

Chem 464
Biochemistry

Multiple choice (4 points apiece):

1. A prosthetic group of a protein is a non-protein structure that is:
 - A) a ligand of the protein.
 - B) a part of the secondary structure of the protein.
 - C) a substrate of the protein.
 - D) permanently associated with the protein.
 - E) transiently bound to the protein.

2. Which of the following is true of the binding energy derived from enzyme-substrate interactions?
 - A) It cannot provide enough energy to explain the large rate accelerations brought about by enzymes.
 - B) It is sometimes used to hold two substrates in the optimal orientation for reaction.
 - C) It is the result of covalent bonds formed between enzyme and substrate.
 - D) Most of it is derived from covalent bonds between enzyme and substrate.
 - E) Most of it is used up simply binding the substrate to the enzyme.

3. Which of the following statements about a plot of V_0 vs. $[S]$ for an enzyme that follows Michaelis-Menten kinetics is false?
 - A) As $[S]$ increases, the initial velocity of reaction V_0 also increases.
 - B) At very high $[S]$, the velocity curve becomes a horizontal line that intersects the y-axis at K_m .
 - C) K_m is the $[S]$ at which $V_0 = 1/2 V_{max}$.
 - D) The shape of the curve is a hyperbola.
 - E) The y-axis is a rate term with units of $\mu\text{m}/\text{min}$.

4. When two carbohydrates are epimers:
 - A) one is a pyranose, the other a furanose.
 - B) one is an aldose, the other a ketose.
 - C) they differ in length by one carbon.
 - D) they differ only in the configuration around one carbon atom.
 - E) they rotate plane-polarized light in the same direction.

5. The basic structure of a proteoglycan consists of a core protein and a:
 - A) glycolipid.
 - B) glycosaminoglycan.
 - C) lectin.
 - D) lipopolysaccharide.
 - E) peptidoglycan.

6. The phosphodiester bond that joins adjacent nucleotides in DNA:
- A) associates ionically with metal ions, polyamines, and proteins.
 - B) is positively charged.
 - C) is susceptible to alkaline hydrolysis.
 - D) links C-2 of one base to C-3 of the next.
 - E) links C-3 of deoxyribose to N-1 of thymine or cytosine.
7. The double helix of DNA in the B-form is stabilized by:
- A) covalent bonds between the 3' end of one strand and the 5' end of the other.
 - B) hydrogen bonding between the phosphate groups of two side-by-side strands.
 - C) hydrogen bonds between the riboses of each strand.
 - D) nonspecific base-stacking interaction between two adjacent bases in the same strand.
 - E) ribose interactions with the planar base pairs.

Essay Questions 10 points each

8. Discuss how the hemoglobin in your body adjusts to changes in altitude. Do this both by talking about the structural changes that occur in Hemoglobin, and by making a rough sketch of the Binding curve (θ vs $[O_2]$) and discussing how the structural changes alter the binding curve, so that more O_2 is released.

At high altitudes the increases the concentration of BPG (2,3-bisphosphoglycerate) This binds to a site between the two β hemoglobin units and stabilizes the T form of the enzyme, and this lowers the affinity of hemoglobin for O_2 . Your rough sketch of the binding curve should look like figure 5-17, and the BPG binding moves the curve toward the right indicating the lower affinity for O_2 .

Why does a lower affinity for O_2 make this forms of Hemoglobin better adapted for high altitude? Well, while this form as a slightly lower affinity for O_2 so it doesn't bind quiet as much O_2 initially, shifting the binding curve to the right, makes the protein release more O_2 when it gets to the muscles, so the net effect is that the overall oxygen released is about the same.

9. To understand enzyme kinetics we usually plot v vs $[S]$, or $1/v$ vs $1/[S]$. For each plot: A. Make a rough sketch of what the plot should look like; B. Describe how you obtain K_M and V_{MAX} from the plot; C describe how the plot would change if a competitive inhibitor was added to the enzyme; and D. Describe how the plot would change if the enzyme were a homotropic allosteric enzyme and it was being modulated by positive effector that enhances the binding of the substrate to the enzyme.

