended that you use UNC format (see sample below).

Sample value: \\server\shared repository location

Repository Data Format

This setting allows you to specify the data file format used when Submit to Repository sends a copy of the molecule data to the central shared folder (location) specified as the Repository location (see above). File format options include: Send Copy of Sci Ed Molecule file (*.cm5) (default file format), Export Data Subset as GenBank (human readable text format that can be easily read by other programs), Send Xml Sci Ed Molecule file (*.cx5) (an xml parsable format).

Sample value: Send copy of SciEd Molecule file (*.cm5)

Setting up Shared Resources

If you are running the program under a multi-user license (Small WorkGroup or Concurrent User license types), you can share enzyme lists and DataBook database files with others in the group. If you are using the Clone Manager Professional suite, you can also share primer collection files.

Files that can be shared

- Enzyme master file, file name SEEnz32.enz
- Set of user lists, file name SEUserList.dat
- List of special enzymes, filename SEUserDef.enz
- GenBank import filter, filename SEKeyList.dat
- DataBook database files, *.dx5

Sequence phrase collection files, *.sx5
Primer collection files, *.px5

Shared resources are placed in one location where everyone will be able to access these files. Each user then identifies this location in File, Preferences, Share Data in their program settings. When shared enzyme lists, shared databook files, or shared primer collection files are opened from this location, they will be opened as read-only resources. Personal user enzyme lists, databook files, and primer collection files can be used, in addition to the shared resources.

Setting up shared resources

A folder should be created for shared resources in an accessible location. To share the enzyme master file, copy the file SEEnz32.enz to this folder. To share a set of user lists, copy the file SEUserList.dat to this folder. To share DataBook database files, copy the databook files (*.dx5) to a subfolder DataBook, in the same shared location. To share sequence phrase collection files, copy the collection files (*.sx5) to a subfolder SeqPhrases, in the same shared location. To share primer collection files, copy the collection files (*.px5) to a subfolder Collections, in the same shared location (see sample, below). In this example, the shared location is the folder Shared_Resources with its path information.

- Shared_Resources
 - SEEnz32.enz
 - SEUserList.dat
 - SEUserDef.enz
 - SEKeyList.dat
 - Collections
 - AListPrimers.px5
 - Project104.px5
 - DataBook
 - CloningVectors.dx5
 - TeachingSamples.dx5
 - SeqPhrases
 - DNA-binding.sx5
 - Homing Endo.sx5

Notes for shared DataBook database files

DataBook files contain links to the complete molecule, primer, or alignment data files so that the files can be opened for use. You might want to consider using the following procedure to set up DataBook database files to share:

Place a copy of molecule files, primer files, or alignment results files in folders on your server or other accessible location. You might want to prevent others from overwriting the files in this location.

At a computer within the workgroup, use the Multiple File Converter module to create DataBook files using the easy batch procedure. These databook files should all have file paths that will allow the files to be opened from computers within the group.

Copy the databook files (*.dx5) you just created and place them in the shared location, as described above. The databook files in this location will be read-only.

If you want to change any of the data in the shared databook files, you can do so at the computer where you created the databook files (since they will be part of your personal databooks at this location). Then copy the modified databook files to the shared location. If you need to change the path (location) of many of the molecule, primer, or data files, you can use Operations, DataBook Tools to do a find and replace operation for the file path.