



AA

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question stem contains an extra stop codon (UAA) before the normal stop codon (UAG) at the end of the template. During protein translation, the **first stop codon** encountered will **bind a release factor**, halting protein synthesis. Therefore, the codon just prior to the first stop codon will be the last codon to add an amino acid. In this case, (**5'-UUG-3'**) is the last codon to add an amino acid to the truncated protein, and this amino acid will be carried by the **5'-CAA-3'** anticodon (codon-anticodon binding occurs in opposite directions [ie, **5' to 3' binds 3' to 5'**]).

(Choice A) Because complementary sequences align in antiparallel fashion, during translation the tRNA anticodons will bind the 5' to 3' mRNA in the (opposite) 3' to 5' direction. Therefore, the **5'-UUG-3'** mRNA codon will bind the **5'-CAA-3'** tRNA anticodon, not the **5'-AAC-3'** anticodon.

(Choices B and E) The **5'-AUC-3'** and **5'-UCG-3'** anticodons will bind to the **5'-GAU-3'** and **5'-CGA-3'** codons, respectively (**5' to 3' binds 3' to 5'**). These are not present in the above mRNA sequence.

(Choice D) The last codon shown in the above mRNA sequence is **5'-UAG-3'** (a stop codon), with the second-to-last codon being **5'-AGC-3'**. Therefore, **5'-GCU-3'** would be the tRNA anticodon responsible for adding the last amino acid to the normal (non-truncated) protein.

Educational objective:

Translation of the mRNA template proceeds in the 5' to 3' direction. Because complementary sequences align in antiparallel fashion, during translation tRNA anticodons will be oriented in the opposite 3' to 5' direction. Stop codons (UAA, UAG, and UGA) halt protein synthesis by binding a release factor; they do not add amino acids to the polypeptide chain.

Genetics

Genetics (General Principles)

Subject

System

Genetic code

Topic

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A researcher develops 2 functional mRNA sequences composed of CUC and CUU trinucleotide repeats, respectively. He subsequently incubates these mRNAs in a solution containing functional ribosomes and tRNAs charged with the appropriate amino acids. After several hours, it is found that both mRNA sequences produce polypeptide chains containing leucine repeats. This observed finding is due to which of the following genetic principles?

- A. Ambiguity (11%)
- B. No punctuation (0%)
- C. Transition (2%)
- D. Universality (7%)
- E. Wobble (78%)

Omitted
Correct answer
E

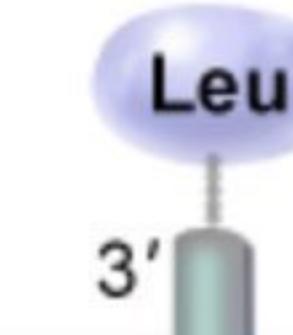
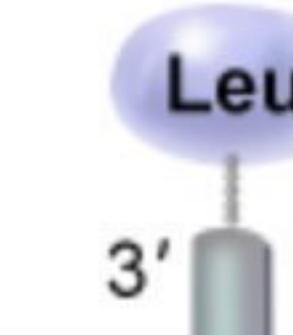
78%
Answered correctly

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Explanation

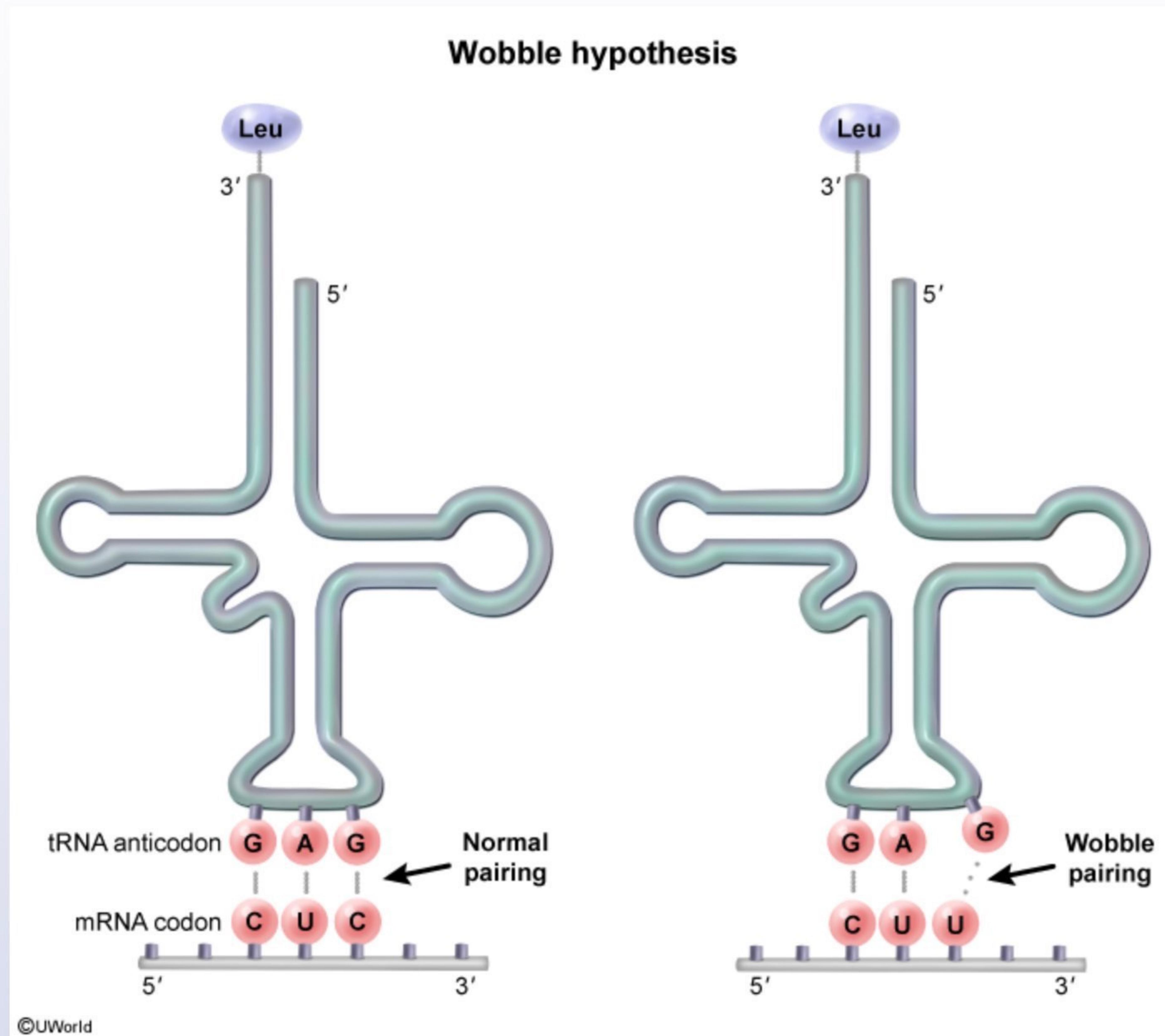
Wobble hypothesis



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There are 61 codons that code for amino acids, but only 20 amino acids are used in protein synthesis. The genetic code is therefore considered "degenerate" because more than 1 codon can code for a particular amino acid.

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acid. For instance, the codons CUC and CUU both code for the amino acid leucine.

Individual tRNA molecules are specific for certain amino acids and recognize the mRNA codons associated with those amino acids. Certain tRNA molecules can recognize **multiple different codons** coding for the **same amino acid**, a phenomenon explained by the **wobble hypothesis**. This hypothesis states that the first 2 nucleotide positions on the mRNA codon require traditional (Watson-Crick) base pairing with their complementary nucleotides on tRNA, whereas the third "wobble" nucleotide position may undergo less stringent (nontraditional) base pairing. In the case of leucine, for example, 1 tRNA molecule recognizes 2 codons (CUC and CUU) because only the first 2 nucleotide positions (CU in the codon) form traditional bonds.

(Choice A) The genetic code is not ambiguous as each codon is associated with only a single amino acid.

(Choice B) The genetic code is read sequentially from a starting point and has no internal punctuation as each codon is adjacent to the next without spacer nucleotides in between.

(Choice C) Genetic transition refers to a point mutation that results in replacement of a purine nucleotide for another purine or a pyrimidine nucleotide for another pyrimidine. In contrast, transversion refers to a point mutation that results in the replacement of a purine nucleotide for a pyrimidine or a pyrimidine nucleotide for a purine.

(Choice D) The genetic code is almost universal as amino acid codons are nearly identical across species; however, mitochondria and some bacteria and single-celled eukaryotes deviate from the standard genetic code.

