Proteopedia cheat sheet

Basic reading and viewing

- Read the text and use the scroll bar on the right to navigate.
- Right-click on hyperlinks to open links in a new tab.
- Click on green links to get a new 3D figure in the Jmol window.
- Look at the 3D figures and use controls at bottom of Jmol window
    - Bigger window: click on magnifier glass
    - Popup window: click on popup (does not update automatically)
    - Toggle spin: click +/- spin

Using the mouse

- Drag to rotate.
- Hover to identify atoms (spin should be off)
- Shift for more mouse functions
    - Zoom; Drag up and down (or two-finger pinch gesture)
    - Z-rotation: Drag left and right
    - Move (translate): double-click and drag (or two-finger drag)
- If you get lost: press the green link again.
- Measuring: double-click an atom
    - Distance: double click second atom
    - Angle: click second and double click third atom
    - Torsion angle: click second and third and double-click fourth atom

Using the Jmol menu

With mouse pointer in Jmol window, control-click or right-click.

- Select submenu (indicates # of atoms selected)
    - Selection halos on or off
    - Protein->By residue name->Ala: select all alanines
    - …
- Style submenu: change representation of selected objects
    - Atoms>100% Van der Waals: spacefilling representation
    - …
- Color submenu:
    - Atoms->Violet
    - …
- Set picking (what clicking on an atom etc does)
    - Center: clicked atom becomes center of rotation
    - Set picking->None (the default behavior).
    - Set picking->Label. Clicking on any atom will add a label, and clicking a second time will delete it again.

Using the console

Open the console using the menu item "Console"

- Finding a residue: "center 72" to center on residue 72
- Changing the representation of a residue: "select 72", and use the menu
- Selecting more than one thing: "select (42, 67, 82) and side chain and _C"
- Add to selection: "select selected and 33"
- Showing hydrogen bond: Select something (e.g. "select backbone and helix"), then type "hbonds calculate" in the console.