PEEBEDU

Protein Builder

Unit 1: Chemistry of Life

Name: ______________________ **Period:** ________ **Date:** ______________

> Open **peebedu.com** and navigate to **Protein Builder**. Click the **Start Building!** button to begin. Read the introduction popup, which describes four levels of protein structure: Primary, Secondary, Tertiary, and Quaternary.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

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

A — Accuracy

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

(b) Identify two things this simulation **oversimplifies or leaves out** about protein structure. Consider what you cannot observe in the simulation that would be important for a complete molecular-level understanding of how proteins fold and function.

P — Purpose

What is the learning goal of this simulation? Explain how the Protein Builder is designed to help you understand how the sequence and chemical properties of amino acid R-groups determine the four levels of protein structure. In your answer, connect at least one specific simulation feature to a biological reason why that structural level matters for protein function.

P — Permanency

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

Small-Group Discussion

With your group, discuss the following:

- How does building the amino acid chain in a specific order help you understand why primary structure matters?
- What are the limitations of using colored spheres to represent R-group interactions?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the progressive unlocking of structure levels reinforce the relationship between primary, secondary, tertiary, and quaternary structure?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Tertiary Structure and R-Group Interactions

> *Simulation Task: Build a chain of at least 12 amino acids that includes two cysteines (C), one positively charged amino acid (R, H, or K), one negatively charged amino acid (E or D), and at least three nonpolar amino acids. Apply the Alpha Helix secondary structure. Then switch to Tertiary Structure and use Drag mode to move R-group spheres until the folding score reaches at least 80%.*

(A) (1 pt) **Describe** how the chemical properties of amino acid R-groups contribute to the three-dimensional shape of a protein's tertiary structure.

(B) (1 pt) **Explain** how hydrogen bonds, hydrophobic interactions, ionic interactions, and disulfide bridges each stabilize the folded shape of a polypeptide chain.

(C) (1 pt) **Predict** what would happen to the three-dimensional shape and function of a protein if a mutation replaced a cysteine involved in a disulfide bridge with a nonpolar amino acid.

(D) (1 pt) **Justify** your prediction using the relationship between R-group interactions and the stability of a protein's tertiary structure.

EK 1.7.A.5

Analyze Model / Visual Representation

Question 2 — Primary Structure Determines Protein Shape

> *Simulation Task: Reset the simulation and build two different chains of 10 amino acids each. For the first chain, use mostly nonpolar amino acids. For the second chain, use a mix of polar, charged, and nonpolar amino acids. Apply the Beta Sheet secondary structure to each chain, then switch to Tertiary Structure and click Auto-Fold Protein for each chain. Compare the folding scores and the types of interactions that form.*

(A) (1 pt) **Describe** how the specific sequence of amino acids in a polypeptide determines both the primary structure and the overall shape of the protein.

(B) (1 pt) **Explain** the relationship between the types of amino acids in a sequence and the variety of R-group interactions that can form during folding.

(C) (1 pt) **Represent** the tertiary structure of a protein.

Draw your diagram here.

(D) (1 pt) **Explain** how a point mutation that changes a single amino acid in a protein's primary structure could alter the protein's shape and ultimately affect natural selection in a population.

EK 1.7.A.3, EK 6.7.A.1, EK 7.2.A.3