Name:	Date:
	Section:
Enzyme l	Environment Activity
Investigating Environmenta	al Effects on Enzyme Function
Phase 1: ENGAGE (5 min	utes)
Getting Started: Open peebedu.com	and navigate to Enzyme Environmental Impact Explorer
Read the introduction popup to underst	and enzyme structure, temperature, and pH effects.
•	nmental conditions affect enzyme structure and function? s have different optimal conditions? What molecular on?
Pre-Activity Predictions:	
Based on your knowledge of protein stru	icture:
• How should temperature affect en	zyme activity?
Which digestive enzyme would wo	rk best in the stomach?

## Phase 2: EXPLORE (20 minutes)

#### Systematic Investigation of Enzyme Conditions

#### Part A: Enzyme Selection and Initial Observations

Select  $\mathbf{Pepsin}$  first

•	Observe	enzyme	structure	at	$25^{\circ}\mathrm{C}$	рН	7.0
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• Enzyme movement: \_\_\_\_\_

• Structural state: Folded / Unfolded

#### Part B: Temperature Investigation

Keep pH at 7.0, vary temperature systematically:

Temperature	Enzyme Activity	Ion Behavior
0°C		
20°C		
40°C 60°C		<del></del>
00 C		
80°C		What happens to ion behavior at 80°C?

## Phase 3: EXPLAIN (10 minutes)

Molecular	Mechanisms	<b>Analysis</b>
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Complete the molecular explanations:  • Low pH $\rightarrow$ excess H+ $\rightarrow$ protonation of groups $\rightarrow$ charge  • Charge repulsion $\rightarrow$ protein $\rightarrow$ loss of	Temperature Effects - Identify Patterns:
Complete the molecular explanations:  • Low pH → excess H+ → protonation of groups → charge  • Charge repulsion → protein → loss of  Structure-Function Relationship: Explain how the simulation demonstrates:  • Primary structure:  • Active site integrity:  Digestive System Adaptation: Match enzyme to digestive location based on optimal pH:	$\bullet$ Pattern 1: Increased temperature $\rightarrow$ increased energy
Complete the molecular explanations:  • Low pH → excess H+ → protonation of groups → charge  • Charge repulsion → protein → loss of  Structure-Function Relationship: Explain how the simulation demonstrates:  • Primary structure:  • Active site integrity:  Digestive System Adaptation: Match enzyme to digestive location based on optimal pH:	
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<ul> <li>Low pH → excess H+ → protonation of groups → charge</li> <li>Charge repulsion → protein → loss of</li> <li>Structure-Function Relationship: Explain how the simulation demonstrates:</li> <li>Primary structure:</li> <li>Active site integrity:</li> <li>Digestive System Adaptation: Match enzyme to digestive location based on optimal pH:</li> </ul>	pH Effects - Cause and Effect:
<ul> <li>Low pH → excess H+ → protonation of groups → charge</li> <li>Charge repulsion → protein → loss of</li> <li>Structure-Function Relationship: Explain how the simulation demonstrates:</li> <li>Primary structure:</li> <li>Active site integrity:</li> <li>Digestive System Adaptation: Match enzyme to digestive location based on optimal pH:</li> </ul>	
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Digestive System Adaptation: Match enzyme to digestive location based on optimal pH:	• Active site integrity:
	(F12 0.0). <u>111111</u>
• Small intestine (pH ~8):	• Small intenting (pH ~9).

# Phase 4: ELABORATE (10 minutes)

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Real-World Applications	
Scenario Analysis:	
Fever Response: Normal body temp: 37°C, Fever: 40°C	
• Which enzymes remain functional?	
• Evolutionary advantage of fever?	
Antacid Effects: Patient takes antacids, raising stomach pH from 2 to 5:	
• Effect on pepsin activity:	
• Alternative solutions:	
Lactose Intolerance: Based on lactase properties:	
• Optimal conditions:	
-	
• Effect of consuming hot beverages with dairy:	

### Phase 5: EVALUATE (5 minutes)

Assessment	Questions
Assessment	Questions

Data Analy	vsis:	Plot	enzyme	activity	curves	for	one	enzyme	showing	വര്:
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- Temperature vs. activity (bell curve)
- pH vs. activity (bell curve)

Explain the molecular basis for each curve shape. (3 pts)

**Pattern Application:** You discover a new enzyme from thermophilic bacteria with optimal temperature of 75°C. Predict:

• Likely structural a	daptations:
• Industrial applicat	ions:
(3 pts)	
Systems Integration: I unfolding) accurately rep	Explain how the simulation's visual elements (movement, charge interactions present:
• Kinetic energy cha	nges:
• Hydrophobic collapted (4 pts)	ose:
Model Evaluation:	
Most accurate repr	resentation:
• Missing element: _	

 $\textbf{Research Challenge:} \ \, \textbf{Investigate one enzyme adaptation:} \\$ 

- Psychrophilic enzymes (cold-adapted)
- Thermophilic enzymes (heat-adapted)

• Acidophilic enzymes (acid-adapted)	
Compare structural features to mesophilic enzymes:	