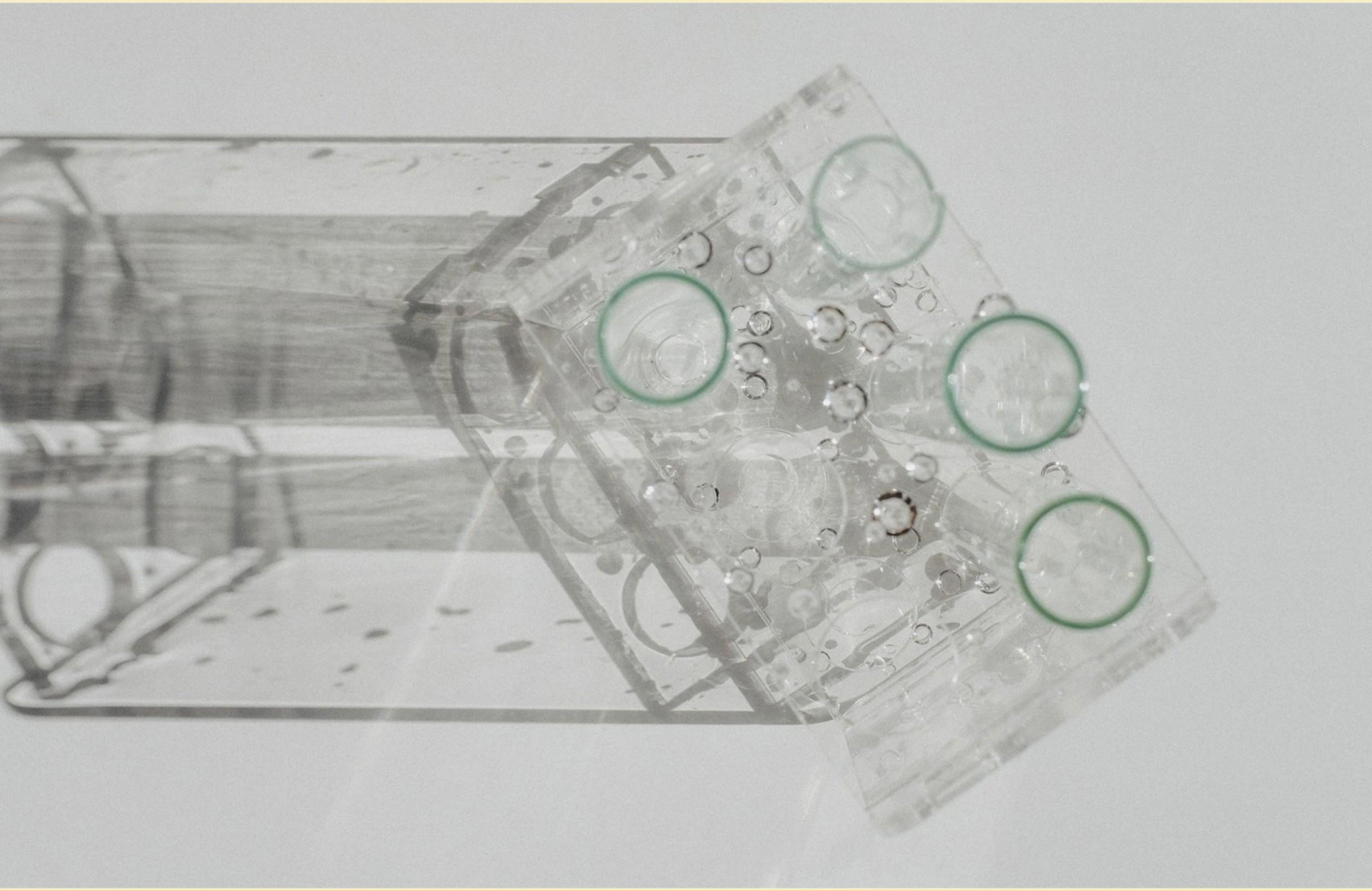
BIOCHEMISTRY MODULE 6 PRACTICE EXAM (SAMPLE)

