

AAMC Chemical and Physical Foundations of Biological Systems (C/P) Full-Length (FL) 2 Practice Test (Sample)

Study Guide



Everything you need from our exam experts!

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Introduction

Preparing for a certification exam can feel overwhelming, but with the right tools, it becomes an opportunity to build confidence, sharpen your skills, and move one step closer to your goals. At Examzify, we believe that effective exam preparation isn't just about memorization, it's about understanding the material, identifying knowledge gaps, and building the test-taking strategies that lead to success.

This guide was designed to help you do exactly that.

Whether you're preparing for a licensing exam, professional certification, or entry-level qualification, this book offers structured practice to reinforce key concepts. You'll find a wide range of multiple-choice questions, each followed by clear explanations to help you understand not just the right answer, but why it's correct.

The content in this guide is based on real-world exam objectives and aligned with the types of questions and topics commonly found on official tests. It's ideal for learners who want to:

- Practice answering questions under realistic conditions,
- Improve accuracy and speed,
- Review explanations to strengthen weak areas, and
- Approach the exam with greater confidence.

We recommend using this book not as a stand-alone study tool, but alongside other resources like flashcards, textbooks, or hands-on training. For best results, we recommend working through each question, reflecting on the explanation provided, and revisiting the topics that challenge you most.

Remember: successful test preparation isn't about getting every question right the first time, it's about learning from your mistakes and improving over time. Stay focused, trust the process, and know that every page you turn brings you closer to success.

Let's begin.

How to Use This Guide

This guide is designed to help you study more effectively and approach your exam with confidence. Whether you're reviewing for the first time or doing a final refresh, here's how to get the most out of your Examzify study guide:

1. Start with a Diagnostic Review

Skim through the questions to get a sense of what you know and what you need to focus on. Your goal is to identify knowledge gaps early.

2. Study in Short, Focused Sessions

Break your study time into manageable blocks (e.g. 30 - 45 minutes). Review a handful of questions, reflect on the explanations.

3. Learn from the Explanations

After answering a question, always read the explanation, even if you got it right. It reinforces key points, corrects misunderstandings, and teaches subtle distinctions between similar answers.

4. Track Your Progress

Use bookmarks or notes (if reading digitally) to mark difficult questions. Revisit these regularly and track improvements over time.

5. Simulate the Real Exam

Once you're comfortable, try taking a full set of questions without pausing. Set a timer and simulate test-day conditions to build confidence and time management skills.

6. Repeat and Review

Don't just study once, repetition builds retention. Re-attempt questions after a few days and revisit explanations to reinforce learning. Pair this guide with other Examzify tools like flashcards, and digital practice tests to strengthen your preparation across formats.

There's no single right way to study, but consistent, thoughtful effort always wins. Use this guide flexibly, adapt the tips above to fit your pace and learning style. You've got this!

Questions

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- 1. What atom is the site of covalent attachment of AMC to the model tetrapeptide used in the studies?**
 - A. I**
 - B. II**
 - C. III**
 - D. IV**
- 2. At pH 7.2, what charge will a lysine side chain typically carry?**
 - A. Neutral**
 - B. Positive**
 - C. Negative**
 - D. Variable**
- 3. Which type of ^{32}P labeled ATP should researchers use for phosphoryl transfer from kinases?**
 - A. $\alpha^{32}\text{P}$ -ATP**
 - B. $\beta^{32}\text{P}$ -ATP**
 - C. $\gamma^{32}\text{P}$ -ATP**
 - D. $\delta^{32}\text{P}$ -ATP**
- 4. What causes duplex DNA with certain (A+T):(G+C) ratios to melt at higher temperatures than those with greater (A+T):(G+C) ratios?**
 - A. Stronger van der Waals forces of pyrimidines**
 - B. Stronger van der Waals forces of purines**
 - C. Increased π -stacking strength**
 - D. Reduced electrostatic repulsion of phosphates**
- 5. What are the characteristics that differentiate acids from bases?**
 - A. Acids accept protons while bases donate protons**
 - B. Acids are always soluble in water while bases are not**
 - C. Acids donate protons whereas bases accept protons**
 - D. Acids are measured by pH levels above 7 while bases are below 7**

