

Solutions to 7.012 Problem Set 1

Question 1

Bob, a student taking 7.012, looks at a long-standing puddle outside his dorm window. Curious as to what was growing in the cloudy water, he takes a sample to his TA, Brad Student. He wanted to know whether the organisms in the sample were prokaryotic or eukaryotic.

a) Give an example of a prokaryotic and a eukaryotic organism.

Prokaryotic:

All bacteria

Eukaryotic:

Yeast, fungi, any animal or plant

b) Using a light microscope, how could he tell the difference between a prokaryotic organism and a eukaryotic one?

The resolution of the light microscope would allow you to see if the cell had a true nucleus or organelles. A cell with a true nucleus and organelles would be eukaryotic. You could also determine size, but that may not be sufficient to establish whether a cell is prokaryotic or eukaryotic.

c) What additional differences exist between prokaryotic and eukaryotic organisms?

Any answer from above also fine here. In addition, prokaryotic and eukaryotic organisms differ at the DNA level. Eukaryotes have more complex genomes than prokaryotes do.

Question 2

A new startup company hires you to help with their product development. Your task is to find a protein that interacts with a polysaccharide.

a) You find a large protein that has a single binding site for the polysaccharide cellulose. Which amino acids might you expect to find in the binding pocket of the protein? What is the strongest type of interaction possible between these amino acids and the cellulose?

Cellulose is a polymer of glucose and as such has many free hydroxyl groups. These hydroxyl groups could make hydrogen bonds with any of the charged or uncharged polar amino acids. You may expect serine, threonine, asparagine, glutamine, tyrosine, arginine, histidine, lysine, aspartic acid or glutamic acid to be associated with the binding of cellulose.

Question 2, continued

In the course of your research you discover a small polypeptide that is associated with cellulose. You want to design an enzyme that will bind this small polypeptide. You design the enzyme shown below.

b) In the table below please indicate which amino acid you placed in each position to give the strongest possible interaction between your enzyme and the small polypeptide. For instance, you would choose an amino acid for position D that most strongly interacts with the carboxyl group of the small polypeptide. Also list what interaction occurs at each position (choose from: covalent bond, ionic bond, hydrogen bond, or van der Waals forces).

Position	Amino Acid(s)	Interaction
A	<i>any amino acid with a hydrophobic side chain</i> <i>alanine isoleucine, leucine methionine, phenylalanine, tryptophan, valine</i>	<i>van der Waals forces</i>
B	<i>any of the charged or uncharged polar amino acid</i> <i>serine, threonine, asparagine, glutamine, tyrosine, arginine, histidine, lysine, aspartic acid or glutamic acid</i>	<i>hydrogen bond</i>
C	<i>any of the charged or uncharged polar amino acid</i> <i>serine, threonine, asparagine, glutamine, tyrosine, arginine, histidine, lysine, aspartic acid or glutamic acid</i>	<i>hydrogen bond</i>
D	<i>any of the positively charged amino acids</i> <i>arginine, histidine, lysine</i>	<i>ionic bond</i>
E	<i>any amino acid with a hydrophobic side chain</i> <i>alanine isoleucine, leucine methionine, phenylalanine, tryptophan, valine</i>	<i>van der Waals forces</i>
F	<i>any of the positively charged amino acids</i> <i>arginine, histidine, lysine</i>	<i>ionic bond</i>

Question 3

One of your classmates, Mike, is working on a new science fiction novel. He approaches you with questions regarding cell membranes.

a) Explain the following to Mike.

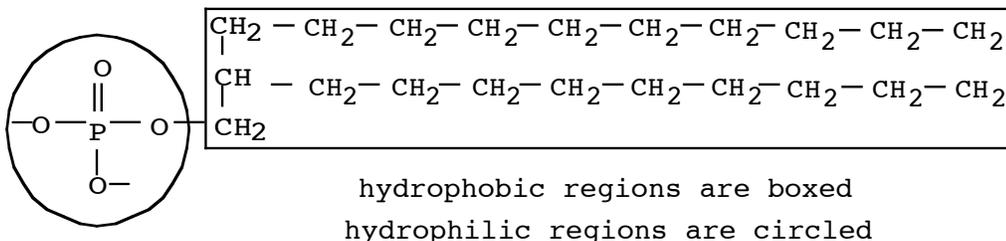
i) What are lipids?

The term lipid refers to a variety of molecules composed mainly of hydrocarbons. They are water insoluble due to the many non-polar covalent bonds.

ii) Why are saturated fatty acids more likely to be solid at room temperature than unsaturated fatty acids?

Saturated fatty acids are composed of hydrocarbon chains containing only single bonds (i.e. the carbon atoms are saturated with hydrogens). Saturated fatty acids are more linear and can be packed more tightly together. Unsaturated fatty acids contain one or more double bond between the carbon atoms. These molecules are less linear and do not pack together as well.

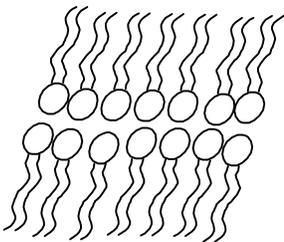
b) On the diagrams below label the hydrophilic and hydrophobic regions of the phospholipids.



c) Why does the structure of the phospholipid molecule favor the formation of bilayers or membranes?

A phospholipid has fatty acid tails that are extremely hydrophobic attached to a phosphate containing head that is hydrophilic. In an aqueous environment, the hydrophobic tails cluster together to exclude water in a manner that allows the hydrophilic end to interact with the water.

d) Mike proposes the following structure for the membranes of an alien life form. What conditions would need to exist to make this arrangement possible?



For this arrangement to be stable, the environment surrounding the phospholipid must be hydrophobic.

Portion of alien membrane

Question 4

Prions (pronounced pree-ahns) are agents that cause a novel type of fatal brain disease. Bovine spongiform encephalopathy (BSE or mad cow disease), sheep scrapie and Creutzfeldt-Jakob disease (CJD) of humans are examples of prion diseases. Prions enter cells and convert normal proteins found within the cells into prions just like themselves. The normal cell proteins have all the same "parts" as the prions--specifically the same amino acid building blocks--but they fold differently.

a) What is the primary structure of a protein? What force or forces (covalent bonds, ionic bonds, hydrogen bonds, or van der Waals forces) are involved in primary structure?

The primary structure of a protein is the linear sequence of the amino acids. Covalent bonds link the individual amino acids

b) What is the secondary structure of a protein? What force or forces (covalent bonds, ionic bonds, hydrogen bonds, or van der Waals forces) are involved in secondary structure?

The secondary structure of a protein is the region or regions within a protein that form α -helices or β -sheets. Hydrogen bonds dictate secondary structure.

c) What is the tertiary structure of a protein? What force or forces (covalent bonds, ionic bonds, hydrogen bonds, or van der Waals forces) are involved in tertiary structure?

The tertiary structure of a protein is the three dimensional shape that a protein takes. All the forces discussed in class work together to stabilize the tertiary structure of a protein.

d) Do you expect both the normal and the infectious versions of a prion protein to have the same primary structure? Why or why not.

If the normal cell proteins have all the same amino acid building block, then the normal and the infectious versions of a prion protein to have the same primary structure.

e) Do you expect both the normal and the infectious versions of a prion protein to have the same tertiary structure? Why or why not.

If the infectious version of a prion protein folds differently, then the normal and the infectious versions of a prion protein have different tertiary structure.