

Making Images of Protein Structures Using Swiss PDB Viewer

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1. Download and install Swiss PDB Viewer program: <http://www.expasy.ch/spdbv/>
2. Download PDB file of interest; unzip if .zip file
3. Start Swiss PDB Viewer program
4. Open PDB file (at startup, or under "File")
5. Several windows will open (or open them manually under "Wind"):
 - input log text file (I usually close this immediately; but it may show info on missing atom locations, etc.)
 - toolbar (should be small window across top of screen, with several small boxes)
 - main window (should show protein in some format)
 - control panel (long narrow window to right of main window, with sequence and boxes)
6. To adjust the molecule display:

Setting the background color

Prefs > Colors > Background (button)

choose new color from window

Turning side chain display on/off

in Control Panel, find residue of interest

click check mark under "side" to turn off side chain display; click again to turn on

NOTE: must have backbone display on to display side chain!

on Mac, hold "Option" key and click anywhere under "side" to turn all side chains on/off

Turning backbone display on/off

as above for side chain display, but use the check marks under "show"

Coloring specific residues

in Control Panel, find residue of interest

make sure pulldown menu under "col" (accessed through black triangle) is set to "backbone + side", or whatever you desire to color

click box for appropriate residue, under "col"

select new color in window

Drawing ribbons

in Control Panel, select all residues under “ribn” (Option-click on Mac)

under “col” pulldown menu, select “ribbon”

color all residue boxes desired color for ribbon (see above, Coloring specific residues)

Ribbon properties

Prefs > Ribbons

Drawing in 3D

Making a surface

Adding labels

“Hiding” part of the protein

7. Manipulating the protein structure:

Rotating the protein

Moving (translating) the protein

Zooming in and out

8. Advanced techniques:

Defining the point of rotation

Displaying and working with multiple structures in one field

Changing which structure is “active” for selections

“Locking” 1 or more proteins in a field

Using lights

Aligning structures

9. See the User Guide for more information: <http://www.expasy.ch/spdbv/text/main.htm>