Looking at structures with Rasmol

1. You need to get the PDB file of the molecule you want to view. Go to
http://www.rcsb.orb
This site is worth exploring. Try getting lysozyme, pdb7lyz.ent
Download the coordinates to your computer. You might rename the file 7lyz.

2. Start Rasmol and open 7lyz. The molecule is displayed.

3. Under Display you can choose several options - wireframe is the default, showing all the atoms as sticks. Probably better for initial view and orientation is Ribbons or Spacefill. Also go to Options and get rid of Hetero atoms.

Rotating and moving the molecule:

Mouse button alone gives rotation in 3-dimensions
Mouse button plus shift changes the magnification
Mouse button plus option translates in x-y plane of screen
Mouse button plus option plus shift rotates in x-y plane of screen

Get "Command line" under windows. Make this screen smaller and move it to the bottom of the main screen, so a couple of lines are below it. Click on the main screen to bring it to the front. Now click on any part of the molecule. The atom you clicked will now be identified on the command line.

Select and color. Choose spacefill and then color code chain segments. Type

select 1-20
color yellow
select 21-40
color blue

If you want to change the display of the whole molecule (to ribbons, wireframe, ...) you first need to type "select all".

You can save the same as an RGB or PICT file or some other format. First it is helpful to get rid of the black background. Type

set background white

Then go to the Export window to save the file.