

## GBCB5874. 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 or VMD (both can be easily installed on any platform, including your laptop). 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?