STUDY GUIDE



SAMPLE STUDY GUIDE WITH LIMITED QUESTIONS

VISIT US ONLINE FOR THE FULL VERSION STUDY GUIDE

https://biochemmodule6.examzify.com

Table of Contents

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

1. What are aminotransferases and which cofactor do they require?

A. Aminotransferases catalyze oxidation of amino acids; require FAD

B. Aminotransferases catalyze transfer of amino groups between amino acids and α-keto acids; require pyridoxal phosphate (PLP)

C. Aminotransferases catalyze decarboxylation of amino acids

D. Aminotransferases transfer phosphate groups

2. What percentage of ribosomes' mass is composed of rRNA?

A. 60%

B. 65%

C. 30%

D. 50%

3. What mechanism transports acetyl-CoA from mitochondria to cytosol for lipid synthesis?

A. Citrate shuttle exporting citrate from mitochondria to cytosol, where it is cleaved to yield acetyl-CoA.

B. Direct transport of acetyl-CoA across inner mitochondrial membrane.

C. Pyruvate transporter.

D. Malate shuttle.

4. Which molecule serves as the two-carbon donor in the first committed step of fatty acid synthesis?

A. Acetyl-CoA

B. Acetoacetyl-CoA

C. Malonyl-CoA

D. Succinyl-CoA

5. What does Km represent in Michaelis-Menten kinetics?

A. Km is the substrate concentration at half-maximal velocity; lower Km indicates higher apparent affinity.

B. Km is the maximum rate.

C. Km is the turnover number.

D. Km is the substrate concentration at half-minimal velocity.

6. Differentiate allosteric enzymes from Michaelis-Menten enzymes.

A. Allosteric enzymes show hyperbolic kinetics and generally lack cooperative binding.

B. Allosteric enzymes show sigmoidal (cooperative) kinetics and are regulated by effectors that modify activity.

C. Allosteric enzymes are inactive; MM enzymes are always active.

D. Both display hyperbolic kinetics and are regulated only by substrate concentration.

7. Non-covalent interactions contribute to the 3D shapes and structures of RNA molecules. Which statement best describes this contribution?

A. Covalent bonds along the backbone stabilize folding.

B. Non-covalent hydrogen bonding between complementary base pairs drives RNA folding.

C. Disulfide bonds stabilize RNA's 3D structure.

D. Ionic bonds between phosphate groups determine secondary structure.

8. The pentose sugar in RNA is ribose.

A. Glucose

B. Deoxyribose

C. Fructose

D. Ribose

9. Purines are characterized by containing two fused rings.

A. They contain a single ring

B. They contain two fused rings

C. They contain three rings

D. They are not nitrogenous bases

10. Which statement best describes the regulatory mechanism of the pyruvate dehydrogenase complex via reversible phosphorylation?

A. PDH is active when phosphorylated and inhibited by phosphorylation

B. PDH is active when dephosphorylated; PDH kinase phosphorylates and inhibits; PDH phosphatase dephosphorylates and reactivates

C. PDH is activated only by phosphorylation and cannot be dephosphorylated

D. Phosphorylation status of PDH does not affect its activity

Answers

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

Explanations

1. What are aminotransferases and which cofactor do they require?

A. Aminotransferases catalyze oxidation of amino acids; require FAD

B. Aminotransferases catalyze transfer of amino groups between amino acids and α-keto acids; require pyridoxal phosphate (PLP)

C. Aminotransferases catalyze decarboxylation of amino acids

D. Aminotransferases transfer phosphate groups

Aminotransferases perform the transfer of amino groups between amino acids and α-keto acids in a reversible transamination reaction. They catalyze the movement of the amino group from a donor amino acid to an acceptor α-keto acid, producing a new amino acid and a new α-keto acid. The essential cofactor is pyridoxal phosphate (PLP), derived from vitamin B6. PLP forms a Schiff base with a lysine in the enzyme and then forms an external aldimine with the amino acid substrate, allowing the amino group to be removed and reattached through stabilized intermediates. This arrangement enables efficient shuttling of the amino group between molecules. The other options describe different enzyme activities: FAD is a redox cofactor used by dehydrogenases, decarboxylases remove carboxyl groups, and kinases transfer phosphate groups.

