

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 – Free Response Questions

Conceptual Analysis

Question 1 – Regulatory Control of Transcription

*Simulation Task: In the Epic Genetics simulator, click **Generate DNA** to create a new sequence. First, attempt to use **RNA Polymerase** without adding a Promoter – observe what happens. Then add the **Promoter** and the **Transcription Factor**, and use **RNA Polymerase** again. Compare the Sim Status panel before and after adding the Transcription Factor, noting the change in transcript count.*

(A) (1 pt) **Describe** how regulatory sequences and regulatory proteins interact to control transcription.

(B) (1 pt) **Explain** why the simulation requires you to activate the promoter before RNA Polymerase can transcribe the DNA, and how adding a transcription factor changes the outcome.

(C) (1 pt) **Predict** what would happen to the type and amount of protein produced if a mutation in the promoter region prevented transcription factors from binding.

(D) (1 pt) **Justify** your prediction by explaining how the phenotype of a cell is determined by the combination of genes that are expressed and the levels at which they are expressed.

Analyze Model / Visual Representation

Question 2 — Alternative Splicing and Differential Gene Expression

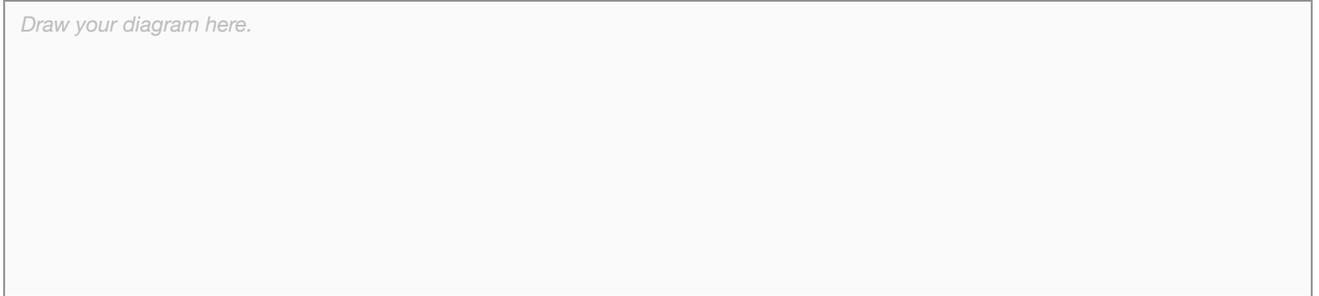
*Simulation Task: Generate a new DNA sequence. Complete the full central dogma pathway: add the **Promoter**, use **RNA Polymerase**, then use the **Spliceosome** to process the pre-mRNA. Note the mature mRNA sequence and resulting protein. Now click **Reset**, generate new DNA, and this time use the **Alt Spliceosome** instead of the standard Spliceosome. Compare the two mature mRNA sequences and the resulting polypeptide chains.*

(A) (1 pt) **Describe** how epigenetic changes and regulatory mechanisms can result in different proteins being produced from the same DNA sequence.

(B) (1 pt) **Explain** the relationship between alternative splicing and cell differentiation.

(C) (1 pt) **Represent** the process of alternative splicing at the molecular level.

Draw your diagram here.



(D) (1 pt) **Explain** how errors in gene regulation, such as a failure to properly silence a gene through epigenetic modification, could lead to uncontrolled cell division.

EK 6.5.A.2, 6.5.A.3