Maestro Elements 1.5 Tutorial: Visualization

Legal Notices

August 2013

Getting Started

Requirements

Before starting this tutorial, please ensure that you have:

- Maestro Elements installed on your Linux or Windows machine
- A 3-button wheel mouse
- Tutorial-specific files, which can be found in your Schrodinger software installation directory, chosen by the person who installed your software. On Windows this directory is likely to be the default: `C:\Schrodinger2012\`

  Please copy this tutorial directory to your Desktop:

`<installation directory>/maestro-v`*`version`*`/tutorial/`

Starting Maestro Elements

If you haven't already, please launch Maestro Elements.

On Windows: double-click the Maestro Elements icon on your desktop.

On Mac: click the Maestro Elements icon in your Applications folder, in the Schrodinger subfolder. Or launch from the commandline as described below for Linux.

On Linux, set the SCHRODINGER environment variable to point to your Schrodinger installation location and run on the command-line: `$SCHRODINGER/maestro -elements &`

Viewing a Molecule

Once you've started Maestro Elements, take note of various features in the main window, as shown in Figure 1.

At the center of the interface is the Workspace, which remains empty until you import structures, build molecules, or open a project.

At the top of the interface is the menu bar, which gives you access to various tools.

On the edges of the Workspace are toolbar buttons for frequently-used tasks.

Please import the structure file `visualization_exercises.mae` from the tutorial directory. To do this, go to the **File** menu and choose **Import Structures....** Navigate to your Desktop, then to the `tutorial/` directory you placed there. Double-click the file `visualization_exercises.mae`.

Your Maestro Elements Workspace should now look like Figure 1. On Windows the toolbar will be attached to the top of the window.

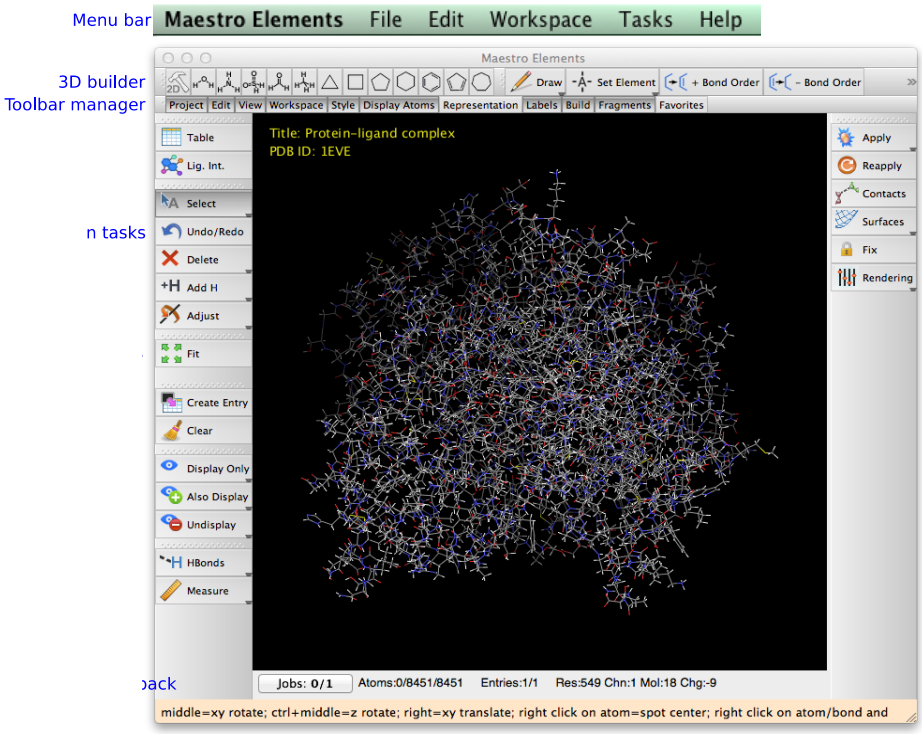

Figure 1: Maestro Elements with file visualization_exercises.mae loaded.