2. What percentage of ribosomes' mass is composed of rRNA?

A. 60%

B. 65%

C. 30%

D. 50%

Ribosomes are ribonucleoprotein complexes, meaning RNA and protein both contribute to their structure and function, but the RNA portion forms the bulk of the mass. The rRNA molecules create the scaffold and the catalytic center, so they make up roughly two-thirds of the ribosome's mass, with ribosomal proteins contributing the remaining one-third. In both bacteria and eukaryotes, this translates to about 60–65% of the mass being rRNA, which is why the commonly cited figure is around 65%.

3. What mechanism transports acetyl-CoA from mitochondria to cytosol for lipid synthesis?

A. Citrate shuttle exporting citrate from mitochondria to cytosol, where it is cleaved to yield acetyl-CoA.

B. Direct transport of acetyl-CoA across inner mitochondrial membrane.

C. Pyruvate transporter.

D. Malate shuttle.

Acetyl-CoA itself can't cross the inner mitochondrial membrane, so the cell moves the carbon for lipid synthesis as citrate. In the mitochondrion, acetyl-CoA condenses with oxaloacetate to form citrate. Citrate is then shuttled out of mitochondria into the cytosol, where ATP-citrate lyase cleaves it back to acetyl-CoA and oxaloacetate. The cytosolic acetyl-CoA is then used for fatty acid synthesis. The other routes don't work for delivering acetyl units to the cytosol: there's no direct acetyl-CoA transporter across the inner membrane, the malate shuttle mainly transfers reducing equivalents (NADH), and the pyruvate transporter moves pyruvate rather than acetyl groups.

4. Which molecule serves as the two-carbon donor in the first committed step of fatty acid synthesis?

A. Acetyl-CoA

B. Acetoacetyl-CoA

C. Malonyl-CoA

D. Succinyl-CoA

In fatty acid synthesis, the chain is extended by a two-carbon unit donated from malonyl-CoA during the first condensation with the starter acetyl group. Malonyl-CoA is decarboxylated as it condenses with the growing chain on the fatty acid synthase complex, delivering two carbons and forming a four-carbon product. This decarboxylative condensation step is what makes malonyl-CoA the two-carbon donor in the initial committed step. Acetyl-CoA provides the initial primer, not the donor in this step. Succinyl-CoA isn't part of this fatty acid synthesis pathway, and acetoacetyl-CoA is the product of the condensation, not the donor.

5. What does Km represent in Michaelis-Menten kinetics?

A. Km is the substrate concentration at half-maximal velocity; lower Km indicates higher apparent affinity.

B. Km is the maximum rate.

C. Km is the turnover number.

D. Km is the substrate concentration at half-minimal velocity.

Km tells you the substrate amount needed to push the reaction to half of its maximum speed. In Michaelis-Menten terms, v = Vmax[S] / (Km + [S]); when [S] equals Km, the velocity is Vmax/2. This makes Km a practical measure of how tightly the enzyme binds the substrate: a smaller Km means the enzyme reaches half-max at a lower substrate concentration, i.e., higher apparent affinity. It is not the maximum rate (that's Vmax) nor the turnover number (kcat). The standard description is the substrate concentration at half-maximal velocity.

6. Differentiate allosteric enzymes from Michaelis-Menten enzymes.

A. Allosteric enzymes show hyperbolic kinetics and generally lack cooperative binding.

B. Allosteric enzymes show sigmoidal (cooperative) kinetics and are regulated by effectors that modify activity.

C. Allosteric enzymes are inactive; MM enzymes are always active.

D. Both display hyperbolic kinetics and are regulated only by substrate concentration.

Allosteric enzymes differ from Michaelis-Menten enzymes in how their activity and kinetics respond to substrate and regulators. Allosteric enzymes have multiple subunits and exhibit cooperative binding, so when substrate or an effector binds at one site, it changes the activity of other sites. This cooperative interaction produces a sigmoidal (S-shaped) rate versus substrate curve rather than a simple, single-peak hyperbola. They're regulated by effectors that bind at allosteric sites (sites other than the active site), which can either enhance or inhibit activity by shifting the enzyme between different conformations (often described as tense and relaxed states). Michaelis-Menten enzymes, on the other hand, typically show hyperbolic kinetics, consistent with non-cooperative binding at a single active site. Their activity is largely governed by substrate concentration, and regulation is usually through substrate availability or classic inhibitors/activators that do not operate through allosteric sites. So, the key distinction is sigmoidal kinetics and regulation by allosteric effectors for allosteric enzymes, versus hyperbolic kinetics and regulation primarily by substrate concentration for Michaelis-Menten enzymes.

