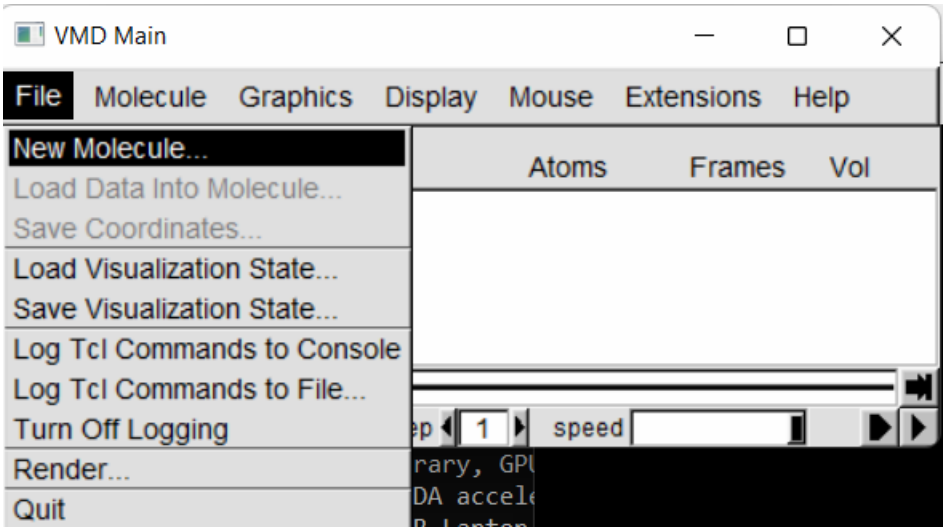
VMD Lab Exercise: Exploring Ubiquitin (1UBQ)

Introduction

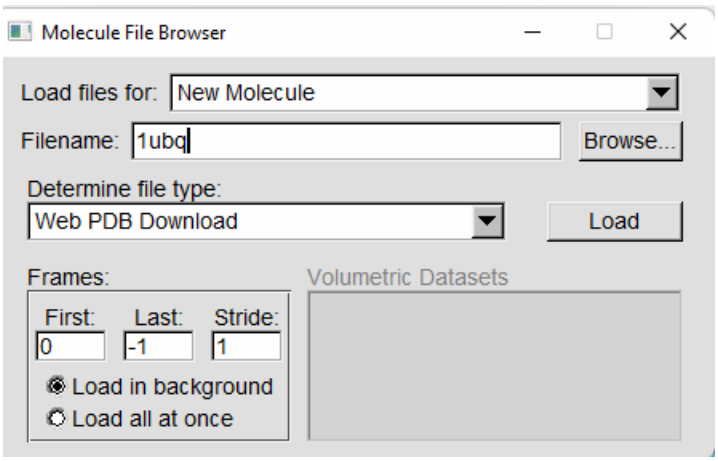
In this lab exercise, we will explore the structure of ubiquitin using Visual Molecular Dynamics (VMD). Ubiquitin is a small regulatory protein found in most tissues of eukaryotic organisms. It plays a crucial role in protein degradation and various cellular processes. The PDB ID for ubiquitin that we'll be using is 1UBQ.

