Extra Homework Assignment H5
(Due: Thursday, 2009/12/03, 12:30 PM)

H5.1. pH-dependent charge states of amino acids. Each charged amino acid is characterized by its own pK_a value, which uniquely described its charged/uncharged state at any given pH. Using the pK_a value of a residue of interest and the corresponding expression for the probability of the uncharged state, the fractions of charged versus uncharged states of this residue can be calculated at any given pH.

(a) Calculate the fraction of positively charged His residues at pH=7. By how much does this fraction increase if pH decreases by 1? The pK_a value of His is 6.08.

(b) Calculate the fractions of negatively charged residues Asp and Glu at pH=4. The pK_a values of Asp and Glu are 3.9 and 4.3, respectively.

H5.2. Membrane Proteins. Consider two ion channel forming membrane proteins A and B with the channel diameters 4Å (protein A) and 8Å (protein B). The free energy of an ion passing from extracellular space through the membrane ion channel increases inside the membrane by:

$$\Delta F \;=\; \frac{+q^2}{4\pi\epsilon\sqrt{\epsilon_w\epsilon_m}R}\,,$$

where R is the radius of the ion channel, $\epsilon_w \approx 80$ and $\epsilon_m \approx 3$ are water and membrane permittivities, respectively.

(a) Calculate the time an ion with a unit charge needs to pass through the membrane ion channel formed by protein A.

(b) By how much does this time increase/decrease if the channel is formed by protein B?

H5.3. Scaling of Protein Size. (*For Honors Undergraduate & Graduate Students*) Simple lattice models of polymers predict the scaling of a polymer's size as a function of the number of monomers. This problems explores whether such a scaling can be applied to proteins. A measure of the size of the protein with total M atoms in a folded state is a radius of gyration R_g:

$$R_g^2 \;=\; \frac{1}{M}\sum_{i=1}^{i=M}(\mathbf{R}_i - \mathbf{R}_{CM})^2$$

where $\mathbf{R}_{CM} = (x_{CM}, y_{CM}, z_{CM})$ is the center of mass:

$$\mathbf{R}_{CM} = \frac{1}{M}\sum_{i=1}^{i=M}\mathbf{R}_i\,.$$

(a) Visit the Protein Data Bank at http://www.rcsb.org/pdb to download the pdb files for a variety of globular proteins: myoglobin, hemoglobin, bovin pancreatic trypsin inhibitor (BPTI), lysozyme, cytochrome c, G-actin, and tubulin.

(b) From the PDB files extract the length of each protein in terms of the number of residues as well as the 3D coordinates of all atoms in each protein. Using the 3D coordinates, calculate the radius of gyration, R_g, of each protein.

(c) Each protein is now characterized by the number of residues N and the calculated R_g. Using data for all 7 proteins, make a graph with $\log(R_g)$ on the y- and $\log(N)$ on the x-axis and fit the curve to the straight line.