University of Toronto (UofT) BCH210H1 Biochemistry I – Proteins, Lipids and Metabolism Midterm Practice Test (Sample)

Study Guide

BY EXAMZIFY

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Questions

1. **How does bicarbonate act as a buffer in the blood when [H+] increases?**
   - A. It directly increases CO_2 production
   - B. It binds with protons to form carbonic acid
   - C. It releases oxygen into the blood
   - D. It converts bicarbonate to hemoglobin

2. **In the context of protein structure, what is tertiary structure?**
   - A. The overall 3D shape of a polypeptide
   - B. The linear sequence of amino acids
   - C. The arrangement of multiple protein chains
   - D. The formation of basic secondary structures

3. **What occurs during the formation of a peptide bond?**
   - A. Two amino acids combine and release hydrogen
   - B. Carboxyl and amino groups bond and release water
   - C. Two amino acids break apart and consume water
   - D. A single amino acid is formed from two polymerized amino acids

4. **What functional group is represented by the formula CHO?**
   - A. Aldehyde
   - B. Amide
   - C. Ester
   - D. Ether

5. **In a Michaelis-Menten graph, what is represented on the x-axis?**
   - A. Rate of reaction
   - B. Substrate concentration
   - C. Enzyme concentration
   - D. Time elapsed

6. Which amino acids are capable of forming disulfide bonds?

- **A. Histidine**
- **B. Cysteine**
- **C. Lysine**
- **D. Glutamine**

7. What type of glycolipid is Glucosylcerebroside?

- **A. Neutral glycolipid**
- **B. Phospholipid**
- **C. Sphingolipid**
- **D. Cholesterol derivative**

8. Which enzyme does not use ATP and can move lipids in either direction across a membrane?

- **A. Flippase**
- **B. Floppase**
- **C. Scramblase**
- **D. Transferase**

9. When selecting a chemical cross-linker, what is a critical factor to consider?

- **A. Cost and availability of the reagent**
- **B. Number and location of accessible functional groups**
- **C. Stability of the protein structure**
- **D. Time required for the reaction**

10. What is a beta turn?

- **A. Segment connecting two alpha helices**
- **B. A regular sequence of five residues**
- **C. A 4 residue segment allowing the peptide chain to turn 180 degrees**
- **D. A feature stabilizing parallel beta sheets**

Answers

1. B
2. A
3. B
4. A
5. B
6. B
7. A
8. C
9. B
10. C

Explanations

1. How does bicarbonate act as a buffer in the blood when [H+] increases?

A. It directly increases CO_2 production

B. It binds with protons to form carbonic acid

C. It releases oxygen into the blood

D. It converts bicarbonate to hemoglobin

Bicarbonate serves as a crucial buffer in the blood, and its role becomes particularly important when the concentration of hydrogen ions ([H+]) increases, which can occur during metabolic acidosis or other conditions that lead to acid accumulation. When [H+] rises, bicarbonate ions in the blood interact with these protons (H+) to form carbonic acid (H_2CO_3). This reaction is catalyzed by the enzyme carbonic anhydrase and can be represented by the equilibrium reaction: $HCO_3^- + H^+ \rightleftharpoons H_2CO_3$ The formation of carbonic acid helps to moderate changes in pH by reducing the free hydrogen ion concentration, effectively neutralizing some of the excess protons. Carbonic acid can then dissociate back into bicarbonate and hydrogen ions, which allows the system to respond dynamically to changes in pH levels. By acting in this manner, bicarbonate provides a buffer system that helps maintain the blood pH within a narrow range necessary for proper physiological function. This buffering mechanism is vital for homeostasis, particularly in maintaining the acid-base balance in the body.