7. Non-covalent interactions contribute to the 3D shapes and structures of RNA molecules. Which statement best describes this contribution?

A. Covalent bonds along the backbone stabilize folding.

B. Non-covalent hydrogen bonding between complementary base pairs drives RNA folding.

C. Disulfide bonds stabilize RNA's 3D structure.

D. Ionic bonds between phosphate groups determine secondary structure.

RNA folding is driven mainly by non-covalent interactions, with hydrogen bonding between complementary bases playing the central role. These hydrogen bonds between A–U and G–C (and occasional G–U) form base pairs that create stems and other secondary structures, bringing distant parts of the molecule into proximity and shaping the overall 3D form. While the covalent backbone bonds hold the chain together, they don't drive folding in the same way; disulfide bonds aren't a feature of typical RNA structure, and although metal ions and electrostatics influence stability, there aren't ionic bonds between phosphate groups that determine the secondary structure. So, the non-covalent hydrogen bonding between bases is the best description of how RNA's 3D shape is stabilized.

8. The pentose sugar in RNA is ribose.

A. Glucose

B. Deoxyribose

C. Fructose

D. Ribose

RNA uses a five-carbon sugar, ribose, as its backbone component. This pentose has a hydroxyl group at the 2' carbon, which distinguishes it from DNA's sugar, deoxyribose, that lacks the 2' OH. The other options are hexoses (glucose and fructose) and do not serve as the sugar in RNA. Therefore, the pentose sugar in RNA is ribose.

9. Purines are characterized by containing two fused rings.

A. They contain a single ring

B. They contain two fused rings

C. They contain three rings

D. They are not nitrogenous bases

Purines have a bicyclic ring system: a six-membered ring fused to a five-membered ring. This two-ring, fused structure is the defining feature of purines (adenine and guanine) and explains why they are larger than the single-ring pyrimidines (cytosine, thymine, and uracil) with which they pair in nucleic acids. The fused rings provide the nitrogen-rich surface needed for hydrogen bonding patterns that help maintain the consistent width of the DNA double helix. So describing purines as containing two fused rings is accurate. A single ring would describe pyrimidines, three rings don't occur for standard nucleobases, and purines are indeed nitrogenous bases.

10. Which statement best describes the regulatory mechanism of the pyruvate dehydrogenase complex via reversible phosphorylation?

A. PDH is active when phosphorylated and inhibited by phosphorylation

B. PDH is active when dephosphorylated; PDH kinase phosphorylates and inhibits; PDH phosphatase dephosphorylates and reactivates

C. PDH is activated only by phosphorylation and cannot be dephosphorylated

D. Phosphorylation status of PDH does not affect its activity

Reversible phosphorylation acts as the on/off switch for pyruvate dehydrogenase activity. The two opposing enzymes are a PDH kinase and a PDH phosphatase. PDH kinase adds a phosphate to the E1 subunit, turning the complex off, while PDH phosphatase removes that phosphate, reactivating it. When PDH is dephosphorylated, it is active and converts pyruvate into acetyl-CoA for entry into the TCA cycle. When PDH is phosphorylated, its activity is reduced, limiting production of acetyl-CoA from pyruvate and slowing flux into the TCA cycle. This regulatory setup lets the cell quickly adjust energy production: high-energy signals favor phosphorylation and inactivation, whereas signals such as increased Ca2+ during activity promote dephosphorylation and activation. Therefore, the description that PDH is active when dephosphorylated, with PDH kinase phosphorylating and inhibiting and PDH phosphatase dephosphorylating and reactivating, is the correct one.

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://biochemmodule6.examzify.com

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