Educational objective:

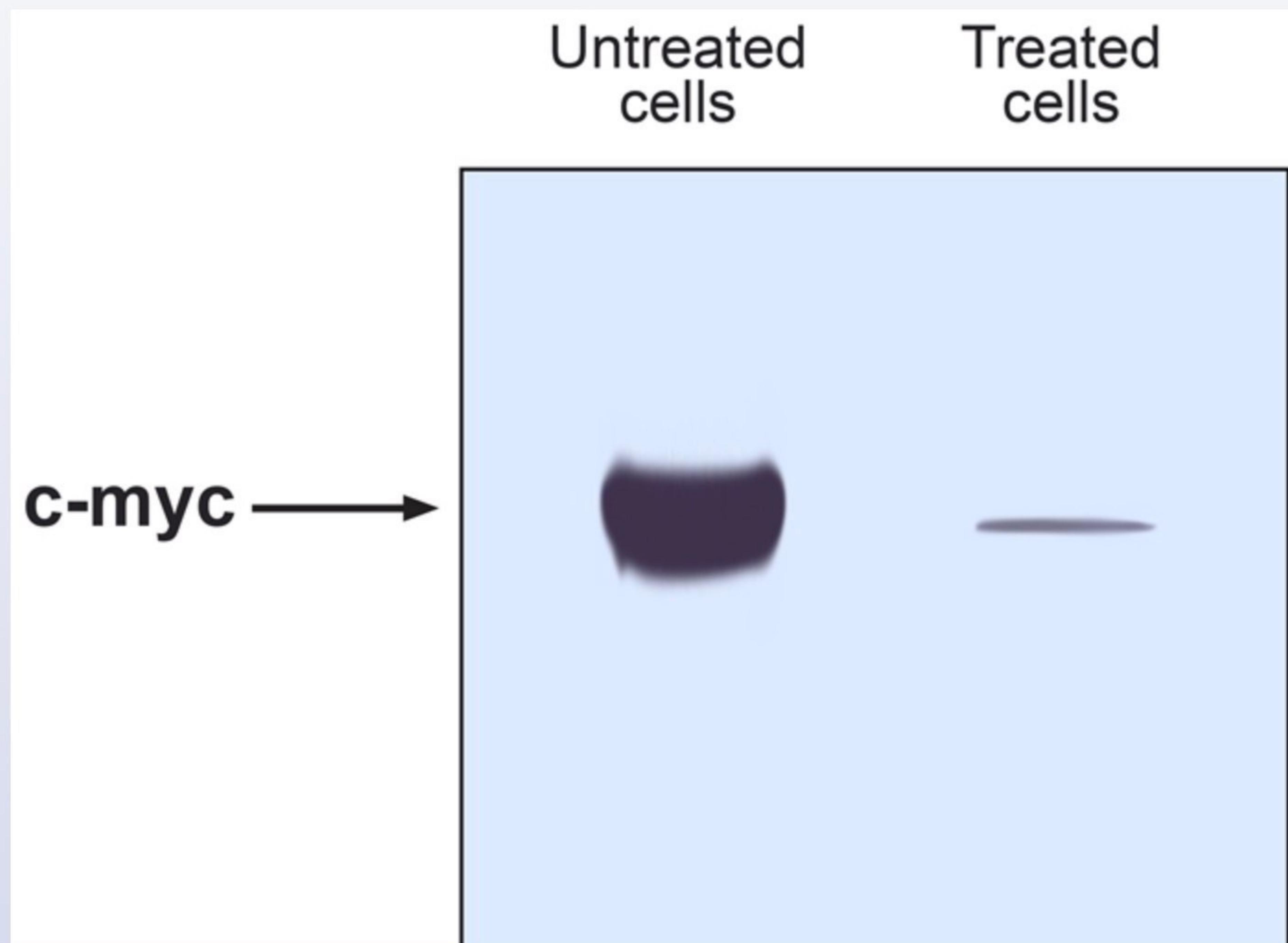
The genetic code is considered "degenerate" because more than 1 codon can code for a particular amino acid. Some of this degeneracy is explained by the wobble hypothesis, which states that the first 2 nucleotide positions on the mRNA codon require traditional (Watson-Crick) base pairing, whereas the third "wobble" nucleotide position may undergo less stringent (nontraditional) base pairing.

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Item 6 of 13 Question Id: 11595

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A pharmaceutical corporation investigating new therapeutic agents for treatment of Burkitt lymphoma synthesizes a double-stranded RNA molecule that is 21 base pairs in length. The RNA molecule has a base pair sequence that is complementary to a region of mRNA encoding c-Myc. Introduction of the RNA molecule into tumor cells results in a significant reduction in cell growth. Western blot analysis of equivalent numbers of treated and untreated cells is shown below.



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Which of the following processes was most likely directly interrupted in the cells exposed to the RNA molecule?

- A. DNA replication (8%)
- B. DNA transcription (17%)
- C. mRNA translation (64%)
- D. Proteasome activity (3%)
- E. Splicing (5%)

Omitted

Correct answer

C



64%

Answered correctly



06 secs

Time Spent



2023

Version

Explanation

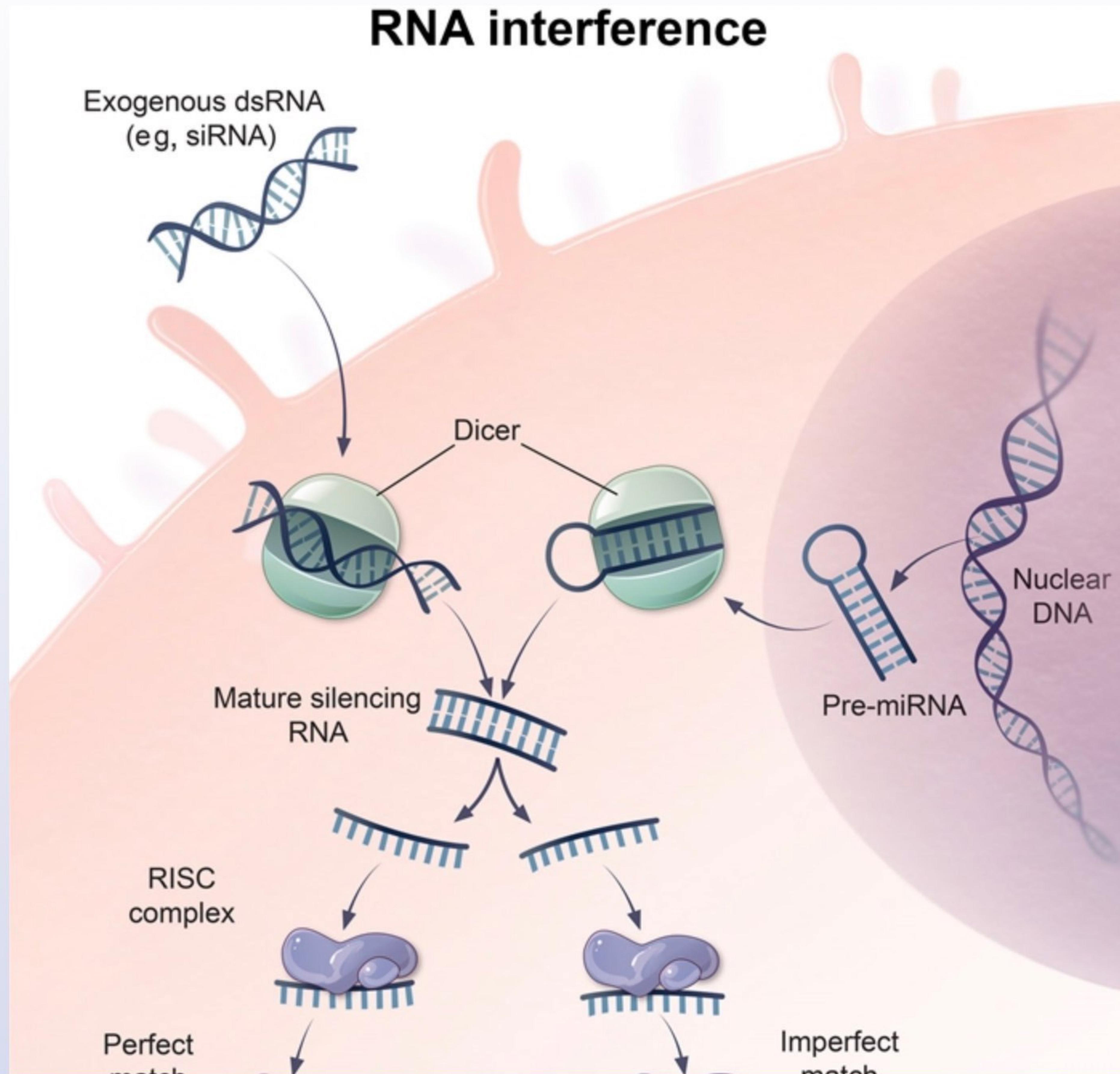
RNA interference

Exogenous dsRNA
(eg, siRNA)

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Mark Question Id: 11595



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The diagram illustrates two mechanisms of RNA interference. On the left, a siRNA duplex perfectly complementary to a segment of mRNA binds to it. This triggers the recruitment of a complex of proteins, leading to the cleavage of the mRNA strand into two fragments. On the right, a siRNA duplex binds to mRNA with some mismatched bases. This imperfect match prevents the ribosome from translating the mRNA into protein, resulting in 'Translation repression'.

mRNA cleavage

Translation repression

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The results of the western blot show that the treated cell line produces less c-myc protein. This is most likely due to RNA interference, a mechanism by which short (20-30 base pair) **double-stranded RNA** sequences induce **posttranscriptional gene silencing**.

Silencing RNA includes both small interfering RNA (siRNA) and microRNA (miRNA). The human genome encodes over 1000 miRNA genes, each one capable of repressing hundreds of target genes; altered expression of miRNA genes are involved in the development of many diseases, including hematologic and solid malignancies. In addition, synthetic siRNA sequences can be introduced into cells to silence specific pathogenic genes (eg, c-Myc oncogene) and are being explored as possible **therapeutic agents**.

After being transcribed, miRNA undergoes processing in the nucleus to form a **double-stranded** precursor that is then exported into the cytoplasm. There, the precursor is cleaved into a short RNA helix by a ribonuclease

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malignancies. In addition, synthetic siRNA sequences can be introduced into cells to silence specific pathogenic genes (eg, c-Myc oncogene) and are being explored as possible **therapeutic agents**.

After being transcribed, miRNA undergoes processing in the nucleus to form a **double-stranded** precursor that is then exported into the cytoplasm. There, the precursor is cleaved into a short RNA helix by a ribonuclease protein called **dicer**. The individual strands are then separated and incorporated into RNA-induced silencing complex (RISC). This multiprotein complex uses its associated miRNA as a template to bind to complementary sequences found on target mRNAs. An exact match generally results in **mRNA degradation**, but a partial match also causes **translational repression** by preventing ribosome and translation factor binding.

(Choice A) DNA polymerase requires a short nucleic acid sequence primer for initiation of DNA synthesis. During DNA replication, these primers are formed from RNA bases by the enzyme DNA primase.

(Choice B) DNA transcription is the process in which RNA is transcribed from a DNA template by an RNA polymerase enzyme. Although certain miRNA sequences can cause transcriptional inhibition, posttranscriptional silencing is the predominant means of RNA interference.

