



Tutorial

Getting started

March 31, 2016

— Sample to Insight —

Getting started

This tutorial introduces the user interface of *CLC Drug Discovery Workbench* and explains how to import your own existing data into the program and how to work with molecules. Finally, 10 tips to get the most out of the workbench are presented.

Workbench Layout

When you open *CLC Drug Discovery Workbench* for the first time, the user interface looks like figure 1.

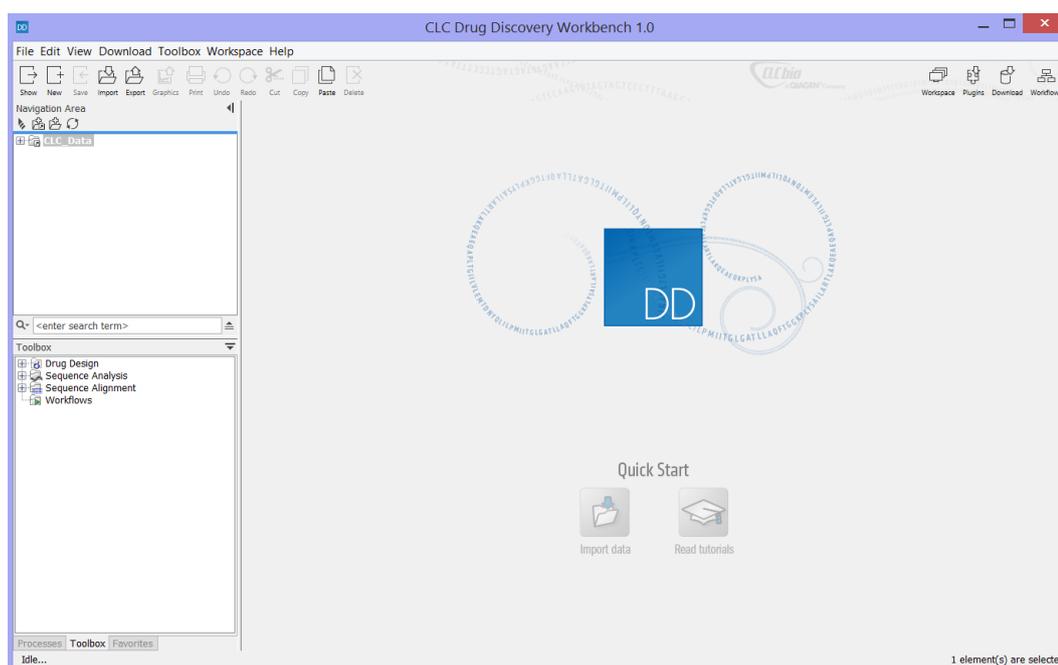


Figure 1: The user interface as it looks when you start the program for the first time. (Windows version of *CLC Drug Discovery Workbench*. The interface is similar for Mac and Linux).

The **Navigation Area** to the left is where you keep all your data for use in the program. Most analyses of *CLC Drug Discovery Workbench* require that the data is saved in the Navigation Area.

The **View Area** is the main area to the right. This is where the data can be viewed. In general, a View is a display of a piece of data, and the View Area can include several Views. The Views are organized in tabs, and can be arranged in split screen setups e.g. by using drag and drop, or even dragged to another screen.

The **Toolbar** found above the Navigation Area contains general tools that apply to all types of data, while the **Toolbox** found below the Navigation Area provides easy access to the analysis and modeling tools available in the workbench.

Import Data

From the **Toolbar**, a number of import and download options are available (figure 2). Molecules in the formats SDF, Mol2, and PDB can be imported.

Dragging a file from the computer file system into the **Navigation Area** will invoke the standard import of the file type (see Tip #1).

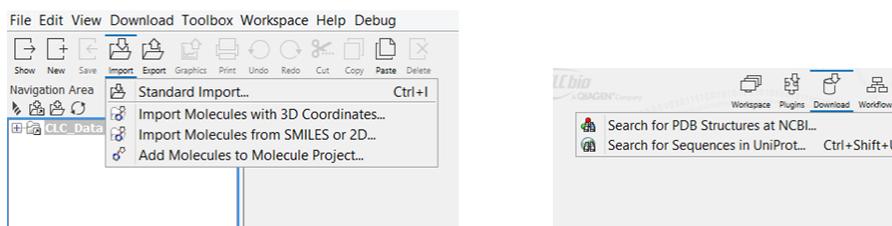


Figure 2: Import and download options found in the Toolbar.

You can also paste molecules represented by SMILES strings directly into a **Molecule Project** (see Tip #2). Double-clicking an object in the **Navigation Area** will open the data in the **View Area**.

Viewing and Working with your Data

All types of data opened in the **View Area** comes with a **Side Panel** containing options for handling and visualizing the specific type of data (see figure 3). Two types of objects are provided to work with molecules:

- **Molecule Projects** (🔗) are used to work with a limited number of molecules in a 3D view and is used to create a binding site setup for molecular docking and for studying molecular interactions.
- **Molecule Tables** (📄) are used to work with small molecules in a table view and can contain an unlimited number of molecules.

Selected molecules can be copied and pasted between tables and projects.