Using the Mouse

At this time, please take a moment to familiarize yourself with the behavior of the mouse in Maestro Elements. Place your mouse cursor over the protein. Now, press and hold while moving the mouse – aka dragging – with each of the 3 mouse buttons in turn. For the middle mouse button you can press on the wheel. If you have a wheel, also try scrolling the wheel.

Dragging with the left mouse button selects atoms in the Workspace, dragging with the middle mouse button rotates the scene in the Workspace, and dragging with the right mouse button moves the molecule in the plane of the Workspace. If your mouse has a scroll wheel, you can use it to zoom in and out. If you do not have a wheel, place the pointer anywhere in the Workspace, hold down the middle and right mouse buttons, and move the mouse to zoom.

Don't worry if you get lost. Just left-click on an empty spot in the workspace to make sure no atoms are selected and then click the Fit to Workspace button in the toolbar on the left side of the workspace. This will move the displayed molecule back to the center.

If you have a preferred mouse behavior, go to the **Edit** menu, choose the **Advanced** submenu and choose **Customize Mouse Actions....** Custom mouse actions can be selected for each button on your mouse. We recommend that you familiarize yourself with rotation, translation, and zooming before modifying these settings.

Try it: focus on the ligand in the protein binding site

Click the Fit to Workspace button in the toolbar on the left side of the workspace, to move the protein into view. Then press the Workspace Style button on the right side of the Workspace. This will highlight the ligand in the protein binding site. Press the letter L on your keyboard to zoom in on the ligand until it occupies a large part of the Workspace. (Alternatively you can scroll with the wheel to zoom, or drag horizontally with the middle and right mouse buttons).

Right-click on an atom in the ligand, to center that atom in the Workspace. Take a moment to test out right-clicking. A short click of the right mouse button on an atom centers the Workspace on that atom. A short click on a bond or on the background does nothing, although if there is an atom hiding behind a bond, a short-click on a bond could center on that atom. A long click of the right mouse button brings up a menu of options, depending on whether you clicked on an atom, a bond, or the background.

