1. What is the most important factor explaining the spontaneous assembly of phospholipids into a bilayer in an aqueous solution?
   a. Increased entropy of lipids, and thereby increased stability of the system
   b. Formation of ionic bonds between the phospholipids, and thereby increased stability
   c. Stabilization of permanent dipole-induced dipole interactions between lipids
   d. Increased Induced dipole induced dipole interactions between the phospholipid head groups
   e. Increased entropy of water, and thereby increased stability of the system

2. Macromolecules in the cytosol need to specifically recognize each other for cellular processes to take place. What are the general properties of this type of intermolecular interaction?

   a. The two surfaces that interact have very similar or even identical properties It involves several covalent bonds so that the macromolecules are held tightly and permanently together.
   b. There are lots of non-covalent bonds formed, which means that the interaction is very strong and will last a long time.
   c. The interacting surfaces on each macromolecule have complementary shape and charge/polarity.
   d. Specific recognition usually only happens within one type of macromolecule, and not between different types

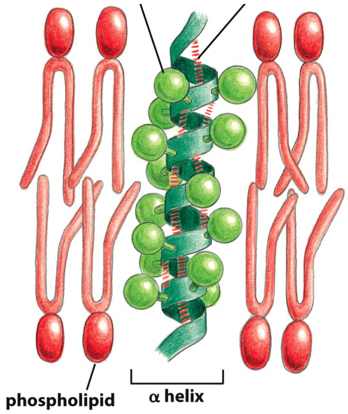
3. Why are phospholipids well suited to be the main structural components of membranes?
   a. They are completely insoluble in water.
   b. They form a structure in which the hydrophobic portion faces outward.
   c. They form a single sheet in water.
   d. They form an impermeable structure.
   e. They can self-assemble into a bilayer

4. Conditions of low pH will affect amino acids and proteins. For some amino acids, side chains that were negatively charged at neutral pH may become neutral and for other amino acids side chains that were neutral may become positively charged. These effects might contribute to altering the tertiary and quaternary structures of a protein by which of the following mechanisms?

   1. Breaking of peptide bonds.
   2. Changing the ionic interactions.
   3. Making new Induced Dipole-Induced Dipole interactions
   4. Changing the amino acid sequence.
   5. Causing charge repulsion.

   a. 2 and 5 probably contribute.
   b. 3 and 4 probably contribute.
   c. 1, 3 and 4 probably contribute.
   d. 1, 2, 3, 4 probably contribute.
   e. All 5 probably contribute.

5. Consider a single transmembrane helix, as shown. Which of the following statements is INCORRECT?



   a. The backbone atoms of the helix interact with each other via hydrogen bonds.
   b. The hydrophilic backbone of the polypeptide chain faces the interior of the alpha helix.
   c. The side chains of the amino acids point outwards from the helix.

   d. The interior of the alpha helix forms a hydrophilic pore for the passage of small molecules.

6. Glucosidase is a soluble, monomeric enzyme that has a glutamate (negatively charged) residue located in the interior of its tertiary structure. In four separate experiments, the glutamate residue was mutated to a different amino acid, resulting in four mutant proteins. Enzyme function was measured for each mutant, and compared to the original enzyme. The results were:

Enzyme	Enzyme function
Original	100%
Mutant 1: Glutamate changed to Aspartate (negatively charged)	95%
Mutant 2: Glutamate changed to Asparagine (neutral polar)	70%
Mutant 3: Glutamate changed to Isoleucine (non-polar)	50%
Mutant 4: Glutamate changed to Arginine (positively charged)	0%

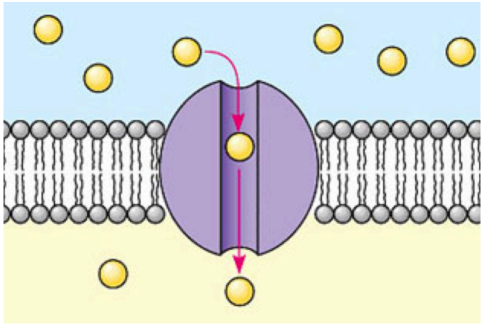
   Based on these data, it is most likely that in the original enzyme, the glutamate interacted with:

   a. water
   b. a neutral polar amino acid
   c. a positively-charged amino acid
   d. a negatively-charged amino acid
   e. a nonpolar amino acid

7. You are given the amino acid sequence of a protein. All 20 of the common amino acids are present in the protein. Which statements are <u>most likely</u> to be correct when considering the final conformation this protein will assume?
    1. H bonds between the atoms of the amino acid R groups will help stabilize the 3° structure.
    2. An alpha helix will form within the protein.
    3. In the 3° structure a disulphide (S-S) bond will form between 2 cysteine residues, which will stabilize the 2° structure.
    4. 2° structures form as a result of repetitive H-bonds between the backbone groups of the polypeptide.
    5. The 1° structure will determine if a beta pleated sheet will form.

    a. 2, 4 and 5 only
    b. 1, 4 and 5 only
    c. 1, 3 and 5 only
    d. 2 and 3 only
    e. 3 and 5 only

For the next two questions: The diagram below shows a channel protein in a lipid bilayer. This channel protein transports magnesium ions (Mg^{2+}) and water molecules.



8. Consider the <u>outside</u> of the channel protein, and the amino acid side chains that are interacting with the lipid tails in the membrane. What properties do most of these amino acid side chains likely have? Choose the most correct and most complete description.
    1. Polar
    2. Nonpolar
    3. Hydrophobic
    4. Hydrophilic
    5. Negatively charged
    6. Positively charged

    a. 1 only
    b. 3 only
    c. 2,3
    d. 2,4
    e. 1,4,5,6

9. Consider the <u>inside</u> of the channel. What properties do most of these amino acid side chains likely have? Choose the most correct and most complete description.
    1. Polar
    2. Nonpolar
    3. Hydrophobic
    4. Hydrophilic
    5. Negatively charged
    6. Positively charged

    a. 1,4,5
    b. 1,4,6
    c. 4,5
    d. 4,6
    e. 1,4,5,6