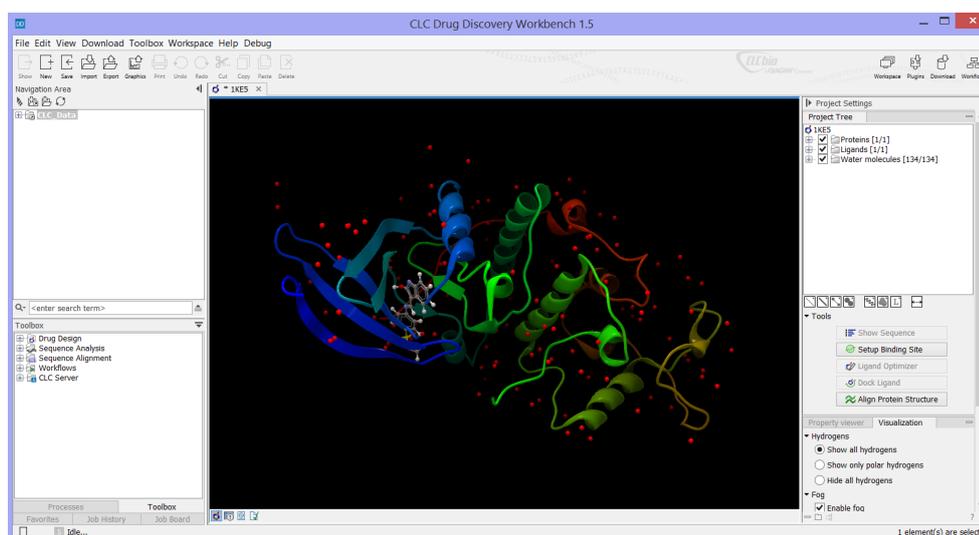


Figure 3: A Molecule Project containing the molecules from PDB ID 1KE5 has been opened. The Side Panel is found to the right of the 3D view and shows three palettes: Project Tree, Property viewer, and Visualization.

In the bottom of the view is found a selection of alternative views on the data. In the case of **Molecule Projects** and **Molecule Tables**, the **Issues** (🔍) view will show an updated list of issues concerning the structure and chemistry representation of the molecules in the project or table.

For **Molecule Tables**, the 2D molecule depictions can be seen in a grid view, if the **Molecule Grid** view  is selected.

Molecule Project Tree

The **Project Tree**, found in the **Side Panel** of **Molecule Projects**, shows a tree view of the project content. In the tree view, check boxes can be used to display or hide molecules from the view. The visualization of molecules selected in the **Project Tree** can be modified using the quick-style buttons found below the tree. Click-hold or right-click a quick-style button, to get a selection of color schemes available for the visualization style. When entries in the **Project Tree** are selected, the right-click context menu presents actions relevant to the selection, and the action buttons Show Sequence, Ligand Optimizer and Dock Ligand, found below the tree, can be used. The Setup Binding Site and Align Protein Structure actions always apply to the whole **Molecule Project**.

10 Tips to get the Most out of the Workbench

1. **Drag and drop files** from your computer into the Navigation Area. This will carry out an automatic import of the data in the file. A PDB file is imported to a Molecule Project, and SDF or Mol2 files to a Molecule Table.
2. From **molecule 2D sketcher programs**, such as ChemDraw and MarvinSketch, select a molecule and Copy As SMILES. Then the molecule can be pasted directly into a Molecule Project, and a 3D structure of the molecule is generated automatically (see the *Dock Ligands from a 2D Molecule Sketch* tutorial).
3. **Select atoms** by clicking them. Hold down Ctrl (Cmd on Mac) to select multiple atoms. Double-click an atom to select the whole residue or molecule. Right-click the *Current* selection in the Project Tree and choose to create an atom group from the selection. Atom groups can be visualized and displayed/hidden the same way as molecules in the tree.
4. From the lower right corner of Molecule Project Side Panels, **custom visualizations of molecules as well as personal Side Panel settings can be saved** and applied later or set as default (☰).
5. The **Show Sequence** action, found below the Project Tree in a Molecule Project, opens a sequence list for the selected protein or nucleic acid chains. The sequences are linked with the Molecule Project such that residues selected on the sequence will make a *Current* selection in the 3D view.

With the sequence in focus, tools in the *Sequence Analysis* folder in the Toolbox can be applied to add annotations to the sequence (see the *Exploring your Protein* tutorial).

Protein sequences are annotated with the PDB residue numbering, to facilitate **finding a particular residue** on the structure.
6. Hold down **Ctrl (Cmd on Mac) while selecting another view** on data (e.g. the Issue list). This will open the new view in a split-screen with the original view.
7. **Double-click an entry in the Project Tree** to zoom-and-fit to the molecule or atom group.
8. **Help is found all around.** Help buttons in dialog boxes and question marks (?) in tool wizards and in the lower right bottom of Side Panels take you to the relevant places in the built-in manual. Tool tips on the parameters in tool wizards offer more detailed descriptions of the settings.
9. In the Toolbox, **the Processes tab** lists the processes run since the workbench was started. Here, running processes can also be paused or stopped.
10. Click-hold-drag to **detach a tab from the View Area or the Side Panel** and move it to somewhere else on your screen(s).