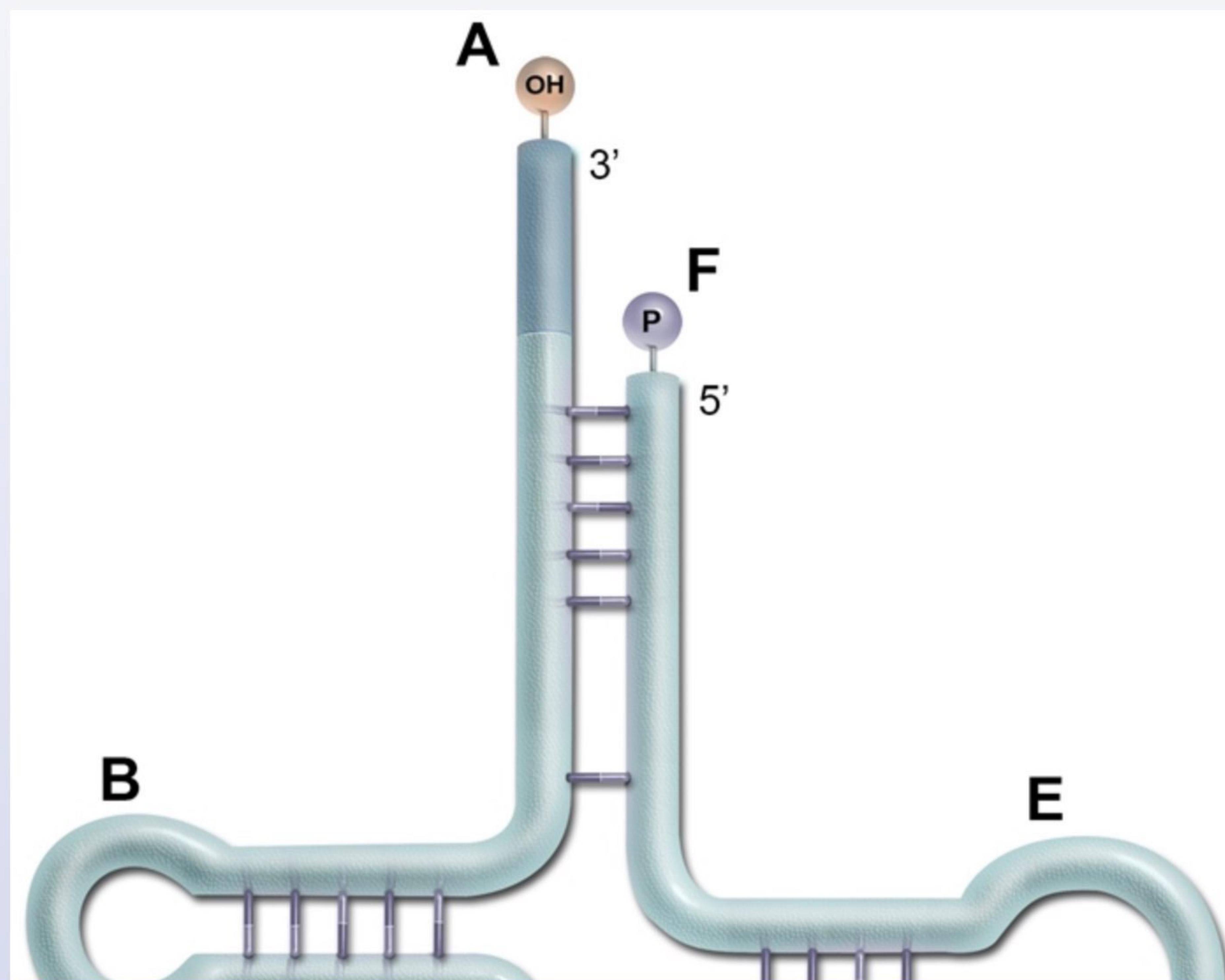
(Choice D) Degradation of proteins and polypeptides occurs in proteasomes and lysosomes. Proteasomes mainly degrade nuclear and cytoplasmic proteins; lysosomes degrade cellular organelles and extracellular proteins.

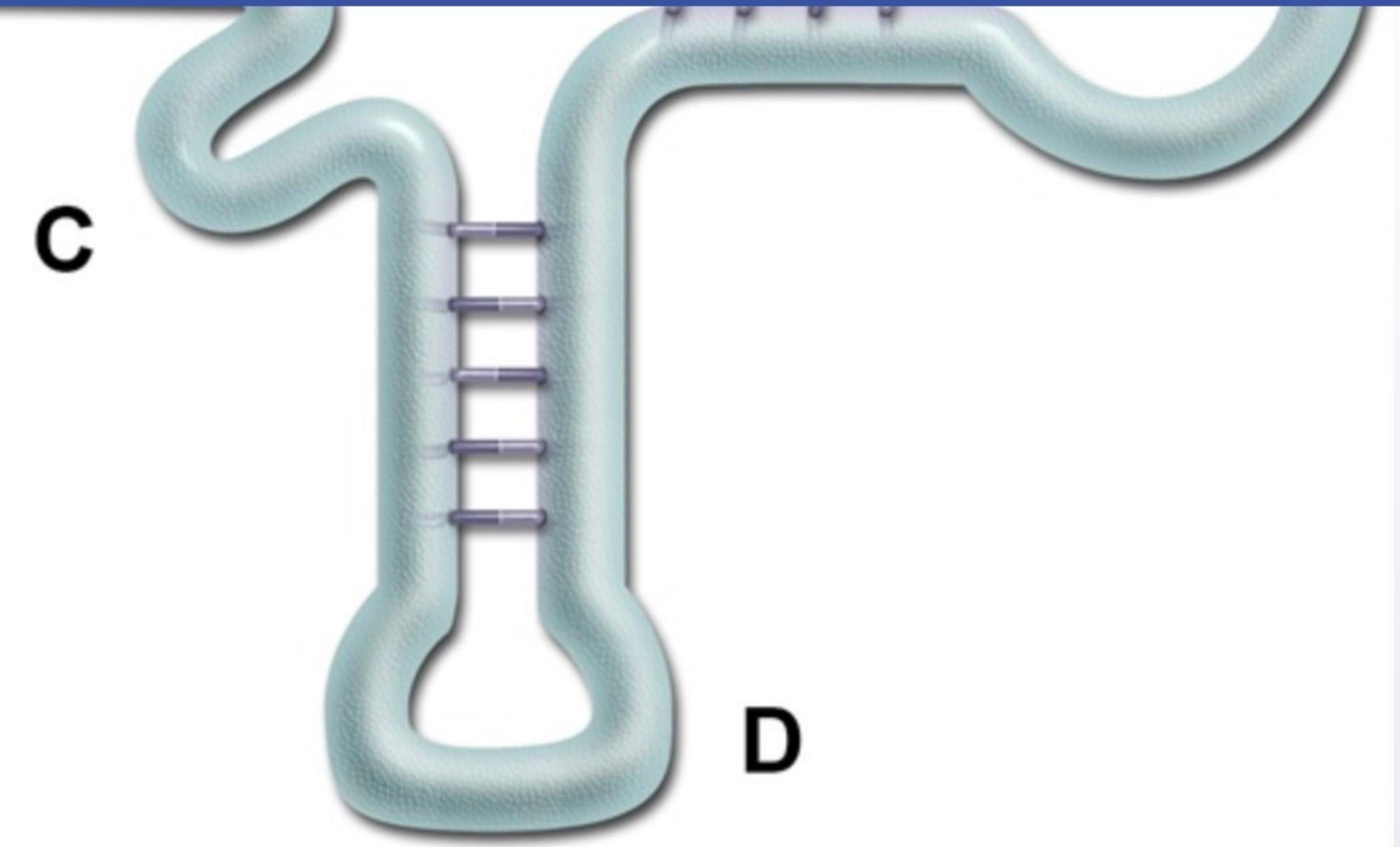
(Choice E) Small nuclear RNA (snRNA) molecules bind to specific proteins to form small nuclear ribonucleoproteins (snRNPs). These snRNPs associate with pre-mRNA to form spliceosomes, which function to remove introns from pre-mRNA during processing within the nucleus.

Educational objective:

Short non-coding RNA sequences (eg, microRNA and small interfering RNA) induce posttranscriptional gene silencing by base-pairing with complementary sequences within target mRNA molecules.

A geneticist is performing an experiment to alter protein structures by incorporating modified amino acids into their polypeptide sequences. During the process, she incubates dermal fibroblasts in a medium containing fluorescently labeled lysine residues. After several hours, she finds that aminoacyl tRNA synthetase in the fibroblasts "loads" lysine residues onto tRNA molecules containing the anticodon UUU. This residue most likely attaches to tRNA at which of the following sites in the image shown below?