Section 1: Downloading and Inspecting the PDB

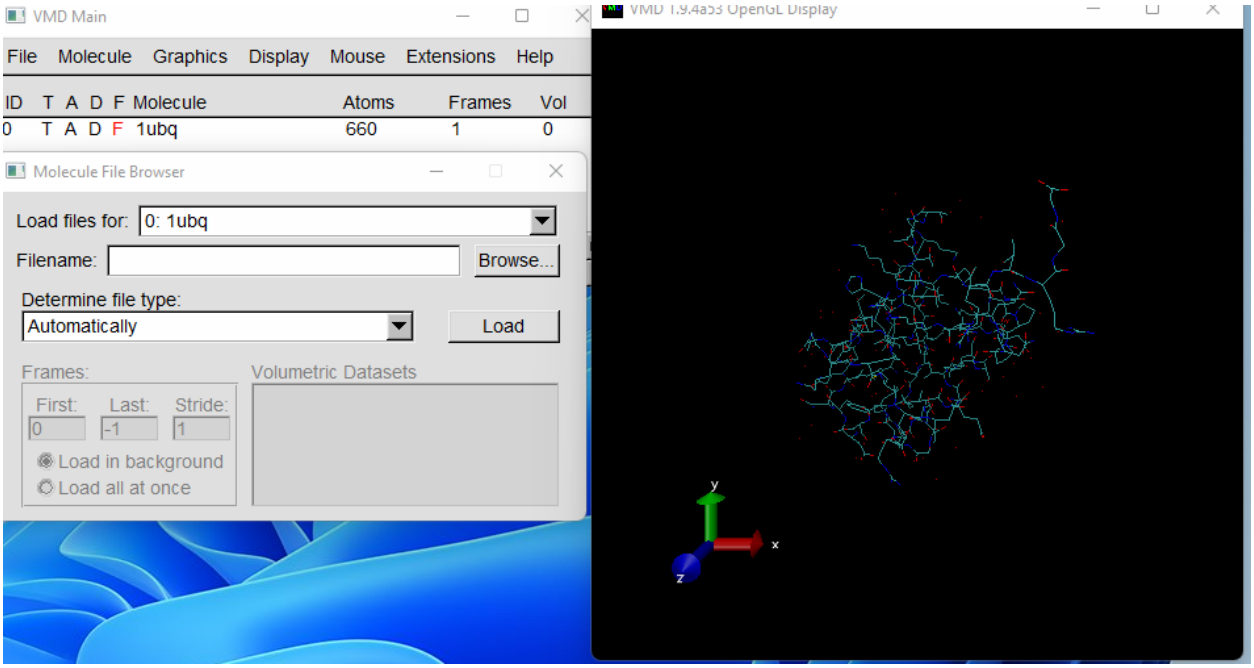
1. Open VMD on your computer.
2. Go to File > New Molecule.



3. In the "Molecule File Browser" window, select "Web PDB Download" from the "Determine file type:" dropdown menu.
4. In the "Filename" field, type "1ubq" and click "Load".



5. Once loaded, you should see the ubiquitin molecule in the VMD OpenGL Display window.

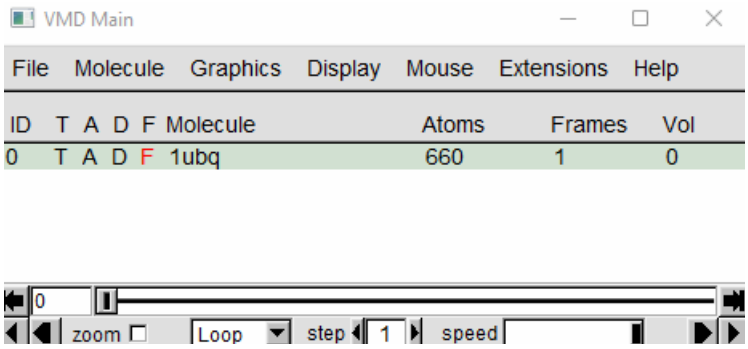


6. Inspect the protein:
    - Use your mouse to rotate and zoom in/out of the molecule.
    - Notice the coloring system: By default, VMD uses a coloring scheme called where different atom types are colored differently (e.g., carbon is cyan, oxygen is red, nitrogen is blue).

