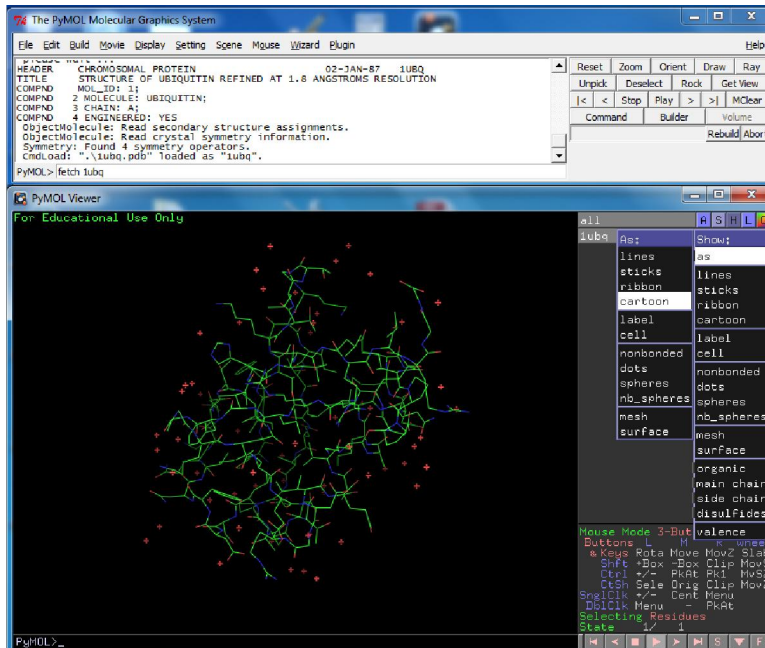


Name:
Date:

TP2 – Guide to using PyMOL

To appreciate the structural features and complexity of proteins, it's best to view them in 3D and manipulate the structures yourself. Using PyMOL, you can explore the different structural features you've learned about, for any protein you can think of. Follow the instructions shown in **bold** to help you explore the interface.



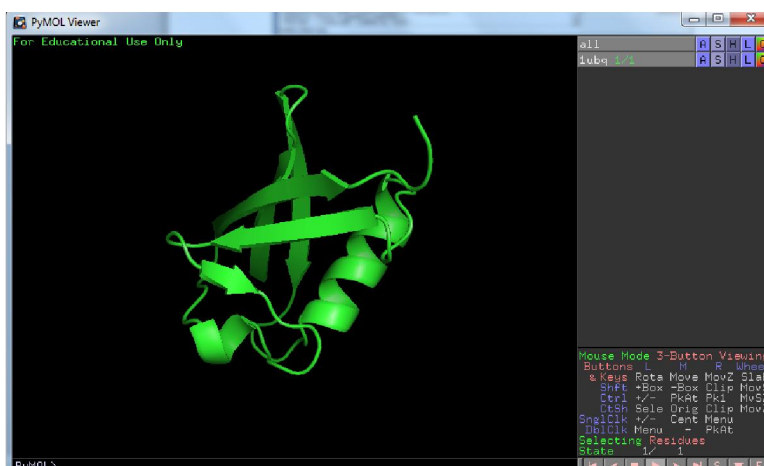
Once you have opened up PyMOL, you can load a protein by entering 'fetch ****' into the command bar. **Load the protein ubiquitin by typing the command 'fetch 1ubq'** into the command bar and pressing enter. You can do this with any protein that you find on the PDB by replacing the code with the code for your desired protein.

Each structure has five types of operation, which you can see in the pane on the right. A=Action, S>Show, H=Hide, L=Label, and

C=Colour. To view the protein as a cartoon model, **click on and follow S>as>cartoon** on this right pane. Note, if you follow the sequence S>cartoon, then the cartoon model will be superimposed onto the current lines view. If you do this, then you can hide the lines view by following H > lines.

The red crosses that you can see represent the water molecules which surround the structure. To make the model clearer, see if you can work out how to **hide the waters**.

You should now have a structure which looks like this. This view should give you a good idea of the secondary structure features (α -helices and β -sheets) in the protein. Using your mouse, manipulate the view of the protein, so you can understand how the protein exists in 3D.



Note that you can change the colour of the protein as you wish, and there are options to colour the protein by secondary structure, or for quaternary proteins, by their chain.

You can zoom in/out of a structure by holding the right mouse button and panning the screen.

Click 'S' in the bottom right-hand corner of the screen. This shows the sequence of amino acid



residues in the primary structure of the protein. If you **colour by secondary structure** as shown, then you will also see the amino acid residues, at the top, coloured. The amino acids are given by their one-letter code, and can be highlighted by clicking on them. It is also worth noting that if there are ligands in the structure, such as ions or heme groups, then they would appear in this top bar also.

One of the most useful features is being able to visualise the hydrogen bonding which gives the protein its shape. Add this to your structure using **A>find>polar contacts>just intra-main chain**. Using this, consider what would happen to the structure, and therefore the function, of the protein, if hydrogen bonding wasn't present.

There are lots of different features available on PyMOL, such as showing the amino acid side chains (**S>side chains>lines**), and showing the surface of the molecule (**S>surface**). If you make a mistake, then try using the hide options. You can delete any features or selections in the right-hand pane using **A>delete**. If you want to remove everything and start again, then enter 'delete everything' into the command bar, and use the 'fetch ****' command to load up a protein. Explore some more features of PyMOL until you feel comfortable with how it works, and how the features can help you to understand protein structure.

A QUICK NOTE ON REPRESENTATIONS

There are a number of different ways to visualise a protein structure. Cycle through these to see how they change the 3D image of the protein.

Lines: Shows the atoms (except hydrogens) and covalent bonds of the entire molecule. This is often most useful when you colour the atoms by element.

Sticks: Similar to lines, but with more width to give a better idea of the 3D nature of the protein. Often lines and sticks can appear complicated as there are many atoms in a protein. This is where the next representations become useful.

Ribbon: Proteins are made up of polypeptides, which are polymers. The polymer backbone can be traced using this view, to show how the chain is folded in space without the distraction of individual atoms and side chains.

Cartoon: Often the most useful representation. This is similar to the ribbon, but represents α -helices and β -sheets very clearly. This shows the secondary structures, and gives a better representation of the entire structure than the ribbon, without overcomplicating the structure with all of the atoms.

Surface/Mesh: These options are both good ways to see the overall 3D shape of the protein. This is especially useful to look at active sites.