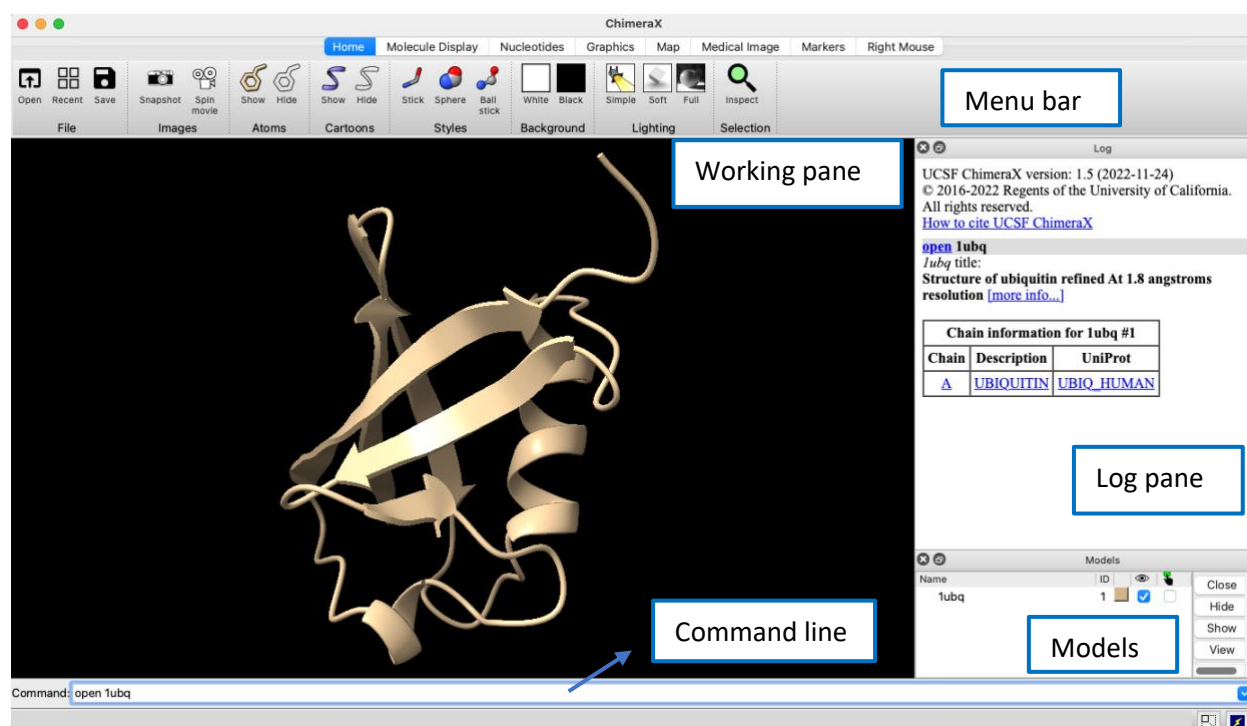


We will be using ChimeraX 1.5 (*download instructions at SUCourse*) .

Example protein: Ubiquitin

To fetch the protein directly from the PDB databank by typing `open 1ubq` in the command line. After you load the file you should see something like this:



You can change the color of the background in Graphics tab. To change the color of the protein chain go to **Actions → Color → All Options**.

Mouse controls:

- Holding the protein with right-click allows you to move the protein about the horizontal and vertical axis.
- Holding the black region with right-click allow syou to rotate the protein clockwise or counter clockwise.
- Holding the protein with left-click allows you to change the pose of the protein you see on the screen.
- If you wish to select a part of the protein, press ctrl and left-click and drag the mouse over that part. To let go of the selection, press ctrl and click anywhere on the black region.

Practicing different representations of a protein:

- Click **Molecule Display** on menu bar. From this tab, you can display the protein surface by clicking **Surfaces → Show** and color it based on electrostatics, hydrophobicity and b-factor. If you have more than one chain, you can color each chain differently. You can also locate one or more residues by clicking **Sequence** on the analysis tab and selecting the residue that you want to display.
- Residue selection is also done by command line. Let's select the first amino acid by typing `select #1:1`. Display the side chain atoms by clicking **Atoms → Show**. Label the residue by typing `label #1:1`. Increase label size by typing `label height 1.4`. It is a Methionine, as in all encoded proteins ! Color the selected residue in **Actions → Color → All Options** by selecting Atoms/bonds and By Heteroatom. You should see that the sulfur atom in methionine side chain colored differently than the carbons.
- You can change the thickness and transparency of the ribbon using the command line. Try out following commands:

```
cartoon style helix width 1.0
cartoon style strand width 1.0
transparency 40 cartoon
```

- To save a high resolution figure of the protein with a transparent background, type in;
`save lubq.png transparentBackground true pixelSize 0.02`

Measured experimental flexibility of a protein and its secondary structure content

- We will now learn more about our molecule; every PDB structure has a column dedicated to the flexibility of each atom as measured from the Debye–Waller factors (also called B-factors; this is only physically meaningful for PDB files whose experimental method is X-ray crystallography). Color the protein by the *b-factor* coloring method. What can you say about the new colors?