6. What is the outcome of adding a strong acid to a solution that contains $[\text{Cu}(\text{NH}_3)_4]^{2+}$?
- A. The concentration of ammonia increases
 - B. The concentration of $[\text{Cu}(\text{NH}_3)_4]^{2+}$ increases
 - C. The concentration of $[\text{Cu}(\text{H}_2\text{O})_2(\text{NH}_3)_2]^{2+}$ increases
 - D. The concentration of $[\text{Cu}(\text{NH}_3)_4]^{2+}$ decreases
7. What kind of energy change occurs in a spontaneous process?
- A. Positive ΔG
 - B. Negative ΔG
 - C. No change in energy
 - D. Neutral energy
8. What is the primary structure of a protein?
- A. The sequence of amino acids in a polypeptide chain
 - B. The folding of the chain into alpha-helices and beta-sheets
 - C. The overall three-dimensional shape of the protein
 - D. The interaction of multiple polypeptide chains
9. Under what condition will tryptophan produce the largest circular dichroism (CD) signal in the near UV region?
- A. As a free amino acid
 - B. Part of an α -helix
 - C. Part of a β -sheet
 - D. Part of a fully folded protein
10. What is the equivalent resistance of a $60\text{-}\Omega$ resistor connected in parallel with a $20\text{-}\Omega$ resistor?
- A. $80\ \Omega$
 - B. $40\ \Omega$
 - C. $15\ \Omega$
 - D. $3\ \Omega$

Answers

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

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Explanations

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1. What atom is the site of covalent attachment of AMC to the model tetrapeptide used in the studies?

- A. I**
- B. II**
- C. III**
- D. IV**

To determine the correct site of covalent attachment of AMC (7-amino-4-methylcoumarin) to the model tetrapeptide, it's important to understand the structure of the peptide and the functionality of the AMC group. Typically, in peptide chemistry, the attachment occurs via nucleophilic attack by an amino group on an electrophilic carbon, often related to a side chain or the N-terminus of the peptide. In this context, the amino acids that form the model tetrapeptide would have different functional groups at specific locations. The atom designated as site I is likely positioned in such a way that it has an accessible functional group suitable for the covalent bond formation with AMC. This can be an amine from an amino acid in the peptide backbone or a side chain from one of the amino acids present. Overall, the attachment of the AMC molecule indicates that it is binding to a site that provides a free amino functional group capable of engaging in a nucleophilic attack, which would typically be found in an N-terminal or an appropriately functionalized side chain within the tetrapeptide. The designation of this specific site as I suggests its structural position optimally facilitates this interaction, making it the most appropriate choice for the covalent bond

2. At pH 7.2, what charge will a lysine side chain typically carry?

- A. Neutral**
- B. Positive**
- C. Negative**
- D. Variable**

At pH 7.2, a lysine side chain typically carries a positive charge. Lysine is an amino acid with a side chain that contains an amino group (-NH₂) that can accept a proton (H⁺). In biological systems, especially at physiological pH levels, this amino group is protonated, forming a positively charged ammonium ion (-NH₃⁺). The pK_a of the side chain amino group of lysine is about 10.5, meaning that at pH values below its pK_a, the amino group will be predominantly protonated and positively charged. Since pH 7.2 is well below the pK_a of the lysine side chain, we can confidently conclude that the lysine side chain will predominantly exist in its protonated, positively charged form at this pH. Other options, such as neutral or negative charges, do not accurately reflect the state of the lysine side chain at this pH. A neutral charge would imply that the amino group is not protonated, which contradicts the conditions near physiological pH. A negative charge is not typical for lysine's side chain at this pH, as the side chain does not have functional groups that would be deprotonated under

3. Which type of ^{32}P labeled ATP should researchers use for phosphoryl transfer from kinases?

- A. $\alpha^{32}\text{P}$ -ATP
- B. $\beta^{32}\text{P}$ -ATP
- C. $\gamma^{32}\text{P}$ -ATP**
- D. $\delta^{32}\text{P}$ -ATP

To effectively carry out a phosphoryl transfer reaction mediated by kinases, researchers should utilize $\gamma^{32}\text{P}$ -ATP. This choice is appropriate because kinases are enzymes that specifically catalyze the transfer of a phosphate group from ATP to a substrate molecule. In ATP, there are three phosphate groups: alpha (α), beta (β), and gamma (γ). The phosphate group at the gamma position is the one that is cleaved off during the phosphorylation process. When kinases transfer a phosphate group to a substrate, they typically do so by cleaving the bond between the beta and gamma phosphates of ATP. Therefore, using $\gamma^{32}\text{P}$ -ATP allows researchers to label the phosphate that is ultimately transferred during the reaction, making it easier to trace the incorporation of radioactive phosphate into the substrate of interest. This specificity for $\gamma^{32}\text{P}$ -ATP distinguishes this option from other forms of labeled ATP, as the alpha and beta phosphate groups are not involved in the transfer during kinase activity.

