PEEBEDU

Epigenetics Simulator (NGSS)

Unit 6: Gene Expression and Regulation

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

> Open **peebedu.com** and navigate to **Epic Genetics**. Click the **Let's Start!** button to begin. Read the introduction popup, which describes how genetic information flows from DNA to RNA to protein through the central dogma. Use the **Generate DNA** button to create a new DNA sequence, then explore the **Molecular Tools** panel on the left side of the screen.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

What type of model is the Epic Genetics simulator? Describe how this computational simulation represents the flow of genetic information from DNA to protein. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about gene expression and its regulation.

A — Accuracy

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

(b) Identify two things this simulation **oversimplifies or leaves out** about gene expression and regulation. Consider what you cannot observe in the simulation that would be important for a complete understanding of how genes are regulated in living cells.

P — Purpose

What is the learning goal of this simulation? Explain how the Epic Genetics simulator is designed to help you understand how regulatory sequences and proteins control transcription and how changes at the DNA level affect the phenotype of an organism. In your answer, connect at least one specific simulation feature to a biological concept related to gene regulation.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries might change or improve a simulation like Epic Genetics. 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 gene expression and regulation?
- 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 molecular steps of gene expression to the concept of phenotype?

Part 2 — NGSS Questions

1.

> *Simulation Task: Click **Generate DNA** to create a new sequence. Add the **Promoter** and then use **RNA Polymerase** to transcribe the DNA. Check the Sim Status panel and note the Transcript count. Now click **Reset**, generate new DNA, and try using **RNA Polymerase** without first adding the Promoter. Compare what happens.*

Explain why the promoter region must be activated before RNA polymerase can begin transcribing DNA into RNA. Describe how this requirement demonstrates that cells control which genes are turned on or off.

HS-LS1-1

2.

> *Simulation Task: Generate a new DNA sequence and add the **Promoter**. Use **RNA Polymerase** once and note the Transcript count. Now add the **Transcription Factor** and use **RNA Polymerase** again. Compare the Transcript count before and after adding the Transcription Factor.*

Describe how the transcription factor changed the amount of RNA produced from the same gene. Explain how specialized proteins that increase or decrease the rate of transcription allow different cell types to produce different amounts of the same protein, even though they share the same DNA.

HS-LS3-2

3.

> *Simulation Task: Generate a new DNA sequence and complete transcription with the **Promoter** and **RNA Polymerase**. Use the **Spliceosome** to process the pre-mRNA into mature mRNA. Note which sections were removed and which were kept. Then click **Reset**, generate new DNA, repeat transcription, and this time use the **Alt Spliceosome** instead. Compare the two mature mRNA sequences.*

Explain how the same DNA sequence produced two different mature mRNA molecules when processed by the standard Spliceosome versus the Alt Spliceosome. Describe how this type of regulation allows one gene to code for more than one protein and why this is important for producing the variety of proteins a cell needs.

HS-LS3-2

4.

> *Simulation Task: Generate a new DNA sequence, add the **Promoter**, and use **RNA Polymerase**. Process the pre-mRNA with the **Spliceosome**, then add the **5' Cap** and the **Poly-A Tail**. Observe how the mature mRNA changes in the visualization area after each modification is applied.*

Describe the modifications that were added to the mRNA after splicing. Explain how these chemical changes to the mRNA molecule help protect it from being broken down and allow it to be recognized by the cell's translation machinery. Connect this to how cells regulate how much protein is ultimately made from a gene.

HS-LS1-1

5.

> *Simulation Task: Generate a new DNA sequence and complete the full pathway: add the **Promoter**, use **RNA Polymerase**, process with the **Spliceosome**, add the **5' Cap** and **Poly-A Tail**, and then use both **tRNA** and **rRNA** to translate the mRNA. Observe the polypeptide chain that appears. Now click **Reset**, generate new DNA, and apply the **Mutagen** before repeating the entire pathway. Compare the two polypeptide chains.*

Describe how the mutation introduced by the Mutagen changed the final protein compared to the unmutated version. Explain how a change in the DNA sequence can alter the structure of the protein produced and how this could affect the traits of an organism.

HS-LS3-2

6.

> *Simulation Task: Generate a new DNA sequence and use **CRISPR** to edit a specific codon in the DNA. Then complete the full pathway (Promoter, RNA Polymerase, Spliceosome, 5' Cap, Poly-A Tail, tRNA, and rRNA). Observe how the targeted edit changed the resulting polypeptide chain compared to the original sequence.*

In the box below, draw a diagram showing how a single change in a DNA codon leads to a different amino acid in the final protein. Label the original DNA codon, the edited DNA codon, the corresponding mRNA codons, and the two different amino acids that result. Include arrows to show the flow of information from DNA to mRNA to protein.

Draw your diagram here.

HS-LS3-2

7.

> *Simulation Task: Generate a new DNA sequence and apply the **Mutagen** to introduce a random mutation. Complete the full pathway and observe the resulting protein. Then click **Reset**, generate the same type of sequence, and this time complete the pathway without any mutation. Compare the two proteins and think about how environmental factors such as UV radiation or chemical exposure could cause similar changes in a living organism.*

Environmental factors such as radiation, chemicals, and diet can cause changes to DNA or affect how genes are regulated. Using evidence from your simulation, explain how an environmental factor could change the proteins a cell produces and how this could affect the traits of an organism or its offspring. Describe one example of how a change in environmental conditions could influence the variation of traits in a population over time.

HS-LS4-5