University of Central Florida (UCF) PCB4524 Molecular Biology II Practice Exam 1 (Sample)

Study Guide



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Questions



- 1. What motif is found in region 2 of sigma 70?
 - B. Zinc finger

 - C. Helix-turn-helix

A. Leucine zipper

- D. Beta-sheet
- 2. What are the two subunits that make up the pincers of RNA polymerase (RNAP)?
 - A. A, B
 - B. B, B'
 - C. Rpb1, Rpb2
 - D. β, α
- 3. Which component is essential for the initiation phase of transcription based on the promoter structure?
 - A. RNA polymerase
 - B. Sigma factors
 - C. Core enzymes only
 - D. Transcription factors only
- 4. What does the evolution of splicing suggest regarding its complexity?
 - A. It has changed from major to minor forms
 - B. It has evolved from group 1 introns to major forms
 - C. It has evolved from group 2 to ATAC minor to major forms
 - D. It shows no evolutionary trend
- 5. What does U2AF65 bind during the splicing process?
 - A. Branch point sequence
 - B. 5' splice site
 - C. Py tract
 - D. Poly-A tail

6. Which element is associated with the initiation of transcription in eukaryotes?
A. Enhancer
B. Silencer
C. TATA box
D. Promoter-proximal element
7. What is the function of TRCF in bacterial transcription?
A. Phosphorylates RNA polymerase
B. Moves upstream along dsDNA and translocates RNAP forward, causing dissociation
C. Enhances RNA stability
D. Recruits elongation factors
8. What is protein targeting?
A. The process by which proteins are synthesized in the ribosome
B. The method of transporting proteins across the cell membrane
C. The process by which proteins are directed to the appropriate location in the cell
D. The mechanism of protein folding into its functional shape
9. Which RNA polymerase subunit is homologous to Rpb2 in RNAP II?
A. A2
Β. α
C. B
D. b
10. What does the process of transcription ultimately produce?
A. Amino acids
B. Protein
C. DNA
D. RNA

Answers



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

Explanations



- 1. What motif is found in region 2 of sigma 70?
 - A. Leucine zipper
 - B. Zinc finger
 - C. Helix-turn-helix
 - D. Beta-sheet

The motif found in region 2 of sigma 70 is the helix-turn-helix structure. This specific motif plays a crucial role in the binding of sigma factors to the promoter regions of bacterial DNA during the initiation of transcription. The helix-turn-helix motif consists of two alpha helices connected by a short strand of amino acids that forms a "turn." This structure allows the protein to fit into the major groove of DNA, enabling specific interactions with the nucleotide sequences necessary for transcription initiation. In the context of sigma 70, the helix-turn-helix is essential for recognizing and binding to specific promoter elements, thereby facilitating the assembly of the RNA polymerase complex. Understanding the significance of the helix-turn-helix motif provides insight into how sigma factors contribute to gene regulation and transcription processes in bacteria. Other motifs, such as leucine zippers, zinc fingers, and beta-sheets, serve different functions or exhibit different DNA-binding characteristics that are not applicable in this specific context.

- 2. What are the two subunits that make up the pincers of RNA polymerase (RNAP)?
 - A. A, B
 - B. B, B'
 - C. Rpb1, Rpb2
 - D. β, α

The pincers of RNA polymerase (RNAP) are formed by two subunits known as B and B'. These subunits play a critical role in the enzyme's function, specifically in the transcription process. In eukaryotic RNA polymerase II, which is central to the transcription of protein-coding genes, the B and B' subunits are essential for the formation of the transcription bubble and the correct positioning of the RNA polymerase on the DNA template. The B subunit is involved in binding to the template DNA and synthesizing the RNA strand, while the B' subunit provides a structural framework that allows for the coordination between the enzyme and the DNA. This pincer-like structure is vital for maintaining contact with the DNA during transcription and facilitating the movement of the enzyme along the DNA strand as it synthesizes RNA. In contrast, the other options present different structures or components that do not represent the specific subunits responsible for the pincers of RNAP. For instance, Rpb1 and Rpb2 refer to the core subunits of RNA polymerase II but do not specifically denote the 'pincer' structure. Similarly, the β and α designations pertain to bacterial RNA polymerase components rather than the euk

- 3. Which component is essential for the initiation phase of transcription based on the promoter structure?
 - A. RNA polymerase
 - B. Sigma factors
 - C. Core enzymes only
 - D. Transcription factors only