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- A. A (67%)
- B. B (2%)
- C. C (2%)
- D. D (17%)
- E. E (2%)
- F. F (9%)

Omitted
Correct answer
A

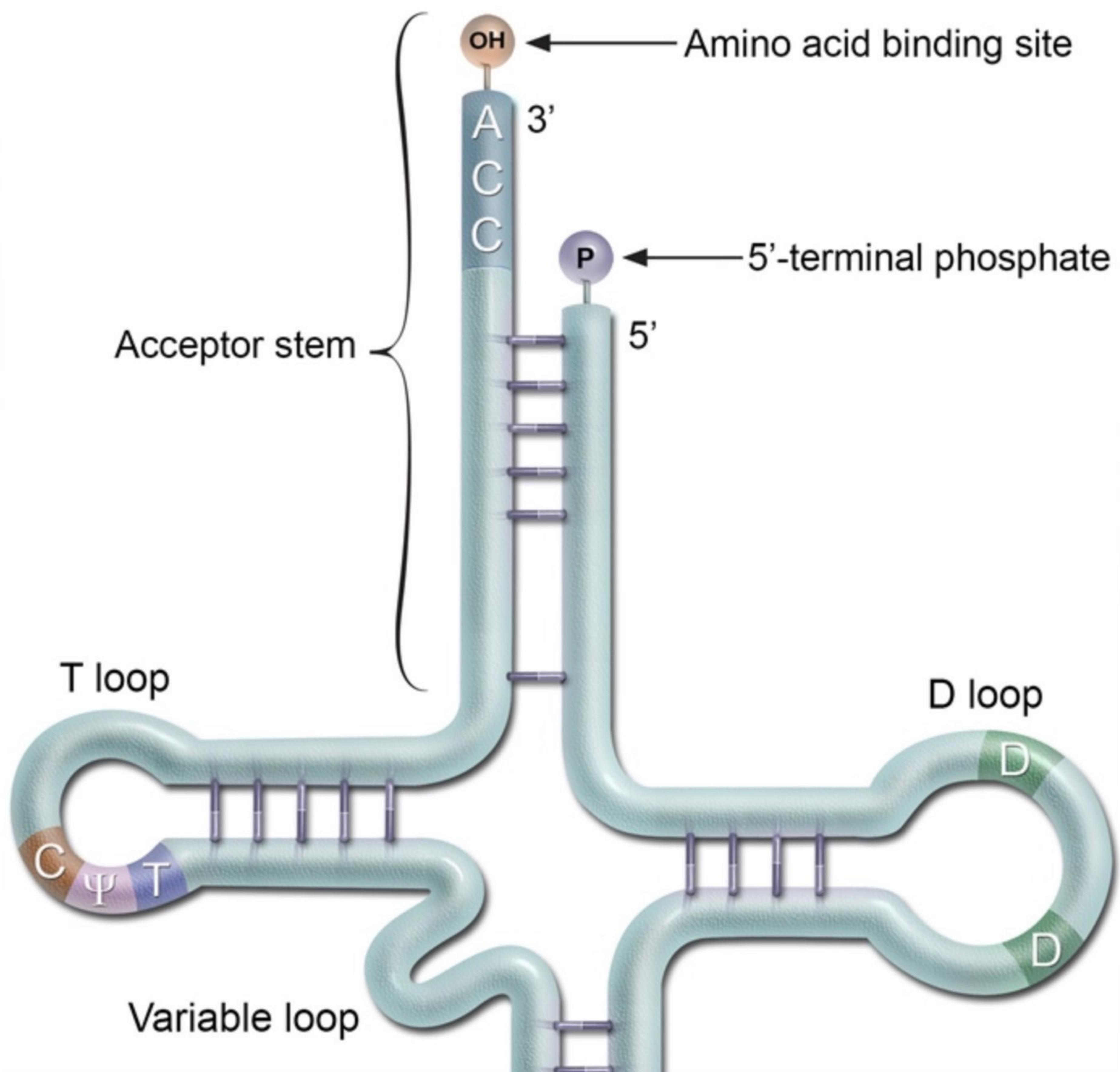
67%
Answered correctly

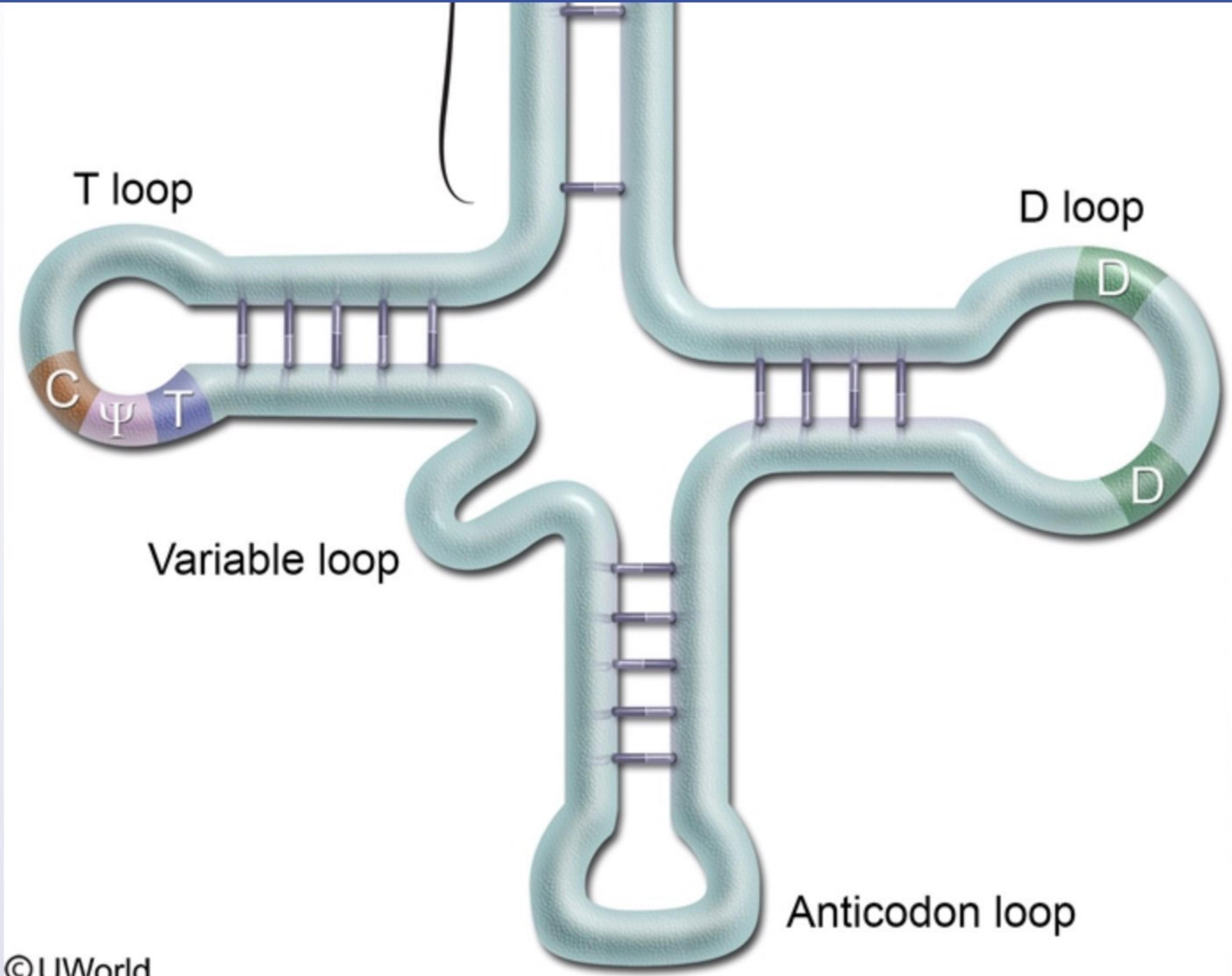
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Explanation

Secondary structure of tRNA





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The image above shows the "cloverleaf" secondary structure of **transfer RNA (tRNA)**, a small, noncoding subtype of RNA that is responsible for transporting amino acids to the site of protein synthesis and introducing them into the growing polypeptide chain at the correct locations.

The acceptor stem of tRNA is created through the base pairing of the 5'-terminal nucleotides with the 3'-terminal nucleotides. It contains the **CCA tail**, which is added to the **3'** end of tRNA as a post-transcriptional modification

The acceptor stem of tRNA is created through the base pairing of the 5'-terminal nucleotides with the 3'-terminal nucleotides. It contains the **CCA tail**, which is added to the 3' end of tRNA as a post-transcriptional modification and serves as the **amino acid binding site**. Aminoacyl tRNA synthetase is the enzyme responsible for "loading" the appropriate amino acid to the 3' terminal hydroxyl group of the CCA tail. The acceptor stem helps mediate correct tRNA recognition by the proper aminoacyl tRNA synthetase.

(Choice B) The T loop contains the TΨC sequence, which is necessary for the binding of tRNA to ribosomes. The TΨC sequence refers to the presence of the chemically modified bases ribothymidine and pseudouridine, and cytidine.

(Choice C) The variable loop contains a variable number of bases that lie between the T and anticodon loops. The variable loop is not present in all tRNAs.

(Choice D) The anticodon loop contains sequences that are complementary to the mRNA codon. During translation, the tRNA anticodon binds to the mRNA codon and assures placement of the proper amino acid in the growing polypeptide chain.

(Choice E) The D loop contains numerous dihydrouridine residues, which are modified bases often present in tRNA. The D loop (along with the acceptor stem and anticodon loop) facilitates correct tRNA recognition by the proper aminoacyl tRNA synthetase.

(Choice F) The 5' end of tRNA contains a terminal phosphate group that does not participate in amino acid or mRNA binding.

Educational objective:

The 3' CCA tail of tRNA serves as the amino acid binding site. Aminoacyl tRNA synthetase is the enzyme responsible for "loading" the appropriate amino acid to the 3' terminal hydroxyl group of the CCA tail.

References

A genetic study performed on a 10-year-old boy reveals a single base substitution mutation involving a DNA segment that encodes a cellular protein, as shown in the image below.

Normal coding strand: 5' --- GCCCAATCT ---- TATAAA ---- CAAGCTCGTCATGCAGGAG --- 3'
Patient's coding strand: 5' --- GCCCAATCT ---- TAGAAA ---- CAAGCTCGTCATGCAGGAG --- 3'

-25 bp +1 bp

This mutation is most likely to affect which of the following processes?

