AR Protein Visualizer

Name: _____　　**Period:** _____　　**Date:** _____

> Open **peebedu.com** and navigate to **AR Protein Visualizer**. Click **Launch Interactive** to open the app. Read the introduction popup, which describes the controls: touch and drag to rotate, pinch to zoom, and two fingers to pan. Click **Start Exploring** to begin. Use the category filter buttons and protein dropdown to select different proteins for viewing.

Part 1 — Model Evaluation (MAPP Framework)

Scientific models are simplified representations of complex biological phenomena. Use the MAPP framework below to evaluate the AR Protein Visualizer as a scientific model.

M — Mode

What type of model is the AR Protein Visualizer? Describe how this computational simulation represents protein structures. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about proteins.

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A — Accuracy

(a) Identify two things this simulation represents **accurately** about protein structure. For each, name the specific simulation feature and explain what structural property of proteins it demonstrates.

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(b) Identify two things this simulation **oversimplifies or leaves out** about protein structure and function. Consider what you cannot observe in the simulation that would be important for understanding how proteins fold and carry out their biological roles.

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P — Purpose

What is the learning goal of this simulation? Explain how the AR Protein Visualizer is designed to help you understand how the four levels of protein structure (primary, secondary, tertiary, and quaternary) determine protein function. In your answer, connect at least one specific protein model from the simulation to a biological process that depends on its three-dimensional shape.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries might change or improve a simulation like the AR Protein Visualizer. Explain why scientific models, including computational protein visualizations, are revised as new evidence becomes available.

Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for protein structure?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the simulation help you connect the amino acid sequence of a protein to its three-dimensional structure and biological function?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Protein Structure Determines Function

Simulation Task: In the AR Protein Visualizer, select the Protein Synthesis category. Load the Protein Factory (Ribosome Complex) and rotate the 3D model to observe its overall shape. Click Protein Information to read about its structure. Then switch to the Metabolism category and load Oxygen Carrier (Hemoglobin). Compare the shapes and structural features of both proteins.

(A) (1 pt) **Describe** how the four levels of protein structure (primary, secondary, tertiary, and quaternary) contribute to the final three-dimensional shape of a protein.

(B) (1 pt) **Explain** how the quaternary structure of hemoglobin, which consists of four polypeptide subunits working together, is essential for its biological function of transporting oxygen in the blood.

(C) (1 pt) **Predict** how a mutation that changes a hydrophobic amino acid in the interior of a hemoglobin subunit to a hydrophilic amino acid would affect the protein's tertiary structure and its ability to carry oxygen.

(D) (1 pt) **Justify** your prediction by explaining how R-group interactions that stabilize tertiary structure would be disrupted by this substitution and why the resulting change in three-dimensional shape would alter the protein's function.

EK 1.7.A.4, 1.7.A.5, 1.7.A.6

Analyze Model / Visual Representation

Question 2 — From Gene to Functional Protein

Simulation Task: In the AR Protein Visualizer, select the Protein Synthesis category and load the Protein Factory (Ribosome Complex). Click Protein Information and read about its function. Then load the Gene Switch (Transcription Factor) from the same category. Rotate both models and compare their structures.

(A) (1 pt) **Describe** the role of ribosomes in translating mRNA into a polypeptide chain.

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(B) (1 pt) **Explain** how the linear sequence of codons in an mRNA molecule is converted into the specific three-dimensional structure of a functional protein, including the role of secondary and tertiary folding after translation.
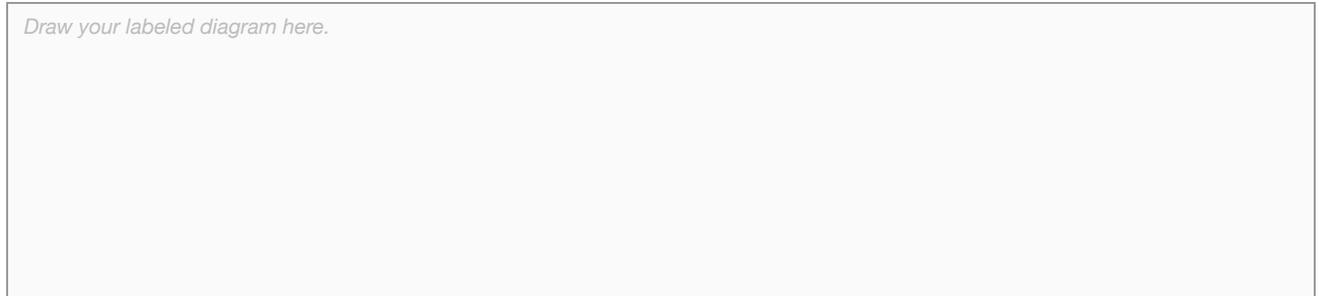
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(C) (1 pt) **Represent** the path from an mRNA molecule to a folded, functional protein.

Draw your labeled diagram here.

(D) (1 pt) **Explain** how a point mutation in the DNA sequence encoding hemoglobin could produce a polypeptide with an altered amino acid sequence that changes the protein's quaternary structure, leading to a phenotype (such as sickle cell trait) that is subject to natural selection in populations where malaria is prevalent.

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EK 6.4.A.1, 1.7.A.4, 1.7.A.5, 1.7.A.6