Assignment 0 (warm-up)

In this assignment you will work on a simple warm-up exercise in structural biology. Please provide TYPED solutions, no more than three pages long, including pictures. When done, just bring the print-out to class.

- Go to `www.rcsb.org/pdb`, find and download any protein whose name starts with the same letter as your last name. To get to the PDB record itself click `EXPLORE`. At the `Download/Display File` window choose `complete with coordinates` and `TEXT`. Ideal protein size for this exercise is 100-300 residues. Consider only ones that are produced by X-ray: search for something like `X-RAY DIFFRACTION` within the PDB file.
- Make a `cartoons` or `ribbons` picture of your protein using something like `rasmol`, `pymol`, `VMD`, or any other structure visualization package. (most can be easily installed on any platform, including your laptop. Links to many of them are available on the PDB site). Attach the picture to your report.
- Find out what the *Ramachandran Plot* is and generate one for your protein. Attach to your report.
- Are there any *alpha*-helices in your protein?
- Very roughly, what percentage of residues in your protein is in *alpha*-helical conformation?