Protein Structure Viewers
Hot Topics – March 2009

Swiss-PdbViewer demo

1. Open (or import) cholera toxin (1xtc) PDB file.

2. Browse main interface
    Rotate, translate zoom
    Display ➔ Render in Solid 3D
    Wind (windows) ➔ Control Panel, Alignment

3. Select by chain or atoms, and/or using Select menu

4. Browse Control Panel
    Chain, secondary structure, group, show (ball and stick), side (chain), label, surface (::v), ribbon, color, backbone/side chain/etc.

5. Preferences (Prefs) menu

6. Change 5 chains of ring (DEFGH) into ribbons
    Prefs ➔ colors

7. Change chain C to orange space-filled

8. Make molecular surface of chains AC
    Prefs ➔ Surfaces
        Check “Ignore Selected Residues”
        Transparency (1 - 100) ➔ 90
    Tools ➔ Compute Molecular Surface

9. Select active site residues and show as red space-filled atoms

10. Save layer (File ➔)

11. Save Pov-Ray Scene (File ➔)

12. Open (or import) E. coli enterotoxin (1tii) PDB file.

13. Browse new display options:
    Control Panel ➔ pull-down menu for structure selection
        Visible? Can move?

14. Fit ➔ Iterative Magic Fit (and then separate)

15. Select active residues and change to space-filling
    Look at Alignment

10. Save Project (File ➔)

11. Save Pov-Ray Scene (File ➔)

12. Go to POV-Ray (or open *.pov file) and Run, generating image of desired size.