The initiation phase of transcription is a critical process in gene expression, and the role of RNA polymerase is essential in this phase. RNA polymerase is the enzyme responsible for synthesizing RNA from a DNA template during transcription. In bacterial systems, the enzyme does not initiate transcription alone; it requires assistance from sigma factors to locate the promoter region of the DNA. The promoter structure includes specific sequences that are recognized by the sigma factor, allowing RNA polymerase to bind and initiate transcription. Once RNA polymerase is correctly positioned at the promoter with the help of sigma factors, it can proceed to unwind the DNA helix and begin synthesizing RNA. In eukaryotes, while RNA polymerase is still a crucial component for transcription initiation, it works in conjunction with transcription factors to recruit to the promoter and form a pre-initiation complex. However, in the context of this question, where RNA polymerase is highlighted as essential, it emphasizes the core function of this enzyme in the transcription process. The other options, while important in their contexts (such as sigma factors being key for bacterial transcription initiation), do not universally represent the essential component needed for the initiation phase across all types of organisms. Thus, the focus on RNA polymerase correctly identifies it as the

- 4. What does the evolution of splicing suggest regarding its complexity?
 - A. It has changed from major to minor forms
 - B. It has evolved from group 1 introns to major forms
 - C. It has evolved from group 2 to ATAC minor to major forms
 - D. It shows no evolutionary trend

The evolution of splicing and its complexity can be understood through the historical progression of intron systems in eukaryotic organisms. The correct answer reflects a path of increasing complexity in the splicing machinery, indicating that initial systems featuring group 2 introns evolved into more complex mechanisms, culminating in the diversity of spliceosomal machinery observed today, which includes both ATAC minor and major spliceosomal forms. Group 1 introns, found in some lower eukaryotes and bacteria, represent a more primitive form of self-splicing. However, more advanced and complex splicing systems, such as those involving group 2 introns, set the stage for further evolutionary development. This pathway eventually led to the emergence of the ATAC and major spliceosomal forms, characterized by more intricate interactions between the spliceosome components and a more refined regulation of splicing processes. The inclusion of ATAC minor forms in the evolutionary context highlights a significant step towards the diversification and specialization of splicing mechanisms, showcasing how functional requirements, such as alternative splicing and regulatory complexities, shaped the trajectory of splicing evolution in eukaryotic cells. Thus, option C accurately encapsulates the complexity evolution perspective, indicating a clear trend towards increasingly sophisticated splicing systems.

5. What does U2AF65 bind during the splicing process?

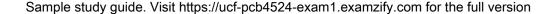
- A. Branch point sequence
- B. 5' splice site
- C. Py tract
- D. Poly-A tail

U2AF65 is a critical component of the spliceosome, which is responsible for the removal of introns from pre-mRNA transcripts during the splicing process. Specifically, U2AF65 binds to the pre-mRNA's pyrimidine-rich tract, also known as the Py tract, that is located upstream of the 3' splice site. The Py tract is essential for the recognition and assembly of the spliceosome on the mRNA. By binding to the Py tract, U2AF65 helps recruit U2 snRNP to the branch point, a step that is crucial for the correct splicing of the mRNA. This binding is integral to facilitating the assembly of other splicing factors and ultimately ensuring that splicing proceeds with fidelity.

6. Which element is associated with the initiation of transcription in eukaryotes?

- A. Enhancer
- B. Silencer
- C. TATA box
- D. Promoter-proximal element

The TATA box is a critical element associated with the initiation of transcription in eukaryotes. This sequence, typically located about 25-30 base pairs upstream of the transcription start site, serves as a binding site for transcription factors, particularly TATA-binding protein (TBP), which is a component of the transcription factor complex that assembles at the promoter region. The binding of TBP to the TATA box encourages the recruitment of other transcription factors and RNA polymerase II, forming the pre-initiation complex necessary for the transcription of protein-coding genes. The role of the TATA box is essential because it helps position the RNA polymerase correctly at the start site, enabling the proper unwinding of DNA and beginning of RNA synthesis. Its presence and function highlight the importance of core promoter elements in controlling gene expression in eukaryotic cells. Other elements like enhancers and silencers act to modify the efficiency and specificity of transcription but do not directly initiate the process. The promoter-proximal elements can enhance transcription but also function to modulate gene activation rather than being essential for the initiation itself.