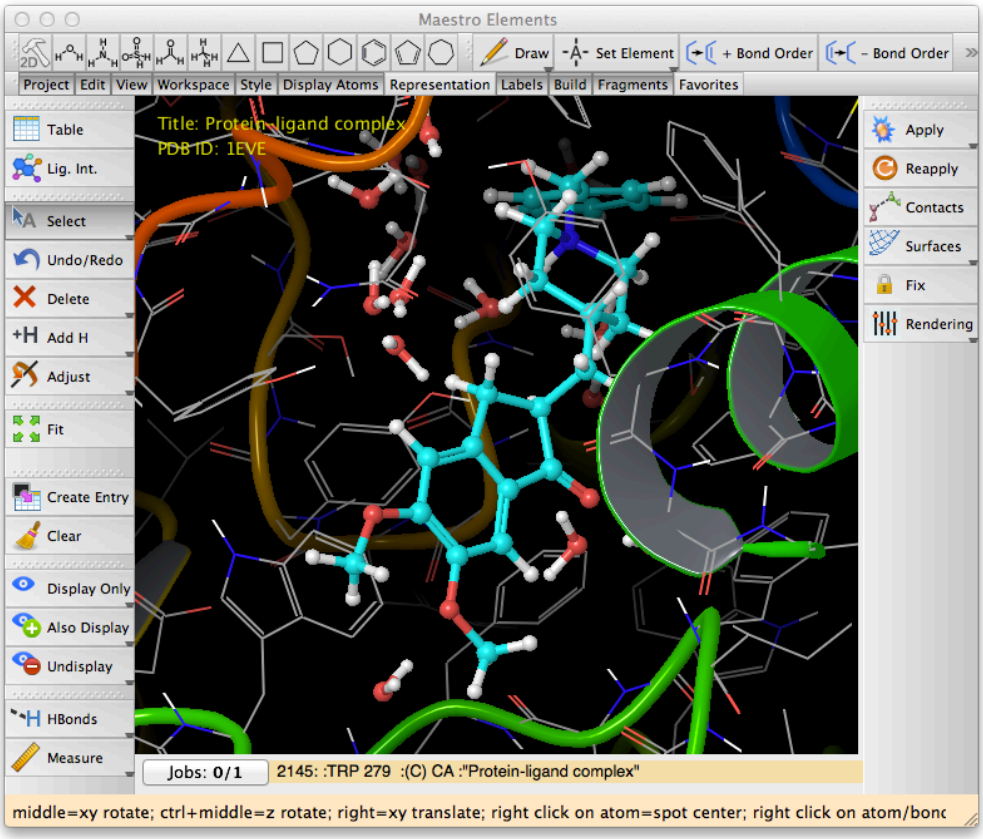

Figure 2. 1EVE binding site

Using the Project Table

The Project Table is where Maestro Elements stores structures that you've imported. It can also be used to plot, sort, and analyze data. For now, though, we'll just use the Project Table to control which molecules are displayed (incuded) in the Workspace. For more information about the Project Table, see Chapter 8 of the *Maestro User Manual*.

Go to the **File** menu and choose **Import Structures...**. Navigate to your Desktop, then to the `tutorial/` directory you placed there. Double-click on `multi-structure_file.sdf` to import it.

Click the Open/Close Project table button  on the toolbar to open the Project Table panel.

In the Project Table, you'll notice that several "entries", represented by various rows with text in them, are highlighted in yellow. These highlighted entries are the structures that you just imported. You'll also notice a tan row with a "–" in the In column. This is the label row for an entry group. When you imported the structures, they were added as a group, named after the file they came from. You can open and close the group by clicking the "–" or "+" mark.

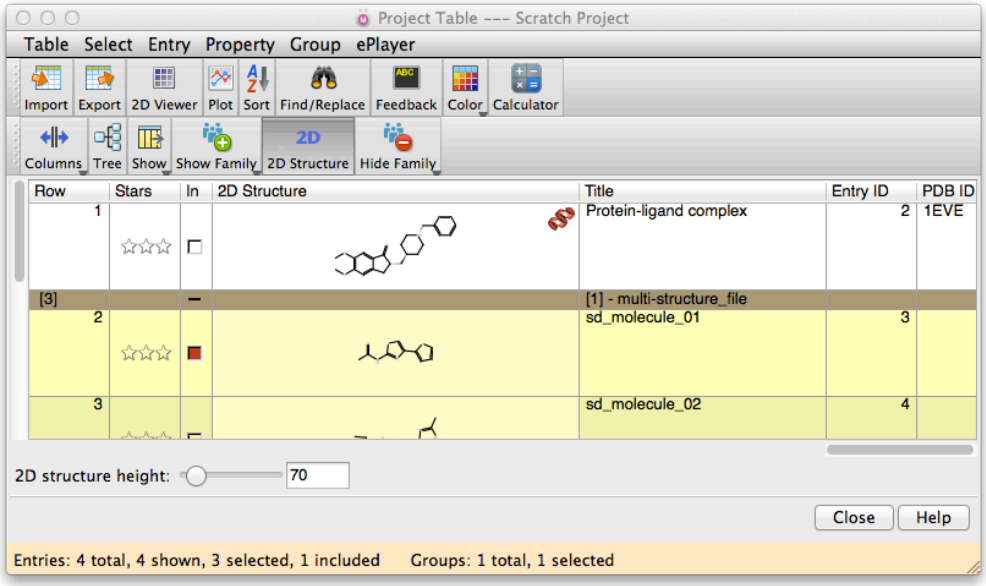

Figure 3. The Project Table

Click the square to the left of the title text (in the In column) to include sd_molecule_03 in the Workspace. The filled square indicates that the structure is currently included in the Workspace.

Pressing the 2D button shows 2D images for the small molecules in the Project Table.  In this mode you may with to decrease the 2D structure height, as shown in Figure 3. The red icon shown in row 1 indicates that this structure includes a protein that cannot be shown in 2D.

