**PEEBEDU**

# Operail (Operon Regulation) (NGSS)

Unit 6: Gene Expression and Regulation

**Name:** ____________________ **Period:** ________ **Date:** ______________

> Open **peebedu.com** and navigate to **Operail**. Click the **Introduction** button and read the popup, which explains how an operon functions using a train analogy: the promoter is a station, RNA polymerase is a locomotive, the operator is a signal switch, and the repressor is a crossing gate. Then explore the simulation by toggling components and clicking **All Aboard!** to run transcription.

## Part 1 — Model Evaluation (MAPP Framework)

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

### M — Mode

What type of model is Operail? Describe how this computational simulation represents operon regulation in prokaryotes. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about gene regulation.

### A — Accuracy

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

**(b)** Identify two things this simulation **oversimplifies or leaves out** about operon regulation. Consider what you cannot observe in the simulation that would be important for a complete molecular-level understanding of how operons function in living cells.

### P — Purpose

What is the learning goal of this simulation? Explain how Operail is designed to help you understand how regulatory sequences, repressors, and transcription factors control gene expression in prokaryotes. In your answer, connect at least one specific simulation feature to a biological scenario where operon regulation is important for a prokaryotic cell.

### P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries might change or improve a simulation like Operail. 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 operon regulation?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the train analogy help (or hinder) your understanding of the molecular mechanisms of gene regulation?

## Part 2 — NGSS Questions

### 1.

> *Simulation Task: Toggle the promoter, operator, and all three genes (A, B, C) ON. Toggle the repressor OFF. Click “All Aboard!” and watch the Event Log as RNA polymerase travels along the DNA track and produces mRNA at each gene.*

Describe the role of the promoter in starting transcription. Explain why RNA polymerase cannot begin reading the genes without a functional promoter and how the mRNA produced at each gene is used by the ribosome to build proteins.

HS-LS1-1

### 2.

> *Simulation Task: Toggle all genes, the promoter, and the operator ON. Toggle the repressor ON. Click “All Aboard!” and observe what happens. Then click “Reset,” toggle the repressor OFF, and click “All Aboard!” again. Compare the two outcomes in the Event Log.*

Explain how the repressor protein controls whether or not the genes in the operon are expressed. Describe what the repressor does at the operator and why this mechanism allows a bacterial cell to turn genes on or off depending on conditions in the environment.

HS-LS1-1

**3.**

> *Simulation Task: Toggle all genes, the promoter, and the operator ON. Toggle the repressor OFF and the transcription factor ON. Click "All Aboard!" and observe the Event Log. Then click "Reset," toggle the transcription factor OFF (keeping everything else the same), and click "All Aboard!" again. Compare the results.*

Describe how the transcription factor (activator) affects the rate of transcription when it is present compared to when it is absent. Explain why a bacterial cell would benefit from having proteins that can speed up or slow down the reading of certain genes.

HS-LS1-1

**4.**

> *Simulation Task: Toggle the operator OFF to simulate a mutation that removes the operator from the DNA. Toggle the promoter, all three genes, and the repressor ON. Click "All Aboard!" and observe whether the repressor can still block transcription.*

Describe what happens to gene expression when the operator is mutated so that the repressor can no longer bind. Explain why a cell with this mutation would continuously produce the proteins encoded by the operon, even when those proteins are not needed.

HS-LS3-1

**5.**

> *Simulation Task: Toggle the promoter OFF while keeping all three genes and the operator ON. Toggle the repressor OFF. Click “All Aboard!” and observe the Event Log to see whether transcription occurs.*

Explain why a mutation that destroys the promoter prevents all three genes in the operon from being expressed, even though the genes themselves are undamaged. Describe how this result shows that a single change in a regulatory DNA sequence can affect the production of multiple proteins at once.

HS-LS3-1

**6.**

> *Simulation Task: Observe the DNA track layout in the simulation. Note the order of the promoter, operator, and genes A, B, and C along the track. Run the simulation once with the repressor ON and once with the repressor OFF.*

In the box below, draw a labeled diagram of the operon in its “ON” state (genes being expressed) and its “OFF” state (genes blocked). Label the promoter, operator, genes, RNA polymerase, and repressor in each diagram. Use arrows to show whether or not transcription proceeds in each state.

*Draw your labeled diagrams here.*

HS-LS1-1

**7.**

> *Simulation Task: Run the simulation several times with different toggle combinations. Consider how the same set of genes can produce different outcomes depending on which regulatory components are active.*

Operons are found in bacteria but not in most multicellular organisms, yet the basic idea of turning genes on and off is shared across all life. Explain how the ability to regulate gene expression could have provided a survival advantage to early single-celled organisms and how this shared mechanism across species supports the idea that modern organisms descended from a common ancestor.

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