A & B. A plot like figure 6-12 and Figure 1 box 6-1 that shows where you find V_{MAX} and K_m

C. With a competitive inhibitor essentially the K_m becomes larger but you can still reach V_{max} at high enzyme concentrations, so in the plot of v_o vs S , you still have a plateau at V_{max} but the center of the curve shifts to the right. In the plot of $1/v$ vs $1/S$ will look like box 6-2 Figure 1, where the y intercept remains the same, but the x intercept moves in toward the center.

D. When you have an allosteric enzyme, the curve shifts from being a pure hyperbolic function to something that looks more like an 'S' curve, like figure 6-34 a. An allosteric effector that increases the binding would decrease K_m and therefore shift the curve to the left.

10. Define the following terms

apoenzyme - an enzyme without its prosthetic group

holoenzyme - an enzyme with its prosthetic group

General base catalysis - a catalysis where an base functional group on the protein is used as part of the mechanism

Specific acid catalysis - a catalysis where H_3O^+ from water is used as part of the mechanism

Induced fit - a catalytic mechanism where the binding of the substrate induces a large structure change in the enzyme as part of the enzyme's mechanism

Pre-steady state - Kinetics that occur before the $[ES]$ stabilizes. The stabilization of $[ES]$ occurs in Briggs & Haldane theory because the rate of production of ES = rate of destruction of ES

allosteric protein - An enzyme whose kinetics is altered by the binding of an effector molecule.

reducing end (of a sugar) - The 1 position of an aldose or the 2 position of a ketose sugar where the oxidizable aldehyde or ketone is.

palindrome - A DNA sequence that is repeated on the opposite strand in the opposite orientation

z-DNA - A form of DNA structure in which the DNA exists in a left-handed helix

11. Lactose ($Gal(\beta 1 \rightarrow 4) Glc$) exists in two anomeric forms, but no anomeric forms of sucrose ($Fru(2\beta \rightarrow \alpha 1) Glc$) have been reported. Why?

In lactose the reducing end of the first sugar is tied up in the linkage between the sugars, but the reducing end of the second glucose is free adopt both α - and β - anomeric forms. In sucrose the reducing ends of both sugars are tied up in the glycosidic linkage, so neither sugar can change from α - to β - so there is only one anomeric form.

12. Discuss the similarities and differences between syndecans and glypicans

Syndecans and glypicans are the two major families of membrane heparan sulfate proteoglycans. In syndecans the protein portion of the molecules is a trans membrane protein with an extracellular domain to which 3-5 heparin sulfate chains are attached; there may also be chondroitin sulfate chains attached to the protein. In glypicans the protein is entirely extracellular, but the protein is anchored to the membrane via a lipid anchor. Both syndecans and glypicans can be found in the extracellular space, detached from the membrane because there are enzymes designed to cleave these proteins near their attachment point to the membrane. Finally in both syndecan and glypicans the carbohydrate is attached to the protein at a serine, in the sequence ser-gly-X-gly.

13. Draw the structure of the DNA dinucleotide pApT hydrogen bonded to a complementary RNA dinucleotide.

I was not looking for great artistry here. My scoring was roughly as follows: 1 point each for the correct structure of A, T, and U in the RNA strand. 1 point for correct hydrogen bonds. 1 point each for correct ribose and deoxyribose sugars. 1 point for correct anti-parallel arrangement of the two strands, 1 point for correct placement of phosphates.

14. Even though the monomers of DNA and RNA are very similar, the three-dimensional structure of a DNA polymer and an RNA polymer are very different. Discuss how and why the 3D structures of DNA and RNA are different.

DNA is almost always observed in the double stranded form. In this form it readily adopts the B-form double helix and makes a structurally boring, extended rod. RNA, on the other hand, is almost always observed in a single stranded form, and in this form the helix is not very stable, because it collapses as the individual bases try to find a complementary base to make hydrogen bonds with. RNA thus is much more structurally interesting because there are kinks and turns and alternate base pairing used to make a much more complex three-dimensional structure.