PEEBEDU

Protein Modification Visualizer

Unit 6: Gene Expression and Regulation

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

> Open **peebedu.com** and navigate to **Protein Modification Visualizer**. Read the introduction popup, which describes how proteins are synthesized at the ER, transported to the Golgi apparatus, modified through glycosylation, phosphorylation, and cleavage, and then delivered to their final destinations. Close the popup and begin the simulation by dragging the protein toward the Golgi.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

What type of model is the Protein Modification Visualizer? Describe how this computational simulation represents the post-translational processing of proteins in eukaryotic cells. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about protein modification and transport.

A — Accuracy

(a) Identify two things this simulation represents **accurately** about protein processing in eukaryotic cells. For each, name the specific simulation feature and explain what aspect of post-translational modification or protein trafficking it demonstrates.

(b) Identify two things this simulation **oversimplifies or leaves out** about protein processing. Consider what you cannot observe in the simulation that would be important for a complete understanding of the endomembrane system and protein modification.

P — Purpose

What is the learning goal of this simulation? Explain how the Protein Modification Visualizer is designed to help you understand how proteins are modified after translation and how those modifications determine protein function and destination. In your answer, connect at least one specific simulation feature to a biological consequence of post-translational modification in a living cell.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries about protein processing might change or improve a simulation like the Protein Modification Visualizer. Explain why scientific models, including computational simulations, 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 post-translational protein processing?
- 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 gene expression (translation) to the final functional form of a protein?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Post-Translational Modification and Protein Function

> *Simulation Task: Drag the protein from the ER toward the Golgi to form a transport vesicle. Once the protein arrives in the Golgi, click **Glycosylate** and then **Phosphorylate** to apply both modifications. Observe the visual changes to the protein after each modification. Then click **Package from Golgi** and drag the vesicle to the **Cell Membrane**.*

(A) (1 pt) **Describe** how proteins synthesized on ribosomes of the rough endoplasmic reticulum undergo post-translational modifications in the Golgi apparatus that alter their structure and function.

(B) (1 pt) **Explain** how glycosylation and phosphorylation observed in the simulation contribute to the final functional form of a protein, and why these modifications are necessary for the protein to carry out its role at its destination.

(C) (1 pt) **Predict** what would happen to a cell if the Golgi apparatus were unable to perform glycosylation on membrane-bound proteins.

(D) (1 pt) **Justify** your prediction by explaining the relationship between post-translational modifications and the function of the gene product, using the concept that the function and amount of gene products determine the phenotype of organisms.

EK 6.4.A.1, EK 6.5.A.3

Analyze Model / Visual Representation

Question 2 — The Endomembrane System and Protein Sorting

> *Simulation Task: Reset the simulation and complete the full protein journey twice. First, drag the protein from the ER to the Golgi, click **Cleave Protein**, package it, and deliver it to the **Lysosome**. Then reset and repeat the journey, but this time click **Glycosylate**, package it, and deliver it to the **Cell Membrane**. Compare the two pathways.*

(A) (1 pt) **Describe** how the type of post-translational modification a protein receives in the Golgi apparatus determines whether it is targeted to the lysosome or the cell membrane.

(B) (1 pt) **Explain** how the sequential processing of proteins through the endomembrane system — from rough ER to Golgi to final destination — demonstrates that gene expression extends beyond transcription and translation.

(C) (1 pt) **Represent** the two protein sorting pathways you observed in the simulation.

Draw your diagram here.

(D) (1 pt) **Explain** how errors in protein sorting, such as lysosomal storage diseases where enzymes meant for the lysosome are secreted outside the cell, demonstrate the connection between disruptions in post-translational processing and changes in cell differentiation and tissue function.

EK 6.4.A.1, EK 6.5.A.3