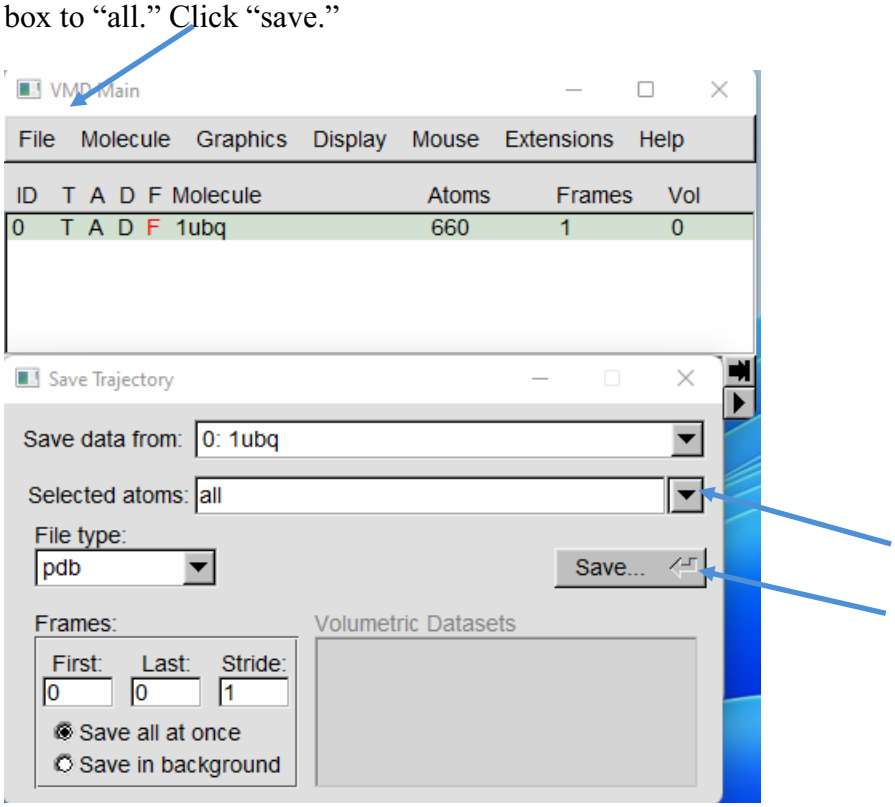
    **Why are there no hydrogens?

    - Most PDB files don't include hydrogen atoms because they're not typically resolved in X-ray crystallography experiments.

7. Save the file:
    - Click on the 1ubq molecule in the VMD main window (this will highlight the correct row in green)



    - Go to File > Save Coordinates. Under “Selected atoms:” change the dropdown box to “all.” Click “save.”



    - Choose a location (Desktop) and name for your file (e.g., "ubiquitin.pdb").

8. Inspect the PDB file:
    - Open the saved PDB file in a text editor.

- Look at the first few lines after the first “Crystal” line. You should see something like

```
ATOM      1  N   MET A   1      27.340  24.430   2.614  1.00  9.67           N
ATOM      2  CA  MET A   1      26.266  25.413   2.842  1.00 10.38           C
ATOM      3  C   MET A   1      26.913  26.639   3.531  1.00  9.62           C
ATOM      4  O   MET A   1      27.886  26.463   4.263  1.00  9.62           O
ATOM      5  CB  MET A   1      25.112  24.880   3.649  1.00 13.77           C
ATOM      6  CG  MET A   1      25.353  24.860   5.134  1.00 16.29           C
ATOM      7  SD  MET A   1      23.930  23.959   5.904  1.00 17.17           S
```

- These lines provide information about each atom's position and properties.

Detailed explanation:

1. Record name: Always "ATOM" for atomic coordinate records.
2. Atom number: Unique number for each atom within the structure.
3. Atom name: Name of the atom (e.g., CA for alpha carbon, N for nitrogen).
4. Residue name: Three-letter code for the amino acid or nucleotide.
5. Chain identifier: Identifies which chain in the structure this atom belongs to.
6. Residue sequence number: Position of this residue in the chain.
7. X coordinates: Position of the atom in 3D space, in Ångstroms.
8. Y coordinates: Position of the atom in 3D space, in Ångstroms.
9. Z coordinates: Position of the atom in 3D space, in Ångstroms
10. Occupancy: Indicates the fraction of time the atom is present at this position (usually 1.00).
11. Temperature factor (B-factor): Indicates the thermal motion of the atom.
12. Element symbol: Chemical symbol of the element.