CRYST1	50.840	42.770	28.950	90.00	90.00	90.00	P 1	1			
ATOM	1	CA	MET	A	1	26.266	25.413	2.842	1.00	10.38	C
ATOM	2	CA	GLN	A	2	26.850	29.021	3.898	1.00	9.07	C
ATOM	3	CA	ILE	A	3	26.235	30.058	7.497	1.00	5.07	C
ATOM	4	CA	PHE	A	4	26.772	33.436	9.197	1.00	4.68	C
ATOM	5	CA	VAL	A	5	28.605	33.965	12.503	1.00	3.87	C
ATOM	6	CA	LYS	A	6	27.691	37.315	14.143	1.00	6.12	C
ATOM	7	CA	THR	A	7	30.225	38.643	16.662	1.00	7.48	C
ATOM	8	CA	LEU	A	8	29.607	41.180	19.467	1.00	14.15	C
ATOM	9	CA	THR	A	9	31.422	43.940	17.553	1.00	19.24	C
ATOM	10	CA	GLY	A	10	28.978	43.960	14.678	1.00	18.74	C
ATOM	11	CA	LYS	A	11	31.191	42.012	12.331	1.00	11.91	C
ATOM	12	CA	THR	A	12	29.542	39.020	10.653	1.00	9.85	C
ATOM	13	CA	ILE	A	13	31.720	36.289	9.176	1.00	11.84	C
ATOM	14	CA	THR	A	14	30.505	33.884	6.512	1.00	9.63	C
ATOM	15	CA	LEU	A	15	31.677	30.275	6.639	1.00	9.03	C
ATOM	16	CA	GLU	A	16	31.220	27.341	4.275	1.00	11.50	C
ATOM	17	CA	VAL	A	17	30.288	24.245	6.193	1.00	8.85	C

Measuring distances and angles:

Now let's focus on the molecular geometry of the first residue. Zoom in and select a covalently bonded sulfur and carbon atom by pressing ctrl+shift and left click. Label the atoms by clicking **Actions** → **Label** → **Atoms** → **Name**. Now go to **Tools** → **Structure Analysis** → **Distances** and click **Create**. Select one more carbon atom and go to **Angles/Torsions** and measure the angle between three atoms.

How big is the protein? Select two atoms on two residues that seem to be the farthest apart and click **Create** on **Distances** tab.

Learning more about your molecule - PDBsum

PDBsum is a database that collects information on deposited PDB structures. Go to the [PDBsum web](#), and type in your pdb ID (and chain info, if any).

From the Protein tab, get the secondary structure diagrams and CATH codes. You can also get conservation scores from ConSurf Database. Predicted tunnels for ligand entry-exit are also provided along with a plethora of other information.

Report (5 pts for general presentation; the report should not exceed 3 pages; please do not change font sizes)

Student name and ID:

- 1. (10 pts) General info on protein:** PDB ID, name, CATH code, known function.
- 2. (15 pts) 3D rendered structure:** Paste your best view below; explain why you choose this particular coloring method and 3D representation.
- 3. (15 pts) Size and shape descriptions:** Describe the size, shape, fold type. What is the aspect ratio of your selected protein (max to min dimensions, and max:min ratio); does it conform to expectations from globular proteins as discussed in class? Why or why not? Paste the ChimeraX views where you make the measurements displaying the measured values.
- 4. (20 pts) Protein flexibility vs. secondary structures:** Make a plot of C_α Debye-Waller factors as a function of residue index. Match the residues with the secondary structure information. Also display your molecule colored by B-factors. Briefly discuss where the most and least flexible residues are and rationalize the observations.
- 5. (20 pts) Residue conservation and positioning.** Using PDBsum, find the ConSurf scores of each residue and display the most conserved ones (score of 9) on the PDB structure. Rationalize the conservation according to the function of the protein. Where are the conserved residues clustered? Are there any which are placed far from the binding site? If so, what might their function be?
- 6. (15 pts) Ligand entry-exit mechanisms.** Using PDBsum, display the tunnels for ligand entry-exit (paste the figures). Briefly explain what purpose these might serve.
- 7. (Bonus if there are any comments with special insight) If there are any additional observations you wish to share, add them here; do not exceed 5 lines.**