Virtual Restriction Digest

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

> Open **peebedu.com** and navigate to **Virtual Restriction Digest**. When the mode selection dialog appears, choose **Case 3: Sickle Cell Screening**. Read the case introduction, which explains how the MstII restriction enzyme is used to screen patients for sickle cell genotypes by cutting the HBB (beta-globin) gene at specific recognition sites.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

What type of model is the Virtual Restriction Digest? Describe how this computational simulation represents the process of restriction enzyme digestion and gel electrophoresis. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about how genetic engineering techniques analyze DNA.

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A — Accuracy

(a) Identify two things this simulation represents **accurately** about restriction digestion and gel electrophoresis. For each, name the specific simulation feature and explain what aspect of the biotechnology technique it demonstrates.

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(b) Identify two things this simulation **oversimplifies or leaves out** about restriction digestion. Consider what you cannot observe in the simulation that would be important for a complete molecular-level understanding of how restriction enzymes interact with DNA.

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P — Purpose

What is the learning goal of this simulation? Explain how the Virtual Restriction Digest is designed to help you understand how genetic engineering techniques can be used to analyze and manipulate DNA. In your answer, connect at least one specific case study (such as sickle cell screening or forensic analysis) to a real-world application of restriction digestion and gel electrophoresis.

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P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries in biotechnology might change or improve a simulation like the Virtual Restriction Digest. Explain why scientific models, including computational simulations of laboratory techniques, are revised as new tools and methods become available.

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Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for restriction digestion?
- 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 process of enzyme cutting to the visible gel electrophoresis banding pattern?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Sickle Cell Screening by Restriction Digest

*Simulation Task: Select **Case 3: Sickle Cell Screening**. Use the MstII restriction enzyme to digest HBB Gene samples from three patients. After the digestion completes, click **View Results** to observe the gel electrophoresis banding patterns. Compare the fragment patterns for a normal (AA), carrier (AS), and affected (SS) individual.*

(A) (1 pt) **Describe** how restriction enzymes recognize and cut DNA at specific nucleotide sequences.

(B) (1 pt) **Explain** how gel electrophoresis separates the DNA fragments produced by MstII digestion, and why the banding pattern differs between a homozygous normal (AA) individual, a heterozygous carrier (AS), and an individual with sickle cell disease (SS).

(C) (1 pt) **Predict** what the gel electrophoresis banding pattern would look like if a new restriction enzyme were discovered that cuts within the sickle cell mutation site (the mutated sequence) but does not cut the normal HBB sequence.

(D) (1 pt) **Justify** how restriction enzyme analysis of the HBB gene can be used as a diagnostic tool for sickle cell disease.

EK 6.8.A.1.i, iv

Analyze Model / Visual Representation

**Question 2 — Restriction Mapping and Fragment Analysis**

*Simulation Task: Select **Standard Lab Mode**. Drag the **Lambda** DNA sample and the **EcoRI** restriction enzyme into the workspace. Click **Perform Digestion**, then **View Results** to observe the gel electrophoresis pattern. Next, repeat the experiment using **HindIII** on the same Lambda DNA. Compare the two gel patterns.*

(A) (1 pt) **Describe** the relationship between restriction enzyme recognition sequences and the number and size of DNA fragments produced during a restriction digest.

(B) (1 pt) **Explain** how the gel electrophoresis results from the simulation demonstrate that smaller DNA fragments migrate farther through the gel than larger fragments.

(C) (1 pt) **Represent** how a restriction enzyme (such as EcoRI) recognizes and cleaves a double-stranded DNA molecule at a palindromic recognition site.

Draw your diagram here.
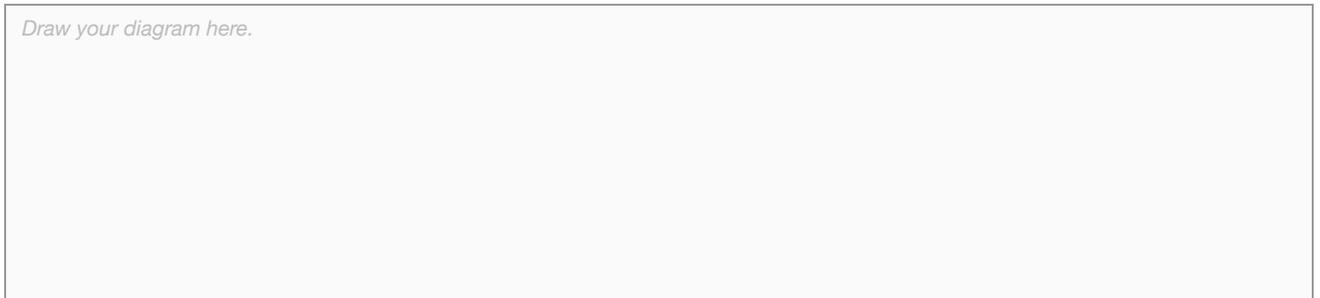
(D) (1 pt) **Explain** how restriction enzyme analysis of the HBB gene reveals that the sickle cell allele (HbS) eliminates an MstII cut site present in the normal allele (HbA).

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