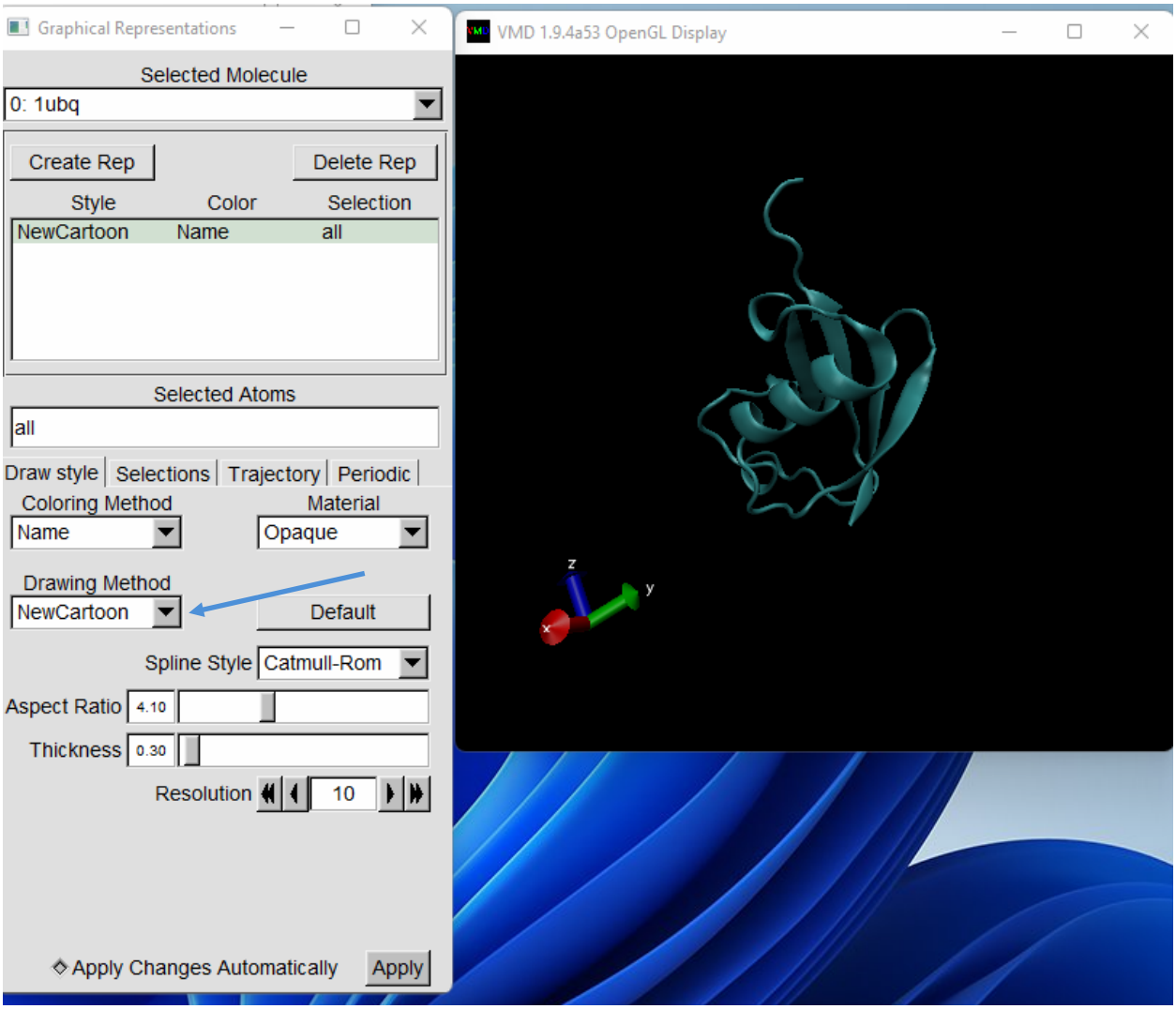
Example: ATOM 1 N MET A 1 27.340 24.430 2.614 1.00 0.00 N

This line represents:

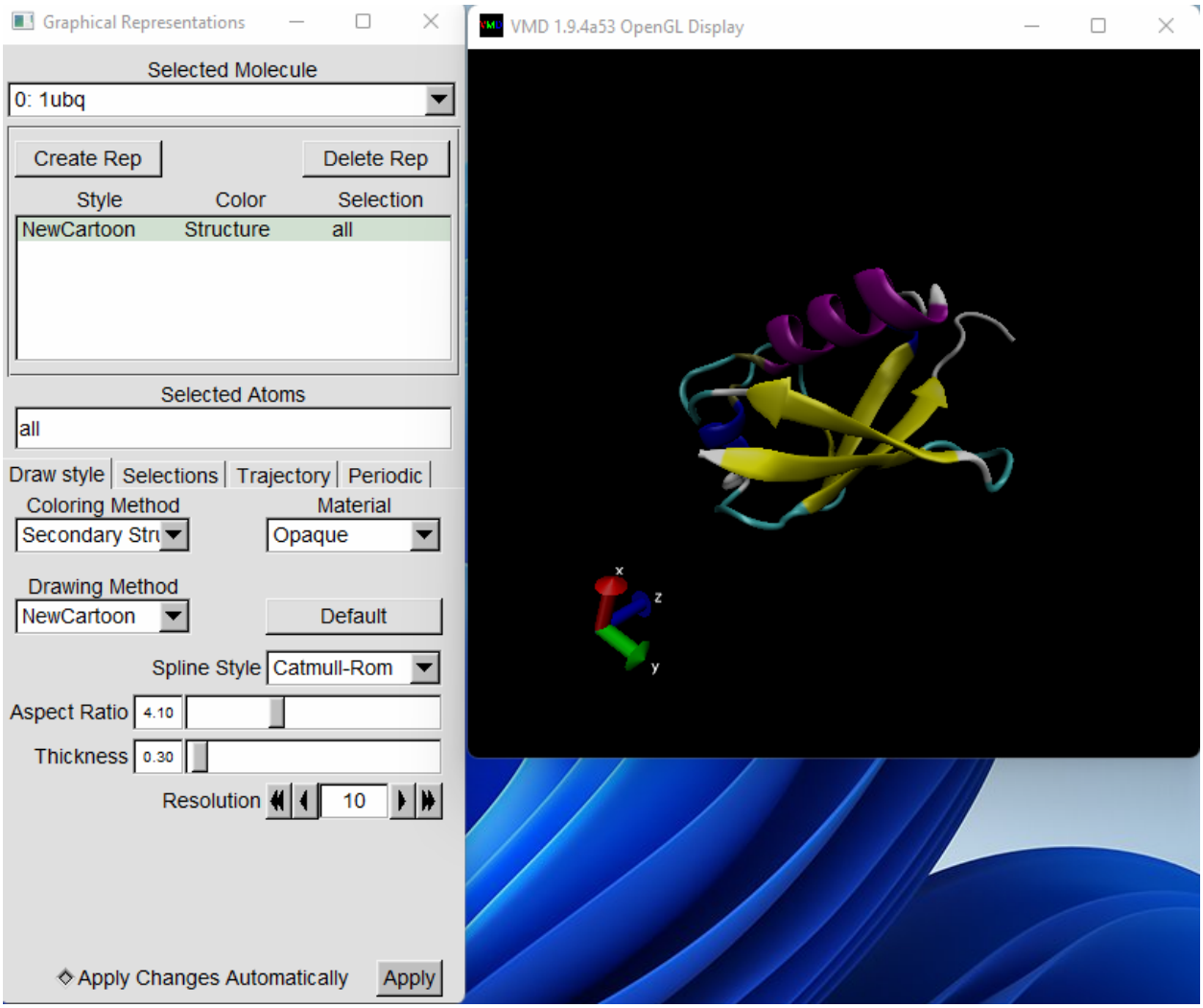
- The first atom in the structure
- It's a nitrogen atom
- Part of a methionine residue
- In chain A
- The first residue in the sequence
- Located at coordinates (27.340, 24.430, 2.614)
- Has full occupancy (1.00) and no thermal motion (0.00)
- The element is nitrogen (N)

Section 2: Coloring and Secondary Structure Analysis

1. Change the representation to "Cartoon":
    - In the VMD Main window, go to Graphics > Representations.
    - In the "Drawing Method" dropdown, select "NewCartoon".



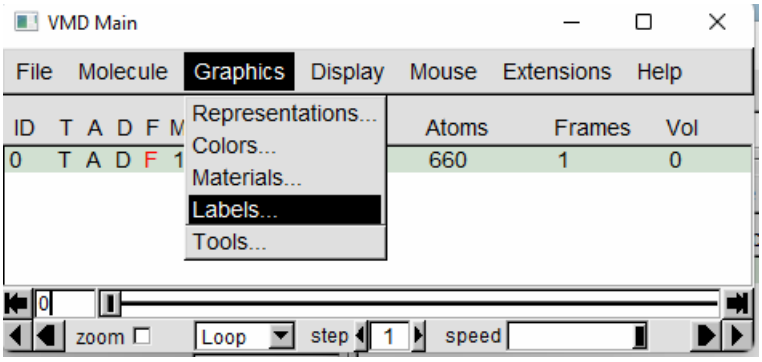
2. Color by secondary structure:
    - In the same Representations window, go to the "Coloring Method" dropdown.
    - Select "Secondary Structure".