2. In the context of protein structure, what is tertiary structure?

A. The overall 3D shape of a polypeptide

B. The linear sequence of amino acids

C. The arrangement of multiple protein chains

D. The formation of basic secondary structures

The tertiary structure of a protein refers to the overall three-dimensional shape of a single polypeptide chain. This structure is pivotal because it determines the protein's functionality and how it interacts with other molecules. The tertiary structure arises from various interactions between the side chains of the amino acids that make up the protein, including hydrogen bonds, ionic bonds, hydrophobic interactions, and disulfide bridges. These interactions fold the polypeptide into a specific 3D conformation that is essential for its biological activity. The other choices provided do not correctly define tertiary structure. The linear sequence of amino acids describes the primary structure of a protein, while the arrangement of multiple protein chains relates to quaternary structure. The formation of basic secondary structures, such as alpha helices and beta-sheets, pertains to secondary structure rather than tertiary structure. Understanding these distinctions is crucial for grasping how proteins are structured and function in biological systems.

3. What occurs during the formation of a peptide bond?

- A. Two amino acids combine and release hydrogen
- B. Carboxyl and amino groups bond and release water
- C. Two amino acids break apart and consume water
- D. A single amino acid is formed from two polymerized amino acids

The formation of a peptide bond is specifically characterized by the interaction between the carboxyl group of one amino acid and the amino group of another. This reaction is a type of condensation reaction, also known as a dehydration synthesis reaction. During this process, a water molecule is released, which results from the removal of a hydroxyl group (–OH) from the carboxyl end of one amino acid and a hydrogen atom (–H) from the amino group of another amino acid. Consequently, the two amino acids are covalently linked together via the newly formed peptide bond. This process is fundamental in building proteins, as it connects amino acids in specific sequences dictated by genetic information. Understanding this reaction is crucial in biochemistry, as it underpins protein structure and function, emphasizing the importance of peptide bonds in biological systems.

4. What functional group is represented by the formula CHO?

- A. Aldehyde
- B. Amide
- C. Ester
- D. Ether

The formula CHO corresponds to an aldehyde functional group. In an aldehyde, the carbon atom is bonded to a hydrogen atom and also has a double bond with an oxygen atom, which is collectively referred to as a carbonyl functional group. Aldehydes are characterized by the presence of this carbonyl group at the end of a carbon chain, giving them their distinct properties. In contrast, an amide contains a carbonyl group bonded to a nitrogen atom, which is not represented by the formula CHO. Esters feature a carbonyl group bonded to an oxygen atom that is also attached to another carbon chain, thus differing in structure from aldehydes. Ethers, on the other hand, contain an oxygen atom bonded to two carbon atoms, which again does not align with the CHO structure. Therefore, the formula CHO accurately portrays the structure of an aldehyde, making it the correct choice in this context.

5. In a Michaelis-Menten graph, what is represented on the x-axis?

A. Rate of reaction

B. Substrate concentration

C. Enzyme concentration

D. Time elapsed

In a Michaelis-Menten graph, the x-axis represents substrate concentration. This choice is foundational to understanding enzyme kinetics, as the relationship between substrate concentration and the rate of enzyme-catalyzed reactions is what the Michaelis-Menten model describes. As substrate concentration increases, more substrate is available for the enzyme to bind with, leading to an increase in the rate of reaction, which is reflected on the y-axis. The graph typically reveals a hyperbolic relationship where, at low substrate concentrations, the reaction rate increases linearly with increasing substrate. However, as the substrate concentration continues to rise, the reaction rate approaches a maximum velocity (Vmax), indicating that all enzyme active sites are occupied, and the enzyme is saturated with substrate. This understanding of how substrate concentration affects the rate of reaction is crucial for predicting and manipulating enzyme behavior in various biological and biochemical contexts.

6. Which amino acids are capable of forming disulfide bonds?

A. Histidine

B. Cysteine

C. Lysine

D. Glutamine

The ability of amino acids to form disulfide bonds is primarily attributed to cysteine. Cysteine contains a thiol (-SH) group in its side chain. When two cysteine molecules come close together, they can undergo an oxidation reaction, resulting in the formation of a covalent bond between their sulfur atoms. This bond is known as a disulfide bond (-S-S-), and it plays a crucial role in stabilizing the three-dimensional structure of proteins, particularly in extracellular proteins where the environment is more oxidizing. In contrast, histidine, lysine, and glutamine do not possess the thiol group necessary for disulfide bond formation. Histidine has an imidazole side chain that does not lend itself to forming such bonds. Lysine has an amino group in its side chain, while glutamine has an amide group, neither of which can oxidize to form disulfide links. Thus, only cysteine is capable of forming these essential bonds in protein structures.