- A. DNA methylation (2%)
- B. Polypeptide folding following translation (3%)
- C. Posttranscriptional RNA splicing (4%)
- D. RNA elongation (2%)
- E. Transcription initiation (82%)
- F. Translation initiation (4%)

Omitted
Correct answer
E

82%
Answered correctly

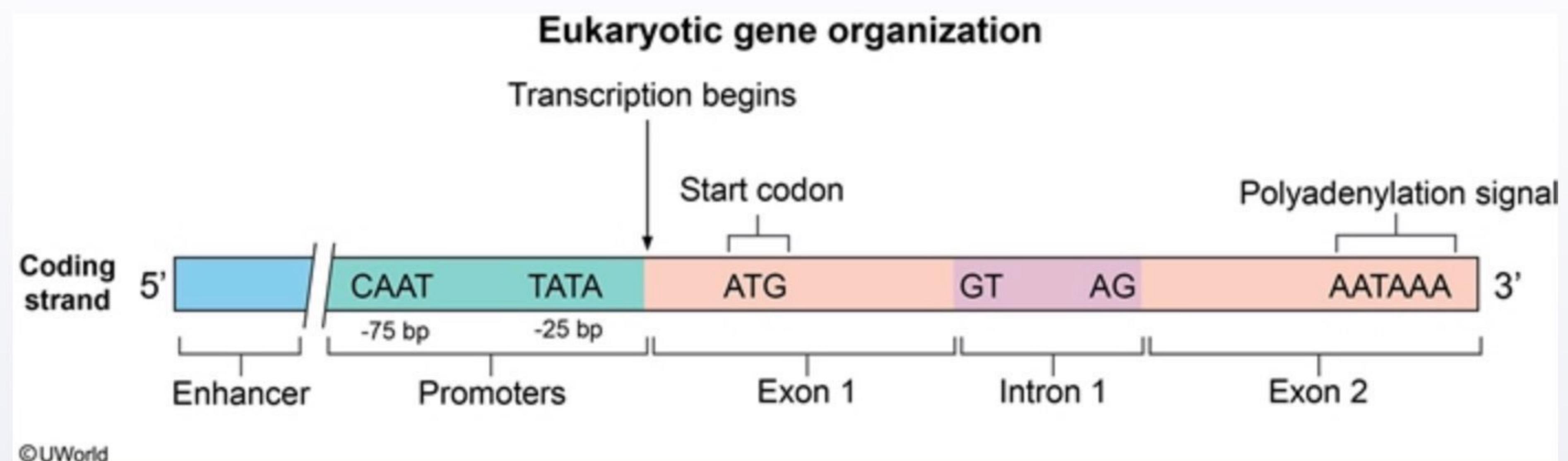
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Explanation

Eukaryotic gene organization

Transcription begins



Genetic information flows from DNA to RNA to proteins. Most eukaryotic DNA sequences consist of coding exons, noncoding introns, and 2 **promoter regions** (the CAAT box and the TATA box). The CAAT box is located 70-80 bases upstream of the beginning (5' end) of the coding region, and the **TATA box** is located **25 bases upstream** from the beginning of the coding region.

Gene transcription begins when **RNA polymerase II** attaches to one of the promoter regions in a process that requires general **transcription factors**. A DNA **enhancer region** then binds activator proteins that associate with transcription factors and RNA polymerase II at the promoter, thereby increasing gene expression. Although promoters are not directly translated into protein, promoter mutations can cause abnormal gene expression by altering the ability of RNA polymerase II and transcription factors to bind.

(Choice A) DNA methylation is part of the epigenetic code. This process is carried out by DNA methyltransferases and serves to silence the genes it affects.

(Choice B) The folding of a formed polypeptide into its secondary and tertiary structures is entirely spontaneous and is determined by the amino acid sequence in the protein's primary structure. Heat shock proteins assist in the spontaneous refolding of proteins.

(Choice C) Posttranscriptional RNA splicing is facilitated by small nuclear ribonucleoproteins (snRNPs) that

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(Choice B) The folding of a formed polypeptide into its secondary and tertiary structures is entirely spontaneous and is determined by the amino acid sequence in the protein's primary structure. Heat shock proteins assist in the spontaneous refolding of proteins.

(Choice C) Posttranscriptional RNA splicing is facilitated by small nuclear ribonucleoproteins (snRNPs) that remove introns from heterogeneous nuclear RNA (hnRNA) containing GU at the 5' splice site and AG at the 3' splice site.

(Choice D) The TATA box only participates in the initiation of transcription. The addition of nucleotides to the forming RNA molecule (RNA elongation) continues until RNA polymerase II encounters a termination signal.

(Choice F) In eukaryotes, translation initiation requires both ribosomal subunits (60S and 40S) with their associated rRNA, mRNA, initiation factors, initiator tRNA charged with methionine, and GTP. The assembled ribosome then recognizes the AUG start codon on mRNA to begin the process.

Educational objective:

The TATA box is a promoter region that binds transcription factors and RNA polymerase II during the initiation of transcription. It is located approximately 25 bases upstream from the beginning of the coding region.

References

- RNA polymerase II transcription initiation: a structural view.

In an experiment, erythrocyte precursor cells are incubated in a medium containing radiolabeled cysteine. These radiolabeled cysteine residues are attached to their appropriate tRNAs by the enzyme aminoacyl-tRNA synthetase. The bound cysteine residues are then chemically modified to form alanine. The end product of this reaction is a tRNA molecule that contains the cysteine anticodon but is mischarged with alanine. Which of the following is most likely to occur to this alanine residue during polypeptide synthesis of alpha-hemoglobin?

- A. It will be incorporated into the polypeptide chain at a site requiring alanine (5%)
- B. It will be incorporated into the polypeptide chain at a site requiring cysteine (69%)
- C. It will be randomly incorporated into the polypeptide chain, halting chain elongation (5%)
- D. It will be rapidly cleaved off tRNA by the enzyme glycosylase (13%)
- E. It will never be incorporated into the polypeptide chain and will remain attached to tRNA (6%)

Omitted

Correct answer

B

 69%
Answered correctly 03 secs
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Explanation

Amino acid activation and attachment to the 3' end of tRNA are catalyzed by **aminoacyl-tRNA synthetases** (AA-tRNA synthetases). Each amino acid/tRNA pair has a specific AA-tRNA synthetase that links them together. These enzymes are responsible for ensuring that each amino acid binds to the tRNA with the proper anticodon. AA-tRNA synthetase activation and binding sites are **highly specific** for their correct amino acids and tRNA molecules. In addition, some AA-tRNA synthetases can "proofread" their specific tRNA molecules and hydrolyze the amino acid bond when their tRNAs are incorrectly charged. The error rate for AA-tRNA

Enzymes are responsible for ensuring that each amino acid binds to the tRNA with the proper anticodon.

AA-tRNA synthetase activation and binding sites are **highly specific** for their correct amino acids and tRNA molecules. In addition, some AA-tRNA synthetases can "proofread" their specific tRNA molecules and hydrolyze the amino acid bond when their tRNAs are incorrectly charged. The error rate for AA-tRNA synthetases is therefore very low, with less than 1 error per 10^4 charges.

During protein synthesis, tRNA acts as an adaptor molecule between the codons found on mRNA and the amino acids being incorporated into the polypeptide chain. The amino acid sequence in a polypeptide chain is dictated by the binding of a tRNA anticodon to its complementary codon on the mRNA molecule being translated.

Erroneous amino acid/tRNA coupling by AA-tRNA synthetase causes the **wrong amino acid** to be **incorporated** into the growing polypeptide chain (**Choice E**).

For example, under normal circumstances, when the ribosome encounters a cysteine codon (eg, UGU) on mRNA, the complementary tRNA anticodon (eg, ACA) binds. If this tRNA is improperly charged with alanine, as described in the experiment above, alanine will be incorrectly incorporated into the growing polypeptide chain in place of cysteine (**Choice A**).

(Choice C) During polypeptide chain elongation, ribosomes move from codon to codon on mRNA in the 5' to 3' direction, sequentially adding amino acids from aminoacyl-tRNA to the peptide chain. This continues until the ribosome encounters a stop codon (ie, UAA, UAG, or UGA). Releasing factors then assist in polypeptide chain termination.

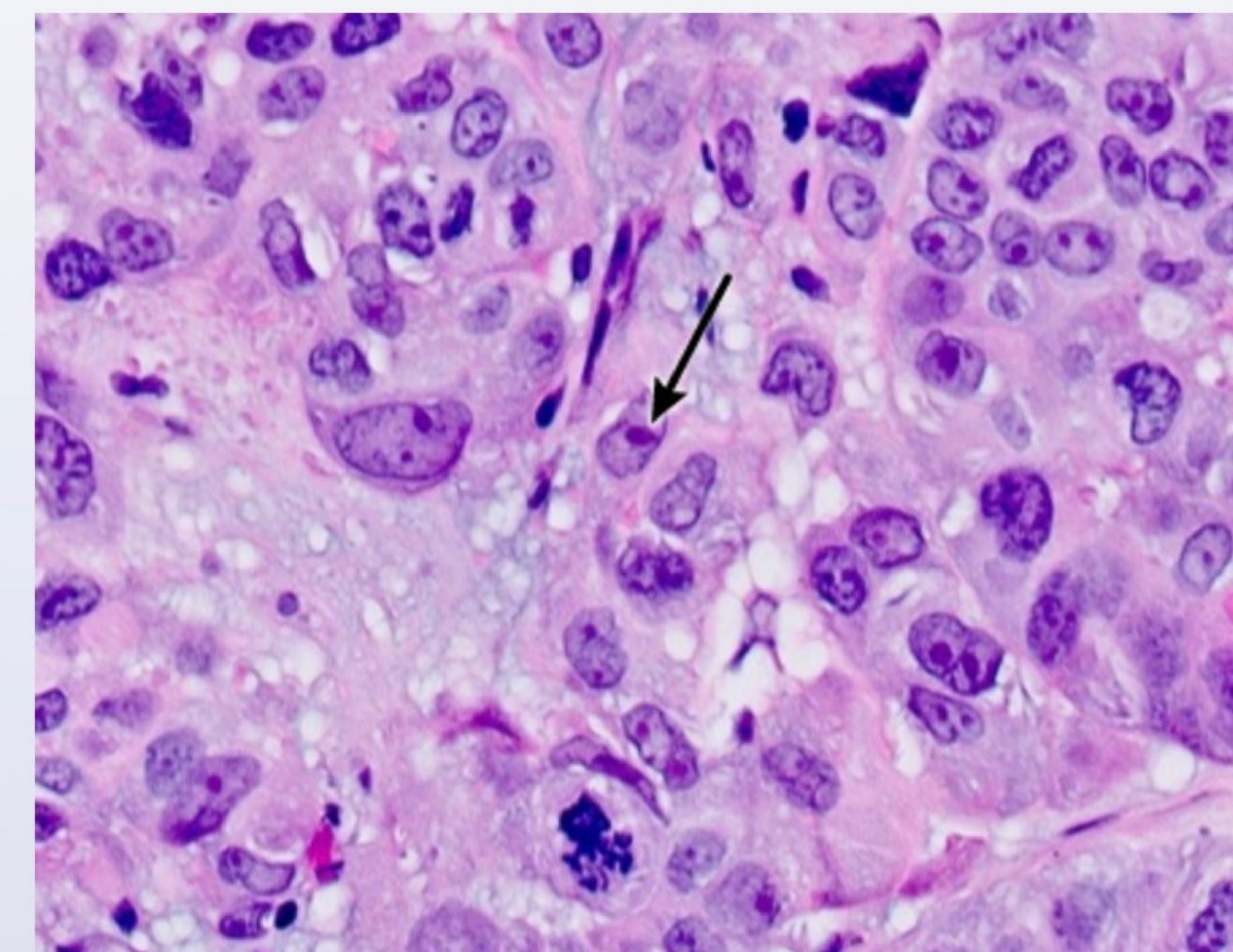
(Choice D) DNA glycosylases are enzymes involved in DNA base excision repair.