To include both sd_molecule_01 and sd_molecule_03 in the Workspace, hold down Control and left-click the square next to the entry for sd_molecule_01. You can then exclude one of these molecules by holding down Control and left-clicking the square next to an entry that is already included in the Workspace. To include all three molecules in the Workspace, left-click the square next to the entry for sd_molecule_01, hold down Shift and left-click the square next to the entry for sd_molecule_03. The `Control` and `Shift` keys behave the same for including entries as they do in other programs, for example row selection in Microsoft Excel. Please take a moment to try including the molecules in the workspace in different combinations.

Clear the Workspace by clicking the Clear Workspace button on the main toolbar.  This automatically excludes all entries from the Workspace.

As you continue to use Maestro you will notice that some Maestro operations act on the "selected" rows in the Project Table. "Selected" rows are colored yellow but are not displayed in the Workspace. This allows you to start calculations on large numbers of molecules without rendering them graphically. You can select a row by clicking on the left side of the row (in the Row column). The `Control` and `Shift` keys operate on row selection the same way they did for inclusion in the Workspace.

Saving Your Project

A Project is a directory of structures and data. Once you save your project, further changes you make to the Project Table are automatically saved for you while you work. This means you can return to this project later.

Go to the **File** menu and choose **Save Project As…** The Save Project dialog box appears.

In the File name box, type a name for your project, such as `tutorial`. Click the **Save** button.

If you quit Maestro and want to re-open this project later, go to the **File** menu and choose **Open Project…** This will open a file chooser so you can select a project.

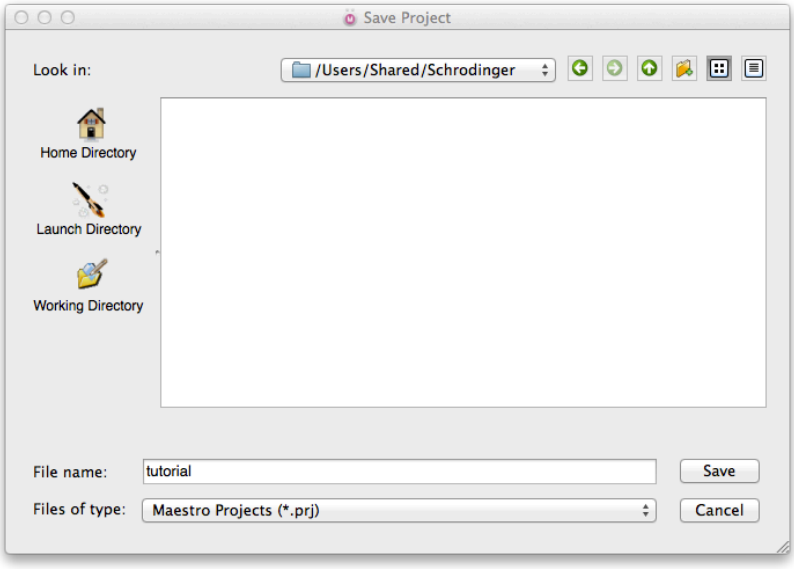

Figure 4. The Save Project dialog box.

Sharing Projects

To share your project:

Go to the **File** menu and choose **Export Project…**

Provide a filename to create a single .zip file of your project that you can share with others.

To open a project that someone has shared with you:

Go to the **File** menu and choose **Open Project…**

Navigate to the location of the .zip file of the shared project, and double-click it to open.

Building and editing molecules

You can build molecules either using fragments or using the “pencil” tool. Please try building the molecule shown in Figure 5.


This structure starts with the cyclopentyl fragment. After placing the first cyclopentyl fragment, click on one of the bonds of the first fragment to fuse the second fragment.


Then place the carbonyl fragment on one end of the structure.


Then place the planar amine fragment twice, on the two adjacent carbons as shown.


Hold down the Set element button, choose S, and click on the appropriate carbon in the workspace to change it to sulfur.