7. What type of glycolipid is Glucosylcerebroside?

- **A. Neutral glycolipid**
- B. Phospholipid
- C. Sphingolipid
- D. Cholesterol derivative

Glucosylcerebroside is classified as a neutral glycolipid because it lacks significant charge on its hydrophilic head group under physiological conditions. Neutral glycolipids typically contain sugar moieties and do not carry a net positive or negative charge, which distinguishes them from charged or polar lipids. In the case of glucosylcerebroside, it consists of a glucose molecule linked to a ceramide backbone, specifically a sphingolipid. While it is accurate to note that glucosylcerebroside fits into the broader category of sphingolipids, its specific characterization as a neutral glycolipid highlights its non-charged nature, which is key to understanding its role in cell membranes and its function in various biological processes. Unlike phospholipids, which contain phosphate groups contributing to their polar characteristics, or cholesterol derivatives, which play different roles in membrane structure, glucosylcerebroside's structure is straightforwardly that of a neutral glycolipid.

8. Which enzyme does not use ATP and can move lipids in either direction across a membrane?

- A. Flippase
- B. Floppase
- **C. Scramblase**
- D. Transferase

Scramblase is the enzyme that facilitates the movement of lipids across a membrane in either direction without the requirement for ATP. This is significant because scramblases operate in response to changes in the concentration of lipids and work by allowing the passive movement of lipids down their concentration gradient. Unlike other enzymes that may be involved in lipid movement, such as flippases and floppases, which typically require ATP to transport lipids in a specific direction (inward or outward, respectively), scramblases do not utilize energy from ATP hydrolysis. This distinctive feature is essential in biological processes, particularly during events like apoptosis, where the asymmetric distribution of phospholipids in the lipid bilayer is altered, needing rapid redistribution. Transferase enzymes, on the other hand, are primarily involved in the transfer of functional groups rather than the direct movement of lipids across membranes. Therefore, scramblase is unique in its ability to facilitate lipid movement bidirectionally and without energy investment.

9. When selecting a chemical cross-linker, what is a critical factor to consider?

- A. Cost and availability of the reagent
- B. Number and location of accessible functional groups
- C. Stability of the protein structure
- D. Time required for the reaction

When selecting a chemical cross-linker, the number and location of accessible functional groups is a critical factor to consider because these functional groups determine the ability of the cross-linker to interact with the target proteins. Cross-linkers work by forming covalent bonds with specific amino acid side chains, such as lysines, cysteines, or aspartates, that contain functional groups capable of reacting with the cross-linker. The availability of these functional groups can significantly influence the efficiency and specificity of the cross-linking process. If there are not enough accessible functional groups or if they are located in inaccessible regions of the protein structure, the cross-linking reaction may be inefficient, leading to incomplete or undesired cross-linking. Therefore, evaluating the number and position of these groups aids in optimizing cross-linking results and enhancing the reliability of subsequent analyses or applications, such as structural studies or functional assays. Other considerations like cost, protein stability, and reaction time do play a role in the choice of cross-linker but do not directly influence the immediate interaction and reactivity between the cross-linker and the protein's functional groups as significantly as the number and location of those groups.

10. What is a beta turn?

- A. Segment connecting two alpha helices
- B. A regular sequence of five residues
- C. A 4 residue segment allowing the peptide chain to turn 180 degrees
- D. A feature stabilizing parallel beta sheets

A beta turn is characterized as a specific structural element in proteins that allows the peptide chain to make a sharp turn or bend, enabling it to reverse direction. This structural feature typically involves a segment of four amino acid residues, allowing the polypeptide chain to pivot approximately 180 degrees. The tightness of this turn is facilitated by hydrogen bonds, often between the first and fourth residues of the turn, which helps stabilize the structure and allows for compact folding of the protein. Understanding the significance of beta turns is crucial since they play a key role in the overall folding and stability of proteins, particularly in regions where the polypeptide backbone needs to change direction sharply. This is essential for creating functional protein domains and for maximizing the variety of structures that proteins can adopt. Other choices describe distinct structural elements in proteins but do not accurately capture the essence of what a beta turn is.