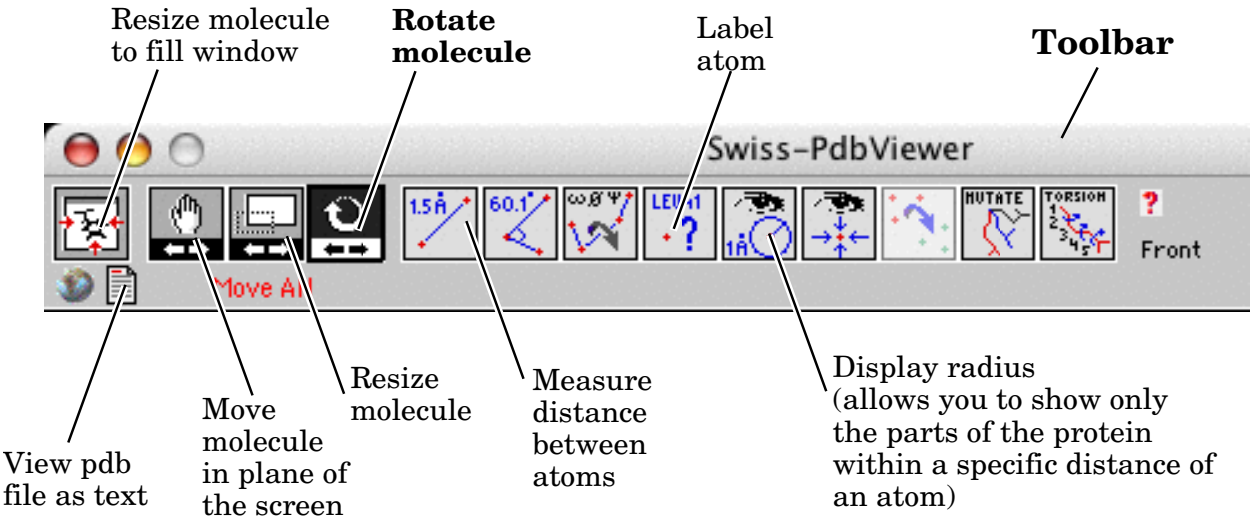
Swiss-PDB-Viewer – Getting Started



Looking at part of a molecule
Three methods are supported by the program:
1. Use the **Select** menu to choose specific residues or parts of a molecule.
2. Use the **Control Panel** – put a √ in the "**Show**" column for any residue you wish to be able to see; remove the √ (by clicking on it) to hide some residue. Alternatively, you can click on the "**Show**" header in the **Control Panel** window; any unselected residues will disappear.
3. Use the **Display Radius** button, click on an atom, and then modify what is displayed using the dialog box. One method is to use "**Display only groups that are within**:" and enter a number between about 5 Å and 10 Å.

Measuring distances
1. Rotate the molecule so that you can see the atoms you wish to measure. (You may wish to deselect other parts of the molecule; see above.)
2. Click the **Measure Distance Between Atoms** button, and click on the 1st atom and then on the 2nd. Note that you will not be able to rotate the molecule again until you click the **Rotate Molecule** button.

Creating a ribbon representation
1. Make sure that no residues are selected (selected residues show up as red in the **Control Panel** window).
2. Click on the "**Show**" header in the **Control Panel** window. The side-chains and backbone should disappear.
3. **Select All** (Control-A, or use the **Edit** menu command).
4. Click on the "**ribn**" header in the **Control Panel**. A wire-frame ribbon trace should appear.
5. Click and hold the small triangle under "**col**" in the **Control Panel**, and select "**ribbon**". You can now alter the color of the ribbon(s) by using the **Color** menu commands.
6. Prettier ribbons can be displayed by selecting "**Render in 3D**" in the **Display** menu.
7. Auto rotate is initiated by the pressing "Shift" and ">"; you may need to alter the preferences (select **Rock and Roll**… in the **Preferences Menu**). Stop rotation by pressing "Esc".