Then choose the methyl fragment, and add 4 methyl groups by clicking on an existing hydrogen to add each methyl. Be careful to create the correct stereochemistry. If you find that you have created the wrong stereochemistry, just use the Invert chirality button to flip the stereocenter. 



Use the carbonyl again with the hydroxyl fragment to create the carboxylic acid.


Finally, press the Clean up geometry button to regularize the geometry of your ligand.

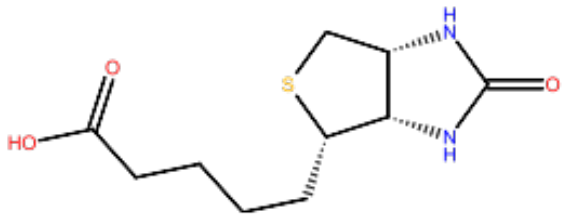

Figure 5. Biotin

Additional information on building:

The Maestro 9.3 tutorial contains more detailed instructions for building aspirin.

Video instructions for building molecules are also provided online:
http://www.schrodinger.com/supportcenter/

Save your molecule:

When you’re done building your molecule, be sure to press Create project entry from Workspace to save your molecule to the Project Table. 

Additional editing tips:

Other toolbar buttons and Tasks are useful during building:

Adding hydrogens is very important. Any energy calculation on your molecule will depend on the current protonation state and tautomer, so make sure the hydrogens and bond orders are correct.

If you make a mistake during building, the Undo button is useful. Only one-step Undo is available.

Hold down the Delete button to see what will be deleted. For building, the default Atoms is the most useful: when the Delete button is toggled on, any atom you click in the workspace will be deleted.

Ligand preparation: If you want the protonation states or tautomers for your ligand to be determined automatically, under **Tasks** and **Ligand Tools** choose **Prepare Ligands (LigPrep)....** If your molecule is in the Workspace, in the LigPrep panel change Use structures from: to **Workspace (included entries).** Also, click the radio button for **Epik** as the method to Generate possible states at target pH. Press **Start...** to generate ionization and tautomer states for your ligand.

After any edits to your ligand, remember to save your molecule to the Project Table! 

Export your molecule:

Select one or more rows in the Project Table for the molecules you wish to save to a file.

Remember, to show the Project Table press the Open/Close Project table button on the toolbar. To select a row, click on the left side of the row, in the Row column. Use the `Control` and `Shift` buttons to select multiple rows.

Right-click on any selected row and choose **Export structures**. In the File name: text box type a filename with the extension of your choice. For example type `mymolecule.mae` to save a Maestro Elements formatted file, or type `mymolecule.sdf` to save an SD-formatted file.

Advanced Visualization

In these exercises you will learn how to set your display preferences for your protein and ligand and also how to use additional visualization aids for your ligand in the protein binding site.

If you have been working on this tutorial from the beginning, you should have an entry in your Project Table called `Protein-ligand complex`.

 Open the Project Table and click the In square for the `Protein-ligand complex` row.

 If your complex is out of view, click the Fit to Workspace button in the toolbar.

If you are restarting the tutorial from this point, Please import the structure file `visualization_exercises.mae` from the tutorial directory. As before, go to the **File** menu and choose **Import Structures....** Navigate to the `tutorial/` directory you created and double-click the file `visualization_exercises.mae`.

Workspace style:

Click the Workspace Style button  once to highlight the ligand in the protein binding site. If you want these settings to always be applied, toggle on the Reapply style when Workspace changes. 

If you prefer a different style, hold down the Workspace Style button  and choose Settings... to change any settings you like. Press OK. Click the Workspace Style button once  to apply these changes.

If you play around with the Workspace Style settings and get into a state you do not like, you can press the Reset button to revert to the default Workspace Style settings. If your protein becomes undisplayed, you can always re-display all atoms: hold down the Also display button and choose All. 

The definition of ligand can also be modified if needed. To find these options, hold down the Workspace Style button  and choose Ligand Detection Settings....