Educational objective:

The sequence of amino acids in a growing polypeptide chain is dictated by the interaction of the mRNA codon with the tRNA anticodon. tRNA that is mischarged with the incorrect amino acid (and not corrected by aminoacyl-tRNA synthetase proofreading) will incorporate the wrong amino acid into the growing polypeptide chain.



A 58-year-old man comes to the office with a persistent dry cough. He also has involuntarily lost 10 kg (22 lb) over the past 3 months. The patient drinks 2 or 3 beers daily and has a 40-pack-year smoking history. Physical examination shows dullness to percussion over the right lower lung base. CT scan of the chest reveals a right-sided pleural effusion and a mass in the lower lobe of the right lung. Microscopic examination of the mass demonstrates malignant cells with large nuclei that contain prominent, round, basophilic bodies, as shown in the image below:



Which of the following enzymes is most likely to function only within this basophilic region of the nucleus?

- A. Peptidyltransferase (10%)
- B. RNA polymerase I (45%)
- C. RNA polymerase II (27%)



Synthesis & function of eukaryotic RNA

| Synthesizing polymerase | Type of RNA produced | Function |
|-------------------------|-------------------------------|--|
| RNA polymerase I | 18S, 5.8S & 28S ribosomal RNA | Forms essential ribosomal components |
| RNA polymerase II | mRNA | Translated by ribosomes to form specific proteins |
| | Small nuclear RNA | Involved in mRNA splicing & transcription regulation |
| | MicroRNA | Causes gene silencing via translation arrest or mRNA degradation |
| RNA polymerase III | Transfer RNA | Adaptor molecule linking codons with specific amino acids |
| | 5S ribosomal RNA | Essential component of 60S ribosomal subunit |

mRNA = messenger RNA.

This patient's biopsy demonstrates malignant cells with prominent nucleoli, which appear as round, dense, basophilic (ie, dark blue to purple) intranuclear bodies on hematoxylin and eosin staining. The **nucleolus** is the primary site of **ribosomal RNA (rRNA) transcription**. Copies of the 45S pre-rRNA gene are arranged in clusters (nucleolar organizing regions) on multiple chromosomes; these regions come together in the nucleus to form the nucleolus. **RNA polymerase I** functions exclusively within the nucleolus to transcribe the 45S pre-rRNA gene into a single transcript that is subsequently processed into mature 18S, 5.8S, and 28S rRNAs.

In addition to rRNA transcription, the nucleolus is involved in the maturation and **assembly of ribosomal**

In addition to rRNA transcription, the nucleolus is involved in the maturation and **assembly of ribosomal subunits**. Ribosomal proteins, which are synthesized in the cytoplasm, are transported into the nucleolus, where they combine with rRNA to form immature 40S and 60S subunits. These subunits are then shuttled via nuclear pores to the cytoplasm, where they ultimately participate in protein synthesis.

The regulation of ribosomal synthesis occurs in part by controlling the number of active rRNA genes. Generally, as cells become more differentiated, growth slows and the cells require fewer ribosomes for protein production. In contrast, **malignant cells** with high metabolic activity usually have a large number of active rRNA genes and **prominent nucleoli**.

(Choice A) Peptidyltransferase catalyzes peptide bond formation during protein synthesis, which occurs in mature ribosomes found in the cytoplasm.

(Choice C) RNA polymerase II synthesizes messenger RNA (mRNA), small nuclear RNA (snRNA), and microRNA (miRNA) in the nucleus. It is the most highly regulated of the 3 RNA polymerases, with its function determined by multiple transcription factors and epigenetic processes.

(Choice D) Ubiquitin ligase attaches ubiquitin molecules to proteins in the cytoplasm, tagging them for degradation in the cell's proteasome complex. The ubiquitin-proteasome pathway is important for the degradation of short-lived, senescent, or abnormal (eg, denatured, misfolded) proteins.

Educational objective

The nucleolus is the site of ribosomal RNA (rRNA) transcription and ribosomal subunit assembly. RNA polymerase I functions exclusively within the nucleolus to transcribe the 45S pre-rRNA gene, which codes for most of the rRNA components (18S, 5.8S, and 28S rRNAs).

Genetics

Subject

Genetics (General Principles System)

Protein synthesis

A pharmaceutical researcher develops a new drug that affects bacterial protein synthesis. In an experiment, *Escherichia coli* is exposed to the drug and serially cultured in media containing tagged nucleotides and amino acids. It is found that the drug inhibits molecules that recognize the highlighted codon in the bacterial mRNA fragment shown in the image below.

5' --- ACG CUA CCA UUG CAA GUU AGC **UAA** AUA GCG UUC --- 3'

Which of the following molecules is the most likely target of this drug?

- A. Charged tRNA (15%)
- B. Elongation factor 2 (7%)
- C. Releasing factor 1 (56%)
- D. snRNP (5%)
- E. Transcription factor II D (3%)
- F. Uncharged tRNA (12%)

Omitted
Correct answer
C

56%
Answered correctly

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Explanation

There are 64 codons in the genetic code, the majority of which code for amino acids. However, because there are only 20 amino acids, most have more than one codon. For example, GUU, GUC, GUA, and GUG all code for the amino acid Valine.

There are 64 codons in the genetic code, the majority of which code for amino acids. However, because there are only 20 amino acids, most have more than one codon. For example, GUU, GUC, GUA, and GUG all code for valine.

In addition, there are codons that call for initiation or **termination of protein synthesis**. The universal start codon is AUG, which codes for methionine. **UAA, UAG, and UGA** are **stop codons**, which do not code for amino acids or bind tRNA. Instead, when the ribosome encounters a stop codon, **releasing factor** proteins bind to the ribosome and stimulate release of the formed polypeptide chain and dissolution of the ribosome-mRNA complex.

(Choice A) Charged tRNA delivers amino acids to the protein synthesis complex. The anticodon on a tRNA molecule recognizes the corresponding codon on mRNA, assuring proper amino acid sequencing.

(Choice B) Elongation factors facilitate tRNA binding and the translocation steps of protein synthesis.

(Choice D) Transcription produces a pre-mRNA molecule containing both introns and exons. Splicing is a post-transcriptional modification in which introns are removed from pre-mRNA via small nuclear ribonucleoproteins (snRNPs).

(Choice E) Initiation of gene transcription is governed by the binding of transcription factors to the regulatory region of the gene. Transcription factor II D binds to the TATA promoter sequence located ~25 bases upstream from the coding region of the gene.

(Choice F) During protein synthesis, uncharged tRNA (lacking an amino acid) does not interact with mRNA and ribosomes.

Educational objective:

Releasing factors recognize stop codons (eg, UAA, UAG, and UGA) and terminate protein synthesis. They facilitate release of the polypeptide chain from the ribosome and dissolution of the ribosome-mRNA complex.



A 32-year-old man is recovering from extensive burns. Fibroblasts near the site of injury actively synthesize precursor mRNA to be used as templates for protein synthesis. After transcription, extensive processing of the precursor RNA occurs to form the finalized mRNA sequence. The finalized mRNA then exits the nucleus and undergoes translation by ribosome complexes before being degraded. Which of the following steps involving the processing and handling of mRNA occurs only within the cytoplasm of cells?

- A. 5'-terminal guanosine triphosphate addition (6%)
- B. Methylation of the 5'-terminal guanine (13%)
- C. Multiple adenine nucleotide attachment to the 3'-end (11%)
- D. Interaction with snRNP (14%)
- E. Removal of intervening sequences (8%)
- F. Interaction with P bodies (44%)

Omitted
Correct answer
F

44%
Answered correctly

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Explanation

After transcription, the preliminary, unprocessed mRNA is known as precursor mRNA, or heterogeneous nuclear RNA (hnRNA). Eukaryotic pre-mRNA undergoes significant posttranscriptional processing before leaving the nucleus, including 5'-capping, poly A tail addition, and intron splicing.

Once mRNA is finalized, it leaves the nucleus bound to specific packaging proteins. Upon entering the



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translation repression and mRNA decay, and contain numerous proteins including RNA exonucleases, mRNA decapping enzymes, and constituents involved in mRNA quality control and microRNA-induced mRNA silencing. P bodies also seem to function as a form of mRNA storage, as certain mRNAs are incorporated into P bodies only to be later released and utilized for protein translation.