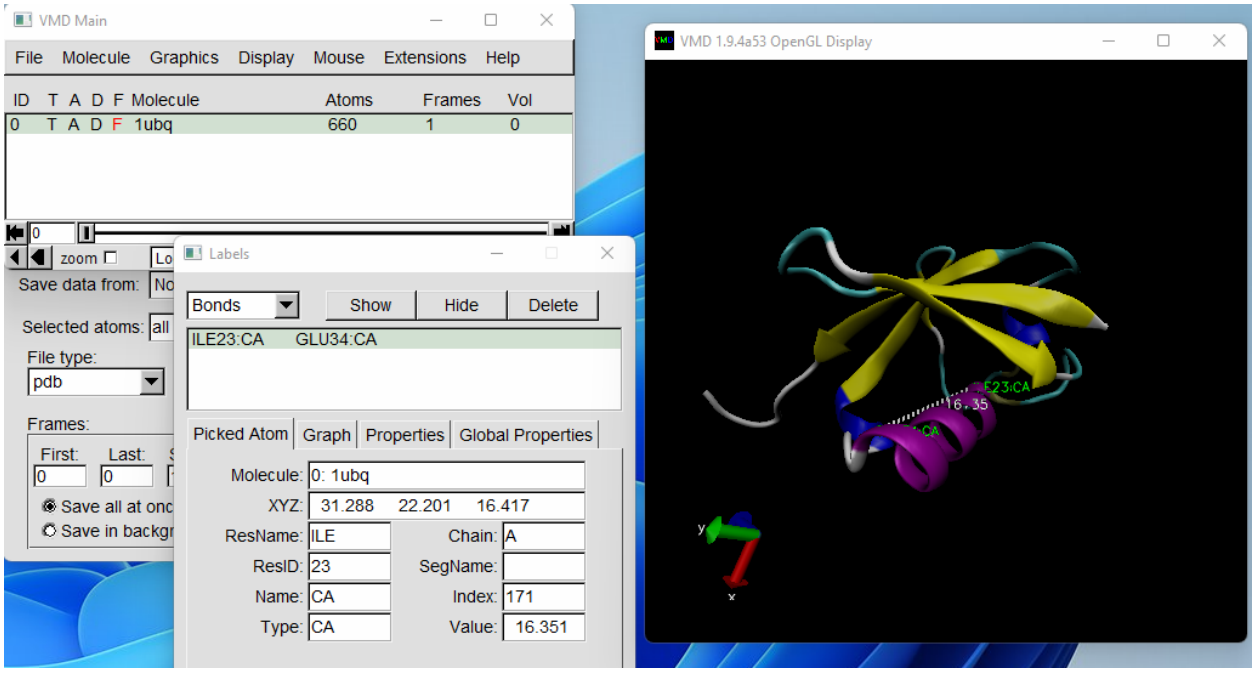
3. Identify secondary structure elements:
    - Alpha helices will appear as spiral ribbons (typically colored purple).
    - Beta sheets will appear as flat arrows (typically colored yellow).
    - Dark blue small turns: These are typically referred to as "turns" or sometimes "coils". They represent short segments of the protein that change the direction of the peptide chain. These are often regions that connect other secondary structure elements like alpha helices and beta sheets.
    - Cyan parts: In VMD's default coloring scheme, cyan usually represents "coils" or "random coils". These are regions of the protein that don't have a regular, defined secondary structure like alpha helices or beta sheets. They're often more flexible parts of the protein.
    - White parts: White in VMD's secondary structure coloring typically indicates regions that are not classified into any specific secondary structure category. These might be disordered regions or parts of the protein where the secondary structure is not well-defined.

Section 3: Calculating Distances Between Atoms

1. Measuring distances in VMD:
    - In the VMD Main window, go to Graphics > Labels to bring up the Labels window and change the dropdown tab to “Bonds.”



