



## HANDS-ON ACTIVITY

# Modeling Protein Synthesis and Mutations

Protein synthesis consists of two main stages: transcription and translation. In transcription, RNA polymerase makes a complementary copy of the cell's DNA. In eukaryotes, this step takes place in the nucleus of the cell. The mRNA strand that is made is complementary, but not identical, to DNA because RNA contains the nitrogenous base uracil instead of thymine.

In eukaryotic cells, mRNA leaves the nucleus and enters the cytoplasm, where translation occurs. Ribosomes facilitate the pairing of complementary tRNA molecules with the mRNA strand. Each tRNA carries an amino acid, the subunit of proteins. The ribosome moves along the mRNA strand, binding together the individual amino acids, and a polypeptide is produced.

One or more polypeptides make up a protein. Polypeptides may undergo further processing and packaging in the endoplasmic reticulum and Golgi apparatus after translation. Once they have taken on their final structures, proteins are transported to various locations in the cell, or delivered to the cell membrane for excretion. Each protein has a specific function that is closely related to its structure. If the protein's structure is incorrect, it may not function correctly.

In this activity, you will model the steps of protein synthesis. You will model transcription and translation using pencil and paper, and then construct a protein out of chenille sticks and beads. Finally, you will analyze the effects of a mutation on the structure of your protein.

**MATERIALS**

- beads (blue, green, purple, yellow)
- chenille sticks
- pencils, colored (blue, green, purple, yellow)

**PROCEDURE**

1. Transcribe the DNA sequence by writing the corresponding mRNA codons. Remember that in RNA, U pairs with A.

DNA sequence:

TAC AAA GAA TAA TGC ATA AGA TTT

CAA ACC TCA TCG GTA CTC GTT ACT

mRNA sequence:

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2. Use the codon chart on the next page to translate your mRNA sequence.

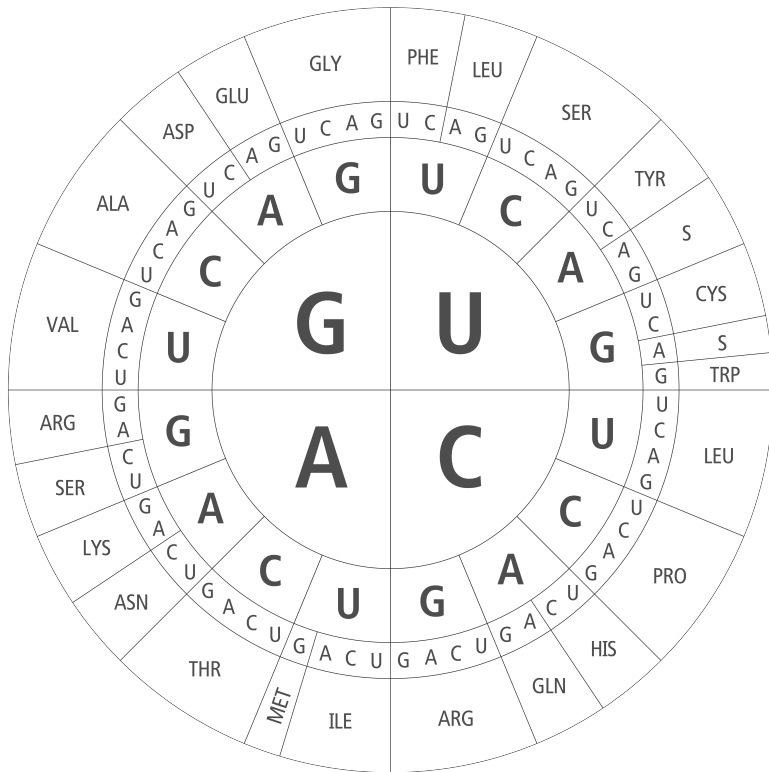
Amino acid sequence:

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Name: \_\_\_\_\_

Date: \_\_\_\_\_



ALA = Alanine	(yellow)
ARG = Arginine	(green)
ASN = Asparagine	(blue)
ASP = Aspartic acid	(purple)
CYS = Cysteine	(no color)
GLN = Glutamine	(blue)
GLU = Glutamic acid	(purple)
GLY = Glycine	(yellow)
HIS = Histidine	(blue)
ILE = Isoleucine	(yellow)
LEU = Leucine	(yellow)
LYS = Lysine	(green)
MET = Methionine	(blue)
PHE = Phenylalanine	(yellow)
PRO = Proline	(yellow)
S = Stop	(no color)
SER = Serine	(blue)
THR = Threonine	(blue)
TRP = Tryptophan	(yellow)
TYR = Tyrosine	(blue)
VAL = Valine	(yellow)

- Use colored pencils to color in the amino acids in the chart according to the colors indicated next to each amino acid's name.
- Build a model of a polypeptide by placing beads of the correct colors on a chenille stick. Use the same color bead as corresponds to the codon chart. When you reach the stop codon, do not place any more beads on the chenille stick.
- Proteins fold into specific shapes that match their function. Use the following folding instructions to fold your polypeptide into a protein:
  - Twist one-half of your protein model around a pencil to make a spiral. This spiral region is called an alpha helix.
  - Bend the other half of your protein molecule into a zigzag shape by making a bend in the opposite direction at each bead. This zigzag region is called a beta-pleated sheet.
  - The alpha helix and beta-pleated sheet represent the secondary structure of a protein.
- Make a drawing in your Evidence Notebook to show the secondary structure of your protein model. Label the alpha helix region and the beta-pleated sheet region on your drawing.
- Twist your protein into a 3D shape according to these protein-folding rules:

Name: \_\_\_\_\_

Date: \_\_\_\_\_

## PROTEIN-FOLDING RULES

AMINO ACID BEAD COLOR	PROPERTIES AND GUIDELINES
Blue	These are hydrophilic (water loving) amino acids. They should be clustered on the outside of the protein.
Green	These are positively-charged amino acids that are attracted to negatively-charged amino acids. Move the green amino acids to touch the purple amino acids.
Purple	These are negatively-charged amino acids that are attracted to positively-charged amino acids. Move the purple amino acids to touch the green amino acids.
Yellow	These are fatty hydrophobic (water-fearing) amino acids. They should be clustered on the inside of the protein.

8. The resulting twisted structure is called the tertiary structure of a protein. Make a drawing in your Evidence Notebook to show the tertiary structure of your protein model.
9. The quaternary structure of a protein is formed when one protein joins another. Join your protein with a partner's, and make a drawing in your Evidence Notebook to show the quaternary structure of your protein model.

## ANALYZE

1. Determine a point mutation that would change the amino acid sequence of the protein. List the new mRNA codon and amino acid resulting from the point mutation here:

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Replace the bead that would change in your protein model, and try re-folding your protein.

2. Did this mutation change the structure of the protein? If so, how?

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3. How might this change in structure affect the protein's function?

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Name: \_\_\_\_\_

Date: \_\_\_\_\_

4. If a new nucleotide were inserted into the first codon of the DNA sequence, how would this change the structure of the resulting protein? Use evidence and examples to explain your answer.

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5. How well did this process model protein synthesis? How could you improve this model to obtain more accurate results?

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