4. What causes duplex DNA with certain (A+T):(G+C) ratios to melt at higher temperatures than those with greater (A+T):(G+C) ratios?

- A. Stronger van der Waals forces of pyrimidines
- B. Stronger van der Waals forces of purines
- C. Increased π -stacking strength**
- D. Reduced electrostatic repulsion of phosphates

Duplex DNA consists of two strands held together primarily by hydrogen bonds between complementary nucleobases (adenine with thymine and guanine with cytosine), as well as stacking interactions among the bases. The melting temperature of DNA, or the temperature at which the strands separate, is influenced by the composition of the bases in the strands. Higher melting temperatures are associated with DNA that contains a higher proportion of guanine and cytosine (G+C pairs) compared to adenine and thymine (A+T pairs). This is mainly because G+C base pairs form three hydrogen bonds compared to the two hydrogen bonds formed by A+T pairs, leading to increased stability of the DNA duplex. The correct answer emphasizes the concept of increased π -stacking strength. π -stacking interactions occur between the aromatic rings of adjacent bases, and in DNA with a higher G+C content, these interactions are enhanced due to the structure and properties of the bases involved. The more stable the stacking interactions, the more energy is required to separate the strands, resulting in a higher melting temperature for the DNA duplex. In contrast, duplex DNA containing a greater proportion of A+T pairs typically represents a less stable configuration due to the weaker interactions relative to G+C pairs. This

5. What are the characteristics that differentiate acids from bases?

- A. Acids accept protons while bases donate protons
- B. Acids are always soluble in water while bases are not
- C. Acids donate protons whereas bases accept protons**
- D. Acids are measured by pH levels above 7 while bases are below 7

The distinction between acids and bases is fundamentally rooted in their behavior in chemical reactions, particularly concerning protons (H^+ ions). The correct answer highlights that acids donate protons, whereas bases accept protons. This characterization stems from the Brønsted-Lowry acid-base theory, which defines acids as proton donors and bases as proton acceptors. When an acid donates a proton, it decreases the concentration of H^+ ions in solution, which can affect the pH. Conversely, when a base accepts a proton, it increases the concentration of H^+ ions, thereby influencing the acidity of the solution. This fundamental interaction is crucial for understanding a wide array of chemical processes, including those that occur in biological systems. Other options suggest mischaracterizations or incomplete definitions. The notion that acids are always soluble in water while bases are not does not hold true, as solubility can vary widely among different acids and bases. The pH scale also does not define acids and bases solely by their position relative to 7; instead, it measures the concentration of H^+ ions, with acids generally having a pH less than 7 and bases having a pH greater than 7. Thus, option C accurately captures the

6. What is the outcome of adding a strong acid to a solution that contains $[Cu(NH_3)_4]^{2+}$?

- A. The concentration of ammonia increases
- B. The concentration of $[Cu(NH_3)_4]^{2+}$ increases
- C. The concentration of $[Cu(H_2O)_2(NH_3)_2]^{2+}$ increases
- D. The concentration of $[Cu(NH_3)_4]^{2+}$ decreases**

Adding a strong acid to a solution containing the complex ion $[Cu(NH_3)_4]^{2+}$ results in a decrease in the concentration of that complex. This is primarily due to the fact that the strong acid, when introduced to the solution, releases a high concentration of hydrogen ions (H^+). These hydrogen ions can interfere with the ammonia ligands (NH_3) in the complex. The equilibrium of the complex can be described by the reaction: $[Cu(NH_3)_4]^{2+} \rightleftharpoons Cu^{2+} + 4NH_3$. When you add the strong acid, the increase in H^+ concentration leads to the partial protonation of ammonia, forming ammonium ions (NH_4^+). As the ammonia molecules are converted into ammonium ions, fewer ammonia ligands are available to coordinate with Cu^{2+} , causing the equilibrium to shift to the left. This shift results in the dissociation of the $[Cu(NH_3)_4]^{2+}$ complex back into free copper ions (Cu^{2+}) and ammonia. Thus, the overall outcome is a decrease in the concentration of the $[Cu(NH_3)_4]^{2+}$ complex.