7. What is the function of TRCF in bacterial transcription?

- A. Phosphorylates RNA polymerase
- B. Moves upstream along dsDNA and translocates RNAP forward, causing dissociation
- C. Enhances RNA stability
- D. Recruits elongation factors

TRCF, or Transcription Repair Coupling Factor, plays a significant role in bacterial transcription by facilitating the translocation of RNA polymerase (RNAP) during transcription elongation. The function of TRCF is primarily to move upstream along double-stranded DNA while simultaneously interacting with RNAP to help it progress through the transcription process. This action induces forward translocation of the polymerase, which can be particularly vital in responding to transcriptional blocks or obstacles that may hinder RNA synthesis. As TRCF moves upstream, it helps to dissociate any stalled complexes, effectively allowing RNA polymerase to continue elongating the RNA transcript. This function is crucial in maintaining transcription efficiency and integrity, ensuring that the transcription machinery can overcome obstacles such as DNA damage or stalled RNA polymerase complexes. By clearing the way for RNAP, TRCF ensures the continuation of gene expression in bacteria, which is essential for their adaptation and survival. In contrast, other options address different aspects of transcription or cellular processes that are not directly related to the specific function of TRCF in assisting the movement of RNAP during elongation. For instance, the phosphorylation of RNA polymerase is typically carried out by different kinases and is not the primary role of TRCF. Enhancing RNA stability is

8. What is protein targeting?

- A. The process by which proteins are synthesized in the ribosome
- B. The method of transporting proteins across the cell membrane
- C. The process by which proteins are directed to the appropriate location in the cell
- D. The mechanism of protein folding into its functional shape

Protein targeting refers to the intricate process by which proteins are directed to the appropriate location within the cell where they will perform their specific functions. This involves signal sequences or tags that are part of the protein's structure, which help guide the protein to various cellular compartments such as the nucleus, mitochondria, endoplasmic reticulum, plasma membrane, or even for secretion outside the cell. This process is crucial because proteins often function in specific regions of the cell and their location can influence their activity and the overall function of the cell. Improper targeting can lead to a breakdown in cellular processes and contribute to various diseases. In contrast, the other options describe different aspects of protein biology but do not capture the essence of targeting. The synthesis of proteins occurs in the ribosome, while transport across the cell membrane might involve different mechanisms like diffusion or active transport, but is not specific to targeting. Additionally, protein folding is an essential step for proteins to achieve their functional form but does not deal with directing proteins to their proper cellular destinations.

- 9. Which RNA polymerase subunit is homologous to Rpb2 in RNAP II?
 - A. A2
 - Β. α
 - C.B
 - D.b

The RNA polymerase subunit that is homologous to Rpb2 in RNA polymerase II is indeed the B subunit. Rpb2 is a core component of RNA polymerase II, playing a critical role in the enzyme's function during transcription. This subunit is involved in forming the catalytic center of the enzyme, facilitating the synthesis of RNA from a DNA template. In prokaryotic systems, the RNA polymerase exists as a simpler structure compared to the eukaryotic RNA polymerases. The B subunit in prokaryotic RNA polymerase (specifically in bacterial RNA polymerase) corresponds to Rpb2, as both share structural and functional similarities necessary for the polymerization of nucleotides. Understanding this relationship helps highlight the evolutionary conservation of key components of the transcription machinery across different domains of life. The other options do not correspond to this homology. The A2 subunit is not present in eukaryotic RNA polymerases, while the α subunit refers more to the assembly and regulation aspects of the bacterial RNA polymerase and does not have a direct homological relationship to Rpb2. Similarly, the b subunit indicates other types of subunits in bacterial RNA polymerase that do not align

- 10. What does the process of transcription ultimately produce?
 - A. Amino acids
 - B. Protein
 - C. DNA
 - D. RNA

Transcription is a fundamental process in molecular biology responsible for synthesizing RNA from a DNA template. During transcription, RNA polymerase binds to a specific region of the DNA known as the promoter, unwinds the DNA strands, and assembles a complementary strand of RNA by incorporating ribonucleotides that are complementary to the DNA template strand. The end result of transcription is the formation of a single-stranded RNA molecule, which can take several forms, such as messenger RNA (mRNA), transfer RNA (tRNA), or ribosomal RNA (rRNA), depending on the gene being transcribed. This RNA molecule then plays a critical role in the next stage of gene expression, where mRNA undergoes translation to become a protein. Thus, the correct answer reflects that the product of transcription is RNA, which serves as the key intermediate in the process of translating genetic information into functional proteins.