Contacts and H-bonds:

 Click the Contacts and H-Bonds button. Check the box for Display receptor-ligand hydrogen bonds. Also check the box for Display receptor-ligand contacts. Press OK.

Surfaces:

Click the Create Binding Site Surfaces... button  once. This opens a panel, as shown in Figure 6. The most common surface to generate is a receptor surface just in the area around the ligand. To create this type of surface, check the box for Create receptor surfaces. Press OK. Rotate the molecule in the workspace (by dragging the middle mouse button) to view the binding site pocket.

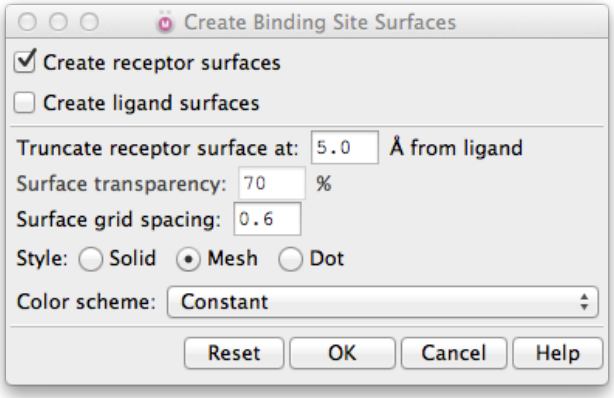

Figure 6. Create Binding Site Surfaces panel

Click the Create Binding Site Surfaces... button again. This time, change the Color scheme: to Electrostatic Potential. Press OK.

To view the electrostatic potential surfaces we created, we need to undisplay the first surface using the Manage Surfaces panel. This panel popped up when you generated your surface, but to find it at any time, hold down the Create Binding Site Surfaces... button and choose Manage....

In the Manage Surfaces panel, undisplay the first surface by holding down the `Control` key and left-click in the black square in the V column. The Manage Surfaces panel inclusion and selection behave the same way as for molecules in the Project Table.

To decrease the transparency of your surface, make sure the relevant surface row is selected (yellow) in the Manage Surfaces panel. Then click Display Options.... In the Surface Display Options panel, slide the transparency slider to the left to create a more solid surface. If you notice that displaying a surface noticeably slows down the Workspace, you may consider changing your surface style to Mesh in the Surface Display Options panel. This option is available just below the transparency slider. Press Apply to view any changes you make in this panel.

Scenes

You can create Scenes as part of your project to save and convey information. Scenes are snapshots of your workspace view that will be saved and can be played back. In Maestro Elements Scenes are available in the Workspace menu under the Scenes submenu.

Your first scene can be of your current workspace view. In the Workspace menu of Maestro Elements, go to Scenes and choose New... Type a short description of your current view in the workspace and press OK.

Move or manipulate the workspace, for example by zooming into the binding site. Create two more scenes the same way, and be sure to type a short description of each scene.

Now that you have three scenes you can view them as a movie by again going to the Scenes menu and choosing View. This will open a player at the bottom of your workspace, as shown in Figure 7. This shows the descriptions you typed and allows you to play through the scenes. Press Exit Scene to return to normal Maestro operation.

These scenes are now saved as part of your project, which can be shared as described earlier in *Sharing Projects.*

