

Instructions

This worksheet explores the fundamental biological process of protein synthesis. Read each question carefully and answer to the best of your ability. You will need to use the provided genetic code chart for Section 3.

Section 1: The Central Dogma - Fill in the Blanks

Complete the following paragraph using the words from the word bank below. Each word should be used only once.

The flow of genetic information in a cell is often described by the central dogma of molecular biology. The process begins in the **1.** _____ of a eukaryotic cell, where a segment of DNA is used as a template to create a molecule of messenger RNA (mRNA). This process is called **2.** _____ and is catalyzed by the enzyme **3.** _____. Before this mRNA molecule can leave the nucleus, it undergoes processing where non-coding regions called **4.** _____ are removed, while the coding regions, known as **5.** _____, are spliced together. The mature mRNA then travels to the cytoplasm and attaches to a **6.** _____. Here, the process of **7.** _____ occurs. The genetic code on the mRNA is read in three-base units called **8.** _____. Molecules of transfer RNA (tRNA) have a corresponding three-base unit called an **9.** _____ and carry a specific **10.** _____. As the ribosome moves along the mRNA, these building blocks are linked together to form a **11.** _____ chain, which will then fold into a functional protein.

Word Bank:

Ribosome
Amino Acid
Transcription
Exons
Anticodon
Polypeptide
RNA Polymerase
Translation
Nucleus
Codons
Introns

Section 2: Comparing Processes

Answer the following questions with detailed explanations.

1. Describe two key differences between transcription and translation in a eukaryotic cell. Consider their location, the molecules involved, and the final product.
2. Explain the functional significance of removing introns from a pre-mRNA transcript. Why is this step crucial for creating a functional protein?

Section 3: From Gene to Protein

Use the DNA sequence and the genetic code chart below to answer the following questions.

Original DNA Template Strand: 3' -TAC GCT CCA TGG AAT ATC-5'

- Write the sequence of the complementary DNA **coding** strand.
- Transcribe the **template** strand into a sequence of mRNA.
- Translate the mRNA sequence from question 3b into a polypeptide chain of amino acids. Use the chart below. (Remember to look for start and stop signals).
- Mutation Analysis 1:** A point mutation occurs in the original DNA **template** strand, changing the 11th base from G to C.
 - Write the new mutated DNA template strand.
 - Write the new mRNA sequence that would be transcribed from this mutated strand.
 - What is the new amino acid sequence?
 - What specific type of point mutation is this (silent, missense, or nonsense)? Explain your reasoning.
- Mutation Analysis 2:** A different mutation occurs in the original DNA **template** strand, causing the 4th base (G) to be deleted.
 - Write the resulting mRNA sequence. (Remember the reading frame will shift).
 - What is this type of mutation called? Explain why it is often more detrimental than a point mutation.

The Genetic Code (mRNA Codons)

	Second Base				
	U	C	A	G	
First Base	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Trp	G
	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met (START)	ACG Thr	AAG Lys	AGG Arg	G
	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Answer Key

Section 1: The Central Dogma - Fill in the Blanks

- Nucleus
- Transcription
- RNA Polymerase

4. Introns
5. Exons
6. Ribosome
7. Translation
8. Codons
9. Anticodon
10. Amino Acid
11. Polypeptide

Section 2: Comparing Processes

1. Possible answers include (any two):

- **Location:** Transcription occurs in the nucleus, whereas translation occurs in the cytoplasm on a ribosome.
 - **Template:** Transcription uses a DNA strand as a template, whereas translation uses an mRNA strand as a template.
 - **Enzyme/Machinery:** Transcription is catalyzed by RNA polymerase, while translation is carried out by ribosomes and tRNA.
 - **Product:** The product of transcription is an RNA molecule (pre-mRNA), while the product of translation is a polypeptide chain (protein).
2. Introns are non-coding sequences that interrupt the genetic code for a protein. Removing them (splicing) is crucial because if they were left in the mature mRNA, the ribosome would try to translate them. This would introduce incorrect amino acids and shift the entire reading frame for the rest of the sequence, resulting in a completely different and almost certainly non-functional protein. Splicing ensures that only the correct, protein-coding exons are joined together to form a coherent genetic message.

Section 3: From Gene to Protein

1. **Complementary DNA coding strand:** 5' -ATG CGA GGT ACC TTA TAG-3'
2. **Transcribed mRNA:** 5' -AUG CGA GGU ACC UUA UAG-3'
3. **Polypeptide chain:** Met - Arg - Gly - Thr - Leu - STOP. (The chain terminates at the UAG stop codon).
4. **Mutation Analysis 1:**
 - a. **New mutated DNA template strand:** 3' -TAC GCT CCA TCG AAT ATC-5'
 - b. **New mRNA sequence:** 5' -AUG CGA GGU AGC UUA UAG-3'
 - c. **New amino acid sequence:** Met - Arg - Gly - Ser - Leu - STOP.
 - d. **Type of mutation:** This is a **missense** mutation. The change in a single nucleotide (G to C in the DNA, resulting in ACC to AGC in the mRNA) led to the incorporation of a different amino acid (Threonine to Serine) in the polypeptide chain.
5. **Mutation Analysis 2:**
 - a. **Resulting mRNA sequence:** 5' -AUG CGA GUA CCU UAU AG...-3'
 - b. **Type of mutation:** This is a **frameshift** mutation (specifically, a deletion). It is often more detrimental because deleting a single base shifts the entire reading frame for all subsequent codons. This scrambles the entire amino acid sequence from the point of the mutation onward, usually leading to a premature stop codon or a completely non-functional protein. It has a much more widespread effect than a single amino acid substitution.