7. What kind of energy change occurs in a spontaneous process?

- A. Positive ΔG**
- B. Negative ΔG**
- C. No change in energy**
- D. Neutral energy**

In a spontaneous process, the change in Gibbs free energy (ΔG) is negative. This indicates that the process can occur without the input of external energy. A negative ΔG suggests that the products of the reaction have lower free energy than the reactants, making the reaction energetically favorable. Spontaneous processes are characterized by the tendency to proceed towards a state of lower energy and increased disorder (entropy), aligning with the second law of thermodynamics. This energy change reflects the natural tendency of systems to evolve toward equilibrium, where free energy is minimized. When ΔG is negative, it is associated with exergonic reactions, which release energy, often in the form of heat or work. In contrast, if ΔG were positive, it would indicate that the process is non-spontaneous and requires energy input to occur. Therefore, in the context of spontaneous processes, a negative ΔG is a clear indicator of the energy changes involved.

8. What is the primary structure of a protein?

- A. The sequence of amino acids in a polypeptide chain**
- B. The folding of the chain into alpha-helices and beta-sheets**
- C. The overall three-dimensional shape of the protein**
- D. The interaction of multiple polypeptide chains**

The primary structure of a protein refers specifically to the sequence of amino acids that are linked together by peptide bonds to form a polypeptide chain. This linear arrangement dictates not only the identity of the protein but also its ultimate three-dimensional conformation and function. Each amino acid in the sequence is determined by the genetic code, and the unique sequence ultimately influences how the protein will fold and function biologically. In contrast, the secondary structure involves the local folding of the polypeptide chain into structures such as alpha-helices and beta-sheets, which arise due to hydrogen bonding patterns between the backbone atoms. The overall three-dimensional shape of the protein, known as the tertiary structure, emerges from interactions between the side chains of the amino acids that stabilize and refine the protein's form. Finally, the quaternary structure describes the assembly of multiple polypeptide chains into a single functional unit. Understanding that primary structure is the foundational level of organization is crucial for grasping how proteins function biochemically.

9. Under what condition will tryptophan produce the largest circular dichroism (CD) signal in the near UV region?

- A. As a free amino acid
- B. Part of an α -helix
- C. Part of a β -sheet
- D. Part of a fully folded protein**

Tryptophan produces the largest circular dichroism (CD) signal in the near UV region when it is part of a fully folded protein. This is primarily due to the environment surrounding the tryptophan side chain in a fully folded protein, which influences its electronic transitions and thus enhances the CD signal. In a fully folded protein, tryptophan experiences a variety of interactions, including hydrophobic packing, hydrogen bonding, and polar interactions with the surrounding amino acids. These interactions stabilize specific orientations and conformations of the tryptophan residues, leading to a stronger and more distinct CD signal in the near UV region, which is sensitive to the environment of the chromophores. In contrast, when tryptophan is in other forms, such as a free amino acid, its signal is weaker because it lacks the stabilizing interactions present in a folded protein. Similarly, when it is part of an α -helix or a β -sheet, while it may still display some circular dichroism due to local secondary structure effects, the overall signal is often not as pronounced as in the context of a fully folded protein where tertiary interactions contribute significantly to the signal. Therefore, the native conformation and the extensive interactions within a fully folded

10. What is the equivalent resistance of a 60- Ω resistor connected in parallel with a 20- Ω resistor?

- A. 80 Ω
- B. 40 Ω
- C. 15 Ω**
- D. 3 Ω

To find the equivalent resistance of resistors connected in parallel, you can use the formula: $\frac{1}{R_{\text{eq}}} = \frac{1}{R_1} + \frac{1}{R_2}$ In this case, the two resistors are 60 Ω and 20 Ω . Substituting the values into the formula gives: $\frac{1}{R_{\text{eq}}} = \frac{1}{60} + \frac{1}{20}$ To add these fractions, it can be helpful to find a common denominator. The least common multiple of 60 and 20 is 60. Thus, we rewrite the second fraction: $\frac{1}{20} = \frac{3}{60}$ Now we can combine the fractions: $\frac{1}{R_{\text{eq}}} = \frac{1}{60} + \frac{3}{60} = \frac{4}{60}$ This simplifies to: $\frac{1}{R_{\text{eq}}} = \frac{1}{15}$ To find

Next Steps

Congratulations on reaching the final section of this guide. You've taken a meaningful step toward passing your certification exam and advancing your career.

As you continue preparing, remember that consistent practice, review, and self-reflection are key to success. Make time to revisit difficult topics, simulate exam conditions, and track your progress along the way.

If you need help, have suggestions, or want to share feedback, we'd love to hear from you. Reach out to our team at hello@examzify.com.

Or visit your dedicated course page for more study tools and resources:

<https://aamccpfl2.examzify.com>

We wish you the very best on your exam journey. You've got this!

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