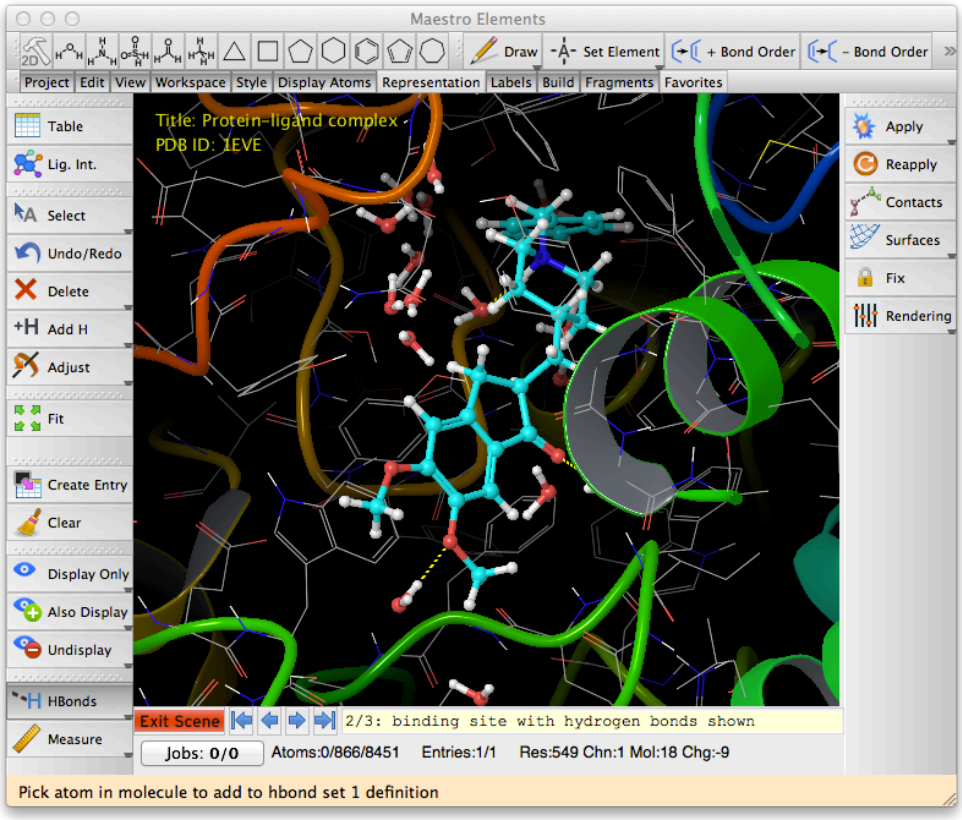

Figure 7. View Scenes player

Ligand Interaction Diagram

If you have been working on this tutorial from the beginning, you should have an entry in your Project Table called `Protein-ligand complex`.

Open the Project Table and click the In square for the `Protein-ligand complex` row to include it in the Maestro workspace. Open the Ligand Interaction diagram from the Tasks menu to generate the diagram as shown in Figure 8. To show the legend, choose LID Legend in the View menu.

Residue colors denote the residue type (as shown in the legend). Hydrogen bonds are shown as dashed pink lines if they are to a residue sidechain but are shown as solid pink lines if they are to a residue backbone. A gray atom background represents the solvent-accessible surface area (SASA) of that atom. In this tutorial example the two methyls on the left side of the image are solvent exposed.