    - In the VMD Main window, go to Mouse > Label > Bond.
    - Click on the first and last CA of the purple alpha helix to measure the distance between them.
    - The distance will be displayed in Ångströms (Å).



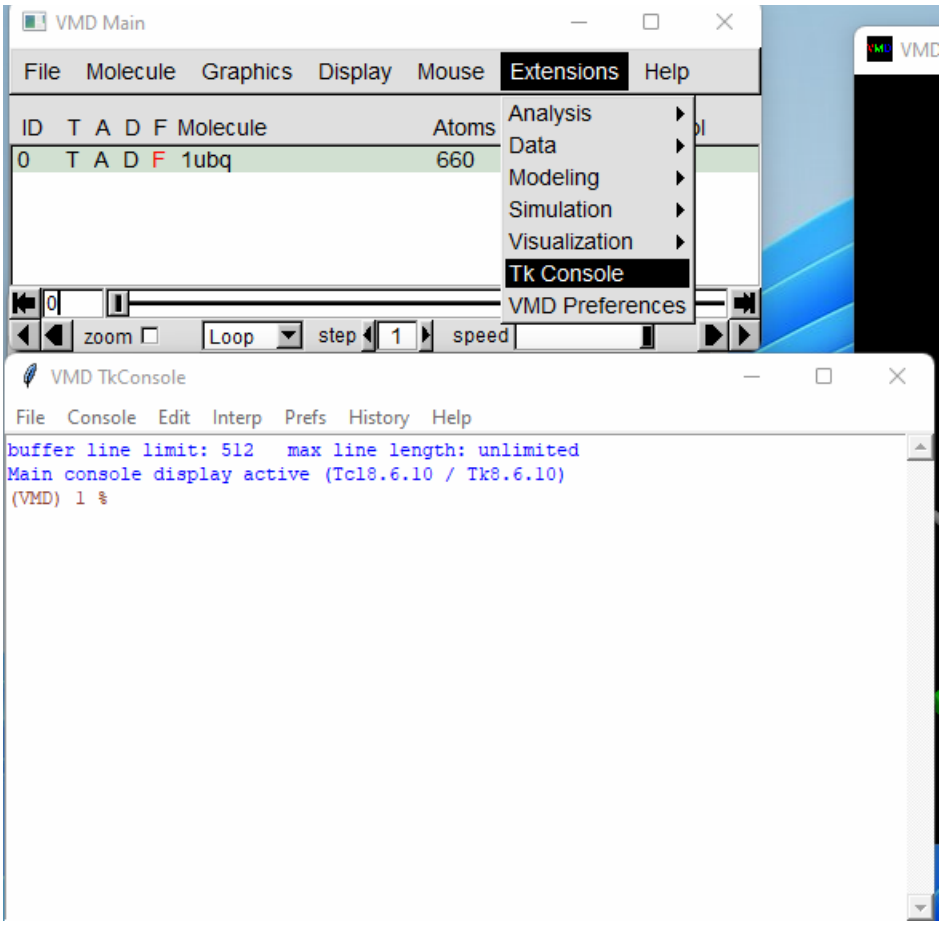
2. Understanding the 3D distance calculation:
    - The distance between two atoms (A and B) in 3D space is calculated using the formula:

Where (x1, y1, z1) are the coordinates of atom A, and (x2, y2, z2) are the coordinates of atom B.