(Choices A and B) The 5' end of all mRNA is capped with a 7-methylguanosine residue by a unique 5' to 5' linkage, which occurs in two stages. The first step is the addition of guanine triphosphate to the 5' end of mRNA in a reaction catalyzed by guanylyltransferase. Methylation of the guanosine cap is then catalyzed by guanine-7-methyltransferase. Capping of the precursor RNA occurs in the nucleus as the RNA is being transcribed. This methylated cap protects mRNA from degradation by cellular exonucleases, and allows it to exit the nucleus.

(Choice C) mRNA is polyadenylated at the 3' end by the polyadenylate polymerase complex, which recognizes a specific sequence (AAUAAA), cleaves the pre-mRNA molecule a few residues downstream from this sequence, and then adds a stretch of 20 - 250 adenine residues called the poly A tail. The addition of the poly A tail occurs before the mRNA exits the nucleus. In the cytosol, the poly A tail is gradually shortened, eventually leading to mRNA degradation.

(Choices D and E) Since pre-mRNA contains both introns and exons, and only exons code for proteins, introns must be excised before translation through a process known as splicing. Splicing of pre-mRNA occurs within the nucleus and is facilitated by the interaction of pre-mRNA with small ribonucleoprotein particles called snRNPs (or "snurps" for short).

Educational objective:

When mRNA is first transcribed from DNA, it is in an unprocessed form called pre-mRNA or heterogeneous nuclear mRNA (hnRNA). Several processing steps are required before finalized mRNA molecules can leave the nucleus, including 5'-capping, poly A tail addition, and intron splicing. Cytoplasmic P bodies play an important role in mRNA translation regulation and mRNA degradation.



A series of experiments is being conducted to determine the structure and function of different types of bacterial RNA. Cultures of *Staphylococcus aureus* are exposed to chemicals that lyse the bacterial cells, and the RNA molecules are then extracted. A specific RNA consisting of 90 nucleotides is purified for further analysis. It is found to contain high amounts of chemically modified bases such as dihydrouridine, pseudouridine, and ribothymidine, and its secondary structure arises from base pairing within the chain. Which of the following is the most likely composition of the 3'-end of this molecule?

- A. AUG (5%)
- B. CCA (41%)
- C. Methylguanosine triphosphate (5%)
- D. Poly-A (30%)
- E. TATA (3%)
- F. UAG (12%)

Omitted

Correct answer

B



41%

Answered correctly



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Time Spent

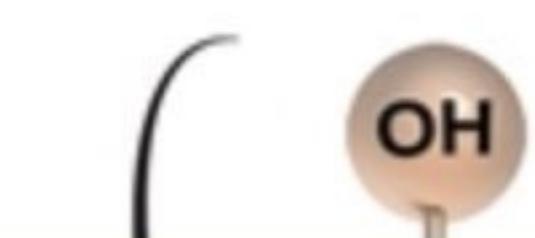


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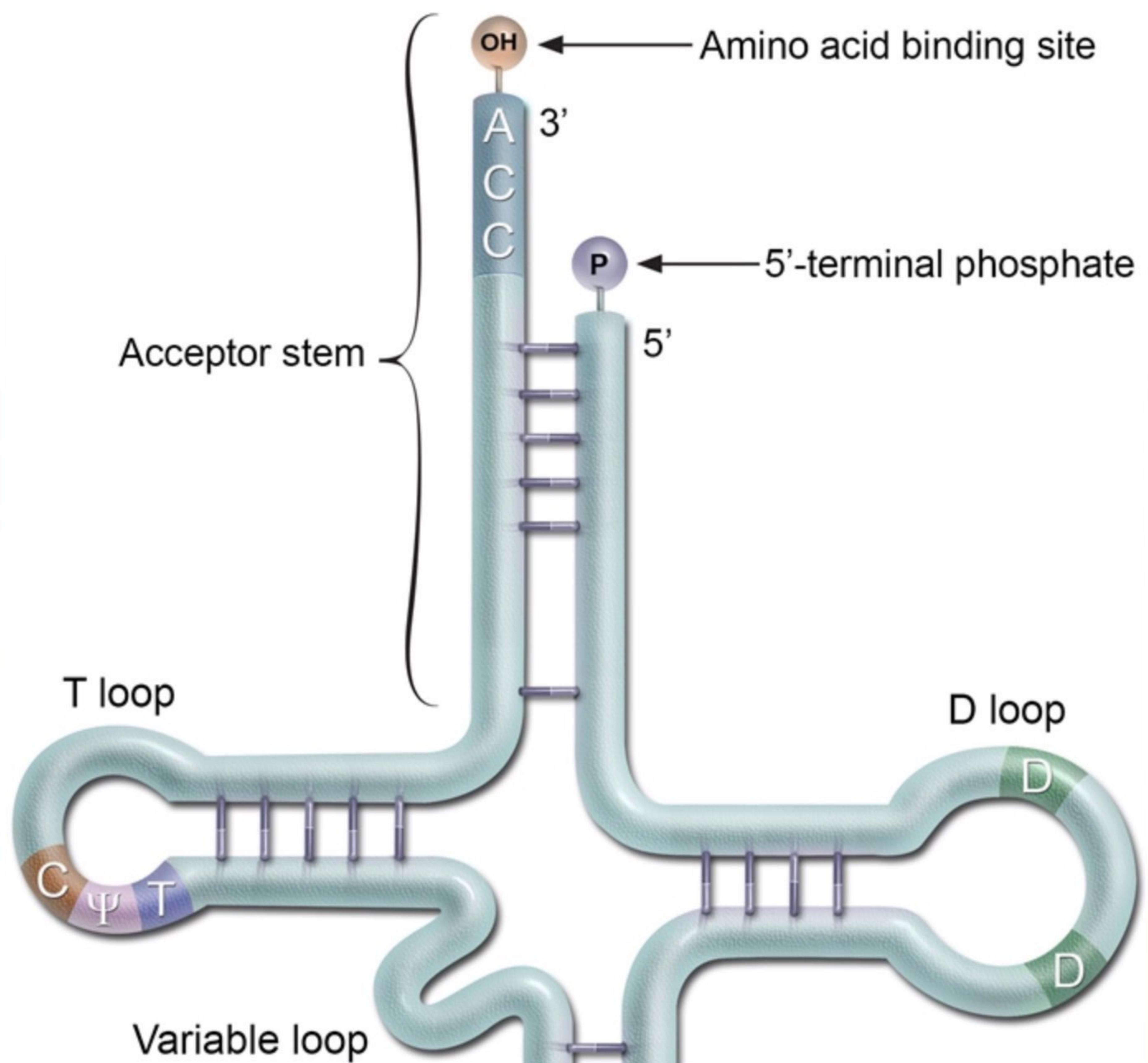
Explanation

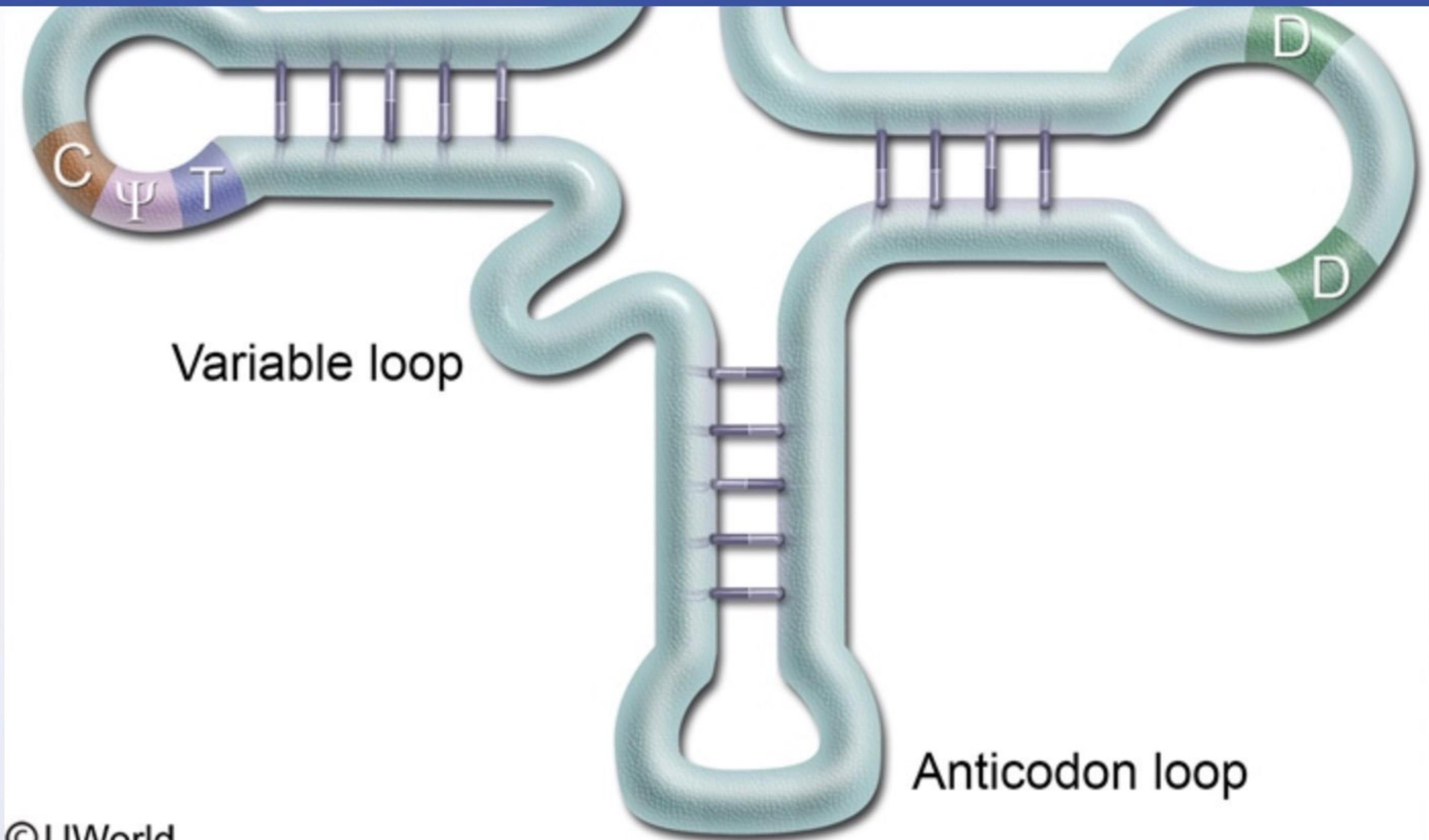
Secondary structure of tRNA



Amino acid binding site

Secondary structure of tRNA





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Transfer RNA (tRNA) is a form of non-coding RNA composed of 74-93 nucleotides. Specific tRNAs transfer certain amino acid residues to the growing polypeptide during translation. tRNA functions by recognizing the 3 base codon on the mRNA being translated through its anticodon region, which contains complementary bases. The secondary structure of tRNA resembles a cloverleaf and contains the following regions:

- The **acceptor stem** is created through the base pairing of the 5'-terminal nucleotides with the 3'-terminal nucleotides. The CCA tail hangs off the 3' end, with the amino acid bound to the 3' terminal hydroxyl group. tRNA is "loaded" with the appropriate amino acid by aminoacyl tRNA synthetase. The acceptor stem helps mediate correct tRNA recognition by the proper aminoacyl tRNA synthetase.
- A **3' CCA tail** is added to the 3' end of tRNA as a posttranscriptional modification in eukaryotes and most prokaryotes. Several enzymes utilize this tail to help recognize tRNA molecules.

- A 3' CCA tail is added to the 3' end of tRNA as a posttranscriptional modification in eukaryotes and most prokaryotes. Several enzymes utilize this tail to help recognize tRNA molecules.
- The **D loop** contains numerous dihydrouridine residues, which are modified bases often present in tRNA. The D loop (along with the acceptor stem and anticodon loop) facilitates correct tRNA recognition by the proper aminoacyl tRNA synthetase.
- The **anticodon loop** contains sequences that are complementary to the mRNA codon. During translation, the ribosome complex selects the proper tRNA based solely on its anticodon sequence.
- The **T loop** contains the TΨC sequence that is necessary for binding of tRNA to ribosomes. The TΨC sequence refers to the presence of ribothymidine, pseudouridine, and cytidine residues.

(Choices A and F) AUG and UAG are mRNA start and stop codons that initiate and terminate translation, respectively.

(Choices C and D) After transcription, eukaryotic pre-mRNA undergoes posttranscriptional modification, which includes the addition of a poly-A tail at the 3' end and methylguanosine cap at the 5' end, and the removal of introns.

(Choice E) A TATA box is an upstream promoter region associated with some genes in eukaryotic organisms. TATA binding protein binds to this promoter during transcription, unwinding the DNA and initiating separation of the strands.

Educational objective:

Transfer RNA (tRNA) is a small, noncoding form of RNA that contains chemically modified bases (eg, dihydrouridine, ribothymidine, pseudouridine). tRNA has a CCA sequence at its 3'-end that is used as a recognition sequence by proteins. The 3' terminal hydroxyl group of the CCA tail serves as the amino acid binding site.

Gene expression and regulation

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Item 1 of 8
Question Id: 2041

Mark

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A 43-year-old man is evaluated for progressive neuropsychiatric symptoms. A year ago, he began feeling depressed and having hallucinations. Five months later, he developed intermittent paresthesias and progressively worsening choreiform movements, myoclonus, and ataxia. These symptoms have not improved despite multiple hospitalizations; an extensive workup has been unrevealing. The patient is a slaughterhouse worker with extensive exposure to bovine offal. As part of the evaluation for prion disease, a tissue sample lysate is processed via gel electrophoresis and transferred to filter paper. Antibodies to a specific prion protein are added to the filter. Next, a marked protein that combines with the antibody-protein complex is used to determine whether the test is positive. Which of the following best describes this test?

- A. Microarray
- B. Northern blot
- C. Southern blot
- D. Southwestern blot
- E. Western blot

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Item 2 of 8
Question Id: 2025

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A 12-year-old boy is evaluated in the clinic due to excessive bleeding following a tooth extraction. The patient also develops large bruises after only minor injury but has had no major bleeding episodes in the past. His maternal uncle died from an intracranial hemorrhage. Laboratory testing reveals decreased coagulation factor VIII activity levels. A referral is made to a clinical geneticist, who suspects that the patient has a deletion mutation in the enhancer sequence of the factor VIII gene. This mutation has resulted in decreased transcription of factor VIII by RNA polymerase II. Which of the following is the most accurate statement regarding the abnormal genetic sequence in this patient?

- A. It can be located upstream, downstream, or within introns of the gene
- B. It can function within only a short distance of the gene
- C. It directly binds RNA polymerase and general transcription factors
- D. It does not require protein binding to affect transcription
- E. It is required to initiate transcription

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Item 3 of 8
Question Id: 2015

Mark

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Full Screen Tutorial Lab Values Notes Calculator Reverse Color Text Zoom Settings

A pharmaceutical researcher performs preclinical testing on a novel chemotherapeutic drug. When rat embryos are exposed to this drug during an early stage of organogenesis, they develop severe skeletal malformations. Further genetic analysis reveals that the drug causes mutations in numerous homeobox genes containing highly conserved 180 base pair DNA sequences. The genes affected by this drug most likely code for which of the following proteins?

- A. Cell surface receptors
- B. Cytoplasmic enzymes
- C. DNA replication enzymes
- D. Structural proteins
- E. Transcription regulators
- F. Transport proteins

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Item 4 of 8
Question Id: 11913

Mark

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Full Screen Tutorial Lab Values Notes Calculator Reverse Color Text Zoom Settings

A researcher is studying the Fas receptor (FasR), a protein widely expressed on cell surfaces. The signaling cascade of programmed cell death is initiated when FasR binds to its ligand (FasL), which is expressed on cytotoxic T cells. In an experiment, cancer cells that escaped elimination by the immune system were found to contain soluble Fas proteins that did not promote apoptosis. The soluble Fas proteins were shorter and lacked the transmembrane domain. DNA analysis of these cells revealed no *FAS* gene mutations. Which of the following is the most likely explanation for the formation of altered Fas proteins in these cancer cells?

- A. Alternative splicing
- B. Defective polyadenylation
- C. DNA methylation
- D. Polycistronic mRNA
- E. Protein ubiquitination

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Item 5 of 8
Question Id: 22214

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A 1-day-old boy is evaluated in the neonatal intensive care unit due to severe hypotonia, poor feeding, and respiratory distress. The patient was born to a 30-year-old woman via vaginal delivery; the pregnancy was complicated by polyhydramnios. The neonate's mother has a history of recurrent muscle cramps, mostly in her hands; her face is long and narrow and lacks expression. She is otherwise healthy. The patient's length, weight, and head circumference are at the 30th percentile. Examination shows profound hypotonia, truncal and appendicular weakness, and marked hyporeflexia. Flexion deformities and clubfoot are present bilaterally. Assuming that the patient and his mother have the same inheritable condition, which of the following mechanisms best explains their different phenotypic presentations?

- A. Genetic anticipation
- B. Genetic heterogeneity
- C. Germline mosaicism
- D. Maternal imprinting
- E. Single nucleotide polymorphism

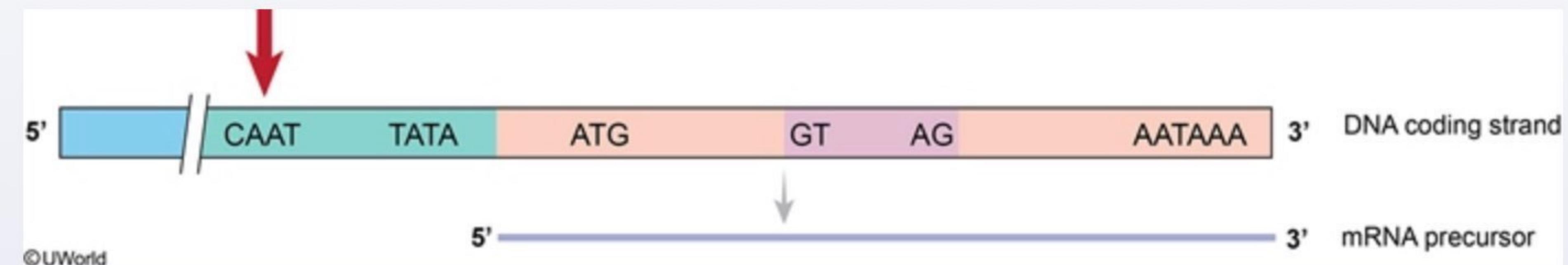
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Item 6 of 8 Question Id: 12263

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A 6-year-old girl with chronic anemia requiring repeated blood transfusions is undergoing genetic testing. The patient's mother and older sibling have a history of mild anemia. Her peripheral blood smear shows hypochromic, microcytic red blood cells, and hemoglobin electrophoresis reveals a predominance of hemoglobins F and A2. Sequencing of the β -globin gene is performed using the patient's erythroblast DNA. A schematic representation of the gene and its transcribed RNA is shown in the image below.



The base sequence indicated by the bold red arrow is responsible for which of the following functions?

- A. Enhancement of transcription
- B. Initiation of transcription
- C. Initiation of translation
- D. Repression of transcription
- E. Termination of transcription

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Item 7 of 8 Question Id: 8276

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A researcher is studying the expression pattern of a particular gene. Messenger RNA is isolated from several tissues, subjected to electrophoresis, blotted, and probed with radiolabeled DNA containing sequences from exon 4 from that gene. An x-ray film is then placed over the blotting membrane, with the results of the autoradiogram shown below:

Which of the following best explains the autoradiogram findings in the different tissues?

- A. Alternate RNA splicing
- B. DNA rearrangement
- C. DNA mutation
- D. Enhancer effect
- E. Transcription factor effect

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