Problem Set #2 – Ch. 5 Structure: From 0.1-10 nm and Larger

1) In class we talked about the RNA world in passing and not too many people had heard of this.
   A) What is the “RNA world”? What is the evidence for an RNA world?
   B) Why do we live in a DNA/Protein world?
   C) As an exercise let’s assume RNA is the method of genetic storage instead of DNA. Estimate or look up the mutation rate for RNA and calculate how long it would take to change a significant portion” of the genetic code. You can estimate how much you think a significant portion is.

2) Go to the PDB and pull up a protein of interest to you. Print the structure out and attach it.
   A) How does the structure of the protein relate to its function?
   B) How do the underlying forces affect the protein’s function?

3) In class we briefly talked about “breathing” of the DNA ends. I hope you were paying attention!
   A) What is breathing in this context?
   B) How many bases will open at room temperature? To figure this out find or estimate the energy required to open a hydrogen bond. From this calculate the energy required to open an A-T base-pair and a G-C base-pair. If you assume the DNA has a 50% GC-content then how many bases will open given the average thermal energy? Now how many will open if you have a fluctuation in thermal energy of 4 times the average?

4) Bioinformatics problem. Predict whether the following sequences of amino acids will be in a transmembrane region of a protein, alpha-helix, or beta sheet. You may want to look up the Kyte-Doolittle hydrophobicity scores in your book and the relative frequencies of amino acids in alpha-helices and beta sheets in a biochemistry text to help you.
   A) IVHHEQRRNKRDGRNKRDKQERLFC
   B) TGGWYVIIT
   C) NPRDSGGKKNDRY
   D) CLMIEEQQFM

5) Your book talks about a fibrous protein called keratin. The shape of hair is actually determined in part by the cysteine residues in keratin.
   A) What types of bonds do cysteine residues form with each other?
   B) How is bonding arranged in straight hair? How could bonding be rearranged to produce curly hair when you go to get a perm?
   C) Aside from the ammonium why might a perm be stinky?

6) In class we talked about two techniques to measure the structures of biomolecules, x-ray crystallography and NMR.
   A) How does each technique work?
   B) What are the limitations of each method?
C) Are there other ways to determine biological structure besides these two techniques?

7) To give you some hints on the last question read the paper: Muller et al., 1999 JMB, “Surface structures of native bacteriorhodopsin depend on the molecular packing arrangement in the membrane.” It is on the course website.
   A) Summarize the important findings of the paper in two sentences. The first sentence should state the problem the paper tries to answer, and the second sentence should relate the author’s conclusions about the stated problem.
   B) List three limitations of x-ray crystallography that are highlighted by the paper. Feel free to use these above as well.
   C) Are there any caveats to using the technique listed in the paper to study protein structure?

8) In class Prof. Carter derived the force between a charge and a permanent dipole as having a $1/r^3$ interaction. She then went on to say that the potential energy for two induced dipoles was a $1/r^6$ interaction. Why is this the case? This is a fairly open ended question. You should do some research – online research probably won’t help – and come up with an answer.