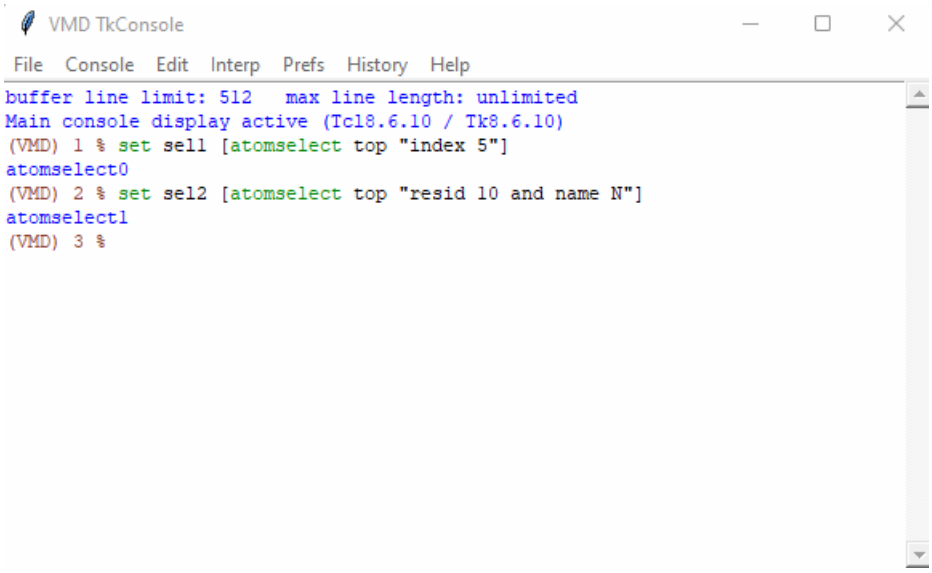
Advanced Atom Selection in VMD for Distance Measurements

Method: Using the Console

1. Open the VMD Main window.
2. Go to Extensions > Tk Console

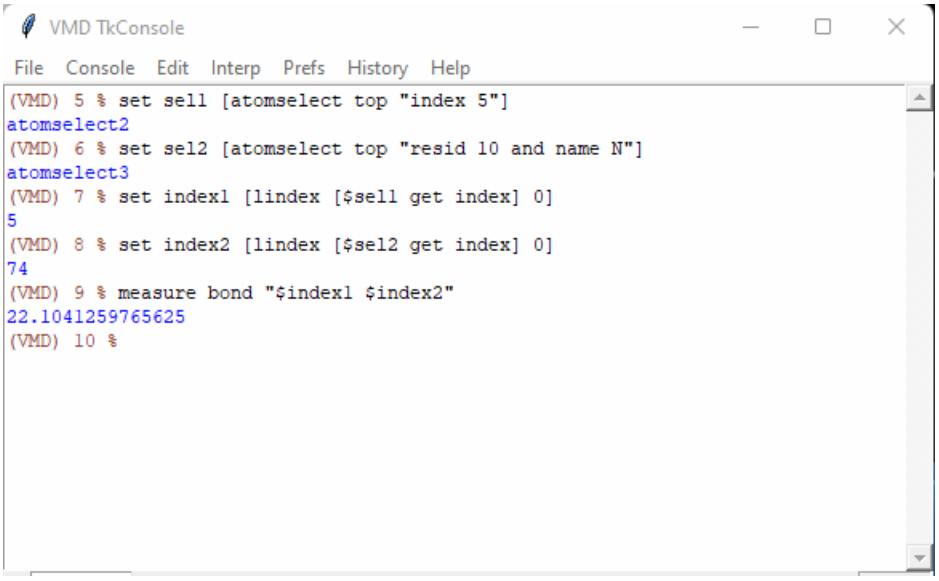


3. Create multiple selections of atoms. Examples:
    - Single atom by index: "index 5"
    - Atom by residue number and name: "resid 10 and name N"



(This creates two selections named “sel1” and “sel2”)

To measure:



Understanding the selections:

- `index 5` selects the atom with index 5.
- `resid 10 and name N` selects the nitrogen atom of residue 10.
- The `lindex` command is used to get the first (and only) index from each selection.

Useful Selection Commands:

- resid X: Select residue number X
- name Y: Select atoms with name Y (e.g., CA for alpha carbon)
- index Z: Select atom with index Z
- chain A: Select all atoms in chain A
- protein: Select all protein atoms
- water: Select all water molecules

Examples:

1. Measure distance between alpha carbons of residues 5 and 10:
    - Selection 1: "resid 5 and name CA"
    - Selection 2: "resid 10 and name CA"
2. Measure distance between the centers of mass of two ranges of residues:
    - Selection 1: "resid 1 to 10"
    - Selection 2: "resid 20 to 30"

3. Practice:
    - Measure the distance between the alpha carbons (CA) of the first and last residues in a beta sheet.
    - Measure the distance between the alpha carbon (CA) of the first residue in an alpha helix and the alpha carbon (CA) of the last residue in a beta sheet.