Practical examples 1

LCVC Module 2 - 2021/2022

Access the Google Colab Notebook at:

https://colab.research.google.com/drive/1NybwMgKclglw8SAHvH9IsOhgoXhjAV1A?usp=sharing

1) Load "mol1.pdb" in PyMOL.

- a. Visualize the structure in various modes: "stick", "cartoon", "spheres" and "surface".
- b. Visualize the structure in two simultaneous modes: "stick" and "cartoon".
- c. Select residue 48 by ID, colour its carbon atoms with a different colour.
- d. Select all ARG residues my name, colour all of their atoms with a different colour.
- e. Employ the "measure" function to calculate the distance between two atoms.
- f. Employ the "measure" function to calculate the phi dihedral angle in residue 48.

2) Setting a backbone dihedral

- a. Load "mol1.pdb" in ProtoSyn
- b. Measure the phi dihedral in Residue #48.
- c. Rotate the phi dihedral in Residue #48 to be 85°.
- d. Measure the phi dihedral in Residue #48 after rotation.
- e. Export the rotated structure to a file and visualize in PyMOL.
- f. Employ the "measure" function (on PyMOL) to calculate the phi dihedral angle in residue 48.

3) Rotating a sidechain dihedral

- a. Load "mol1.pdb" in ProtoSyn (again)
- b. Rotate the chi1 dihedral in Residue #48 by +10°.
- c. Export the rotated structure to a file and visualize in PyMOL in comparison with the original structure.
- d. On ProtoSyn, generate a trajectory of structures by rotating the chi1 dihedral in Residue #48 by +10° 35 times.
- e. Export the generated trajectory and visualize in PyMOL.