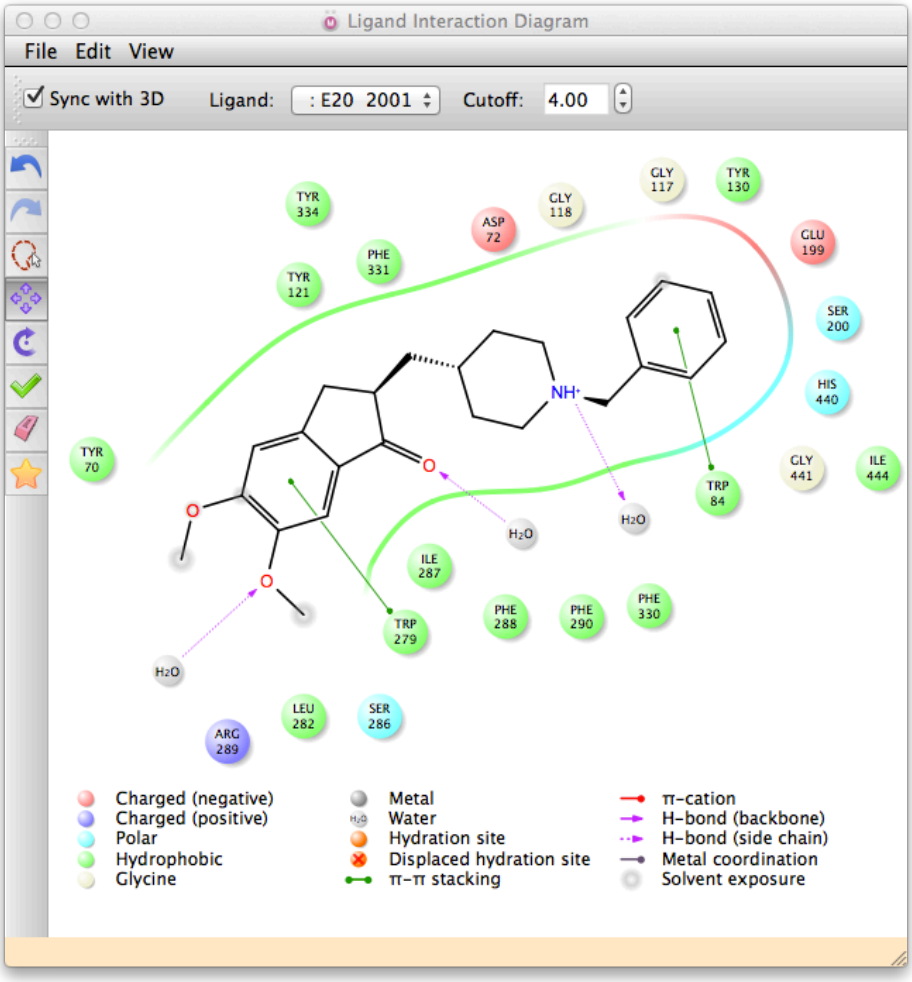

Figure 8: Ligand Interaction Diagram

Maestro Viewer Control for PowerPoint

To use the Maestro Viewer Control for PowerPoint, this must be installed separately from Maestro Elements. To test if it has been installed, try the steps in the **In Powerpoint** section and see if the necessary controls are available.

To install the Maestro Viewer Control for PowerPoint, download the installer from our Download page http://www.schrodinger.com/downloadcenter/ from the link under Other Downloads. Follow the README instructions in the downloaded ZIP file.

The Maestro Viewer Control for PowerPoint is supported for PowerPoint 2002/2003, PowerPoint 2007, and PowerPoint 2010.

In Maestro Elements

Create a workspace view in Maestro Elements the way you would like the workspace to look in PowerPoint. Make sure the center of the workspace rotation is in an appropriate place. As a reminder, right-click on an atom to center it in the workspace. Press CONTROL-C to copy the Maestro Elements workspace.

In PowerPoint

Control location in PowerPoint 2002/2003: Under View, choose Toolbars, then choose the Control Toolbox to open the Control toolbox panel. In that panel, press the button for More Controls. In the menu that opens, choose Schrödinger Maestro Viewer.

Control location in PowerPoint 2007: Click the Microsoft Office Button (in the upper left), and then click PowerPoint Options. Click Popular, and then click to select the Show Developer tab in the Ribbon check box under Top options for working with PowerPoint, and then click OK. On the Developer tab, press the button for More Controls. In the menu that opens, choose Schrödinger Maestro Viewer.

Create a new slide in PowerPoint. When you choose Schrödinger Maestro Viewer in the PowerPoint control, your mouse will change to a + symbol. Drag on the PowerPoint slide to create a large rectangle. After you make the rectangle, it will become a gray rectangle containing instructions on how to add content and how to activate the slide during a presentation.

To add your Maestro Elements workspace to the PowerPoint slide: start the slide show, navigate to that slide, click on the Maestro Viewer (the gray box), CONTROL-V to paste your Maestro Elements workspace into PowerPoint.

You may now send this PowerPoint presentation to others (as long as they have the Maestro Viewer Control for PowerPoint installed). They do not need to install Maestro Elements; just the Powerpoint plugin: http://www.schrodinger.com/downloadcenter/