

AP[®] BIOLOGY
2013 SCORING GUIDELINES

Question 5

The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

Species	Relative Amino Acid Position									
	1	2	3	4	5	6	7	8	9	10
I	Val	His	Leu	Val	Glu	Glu	His	Val	Glu	His
II	Val	His	Leu	Lys	Glu	Glu	His	Val	Glu	His
III	Val	His	Leu	Val	Glu	Glu	His	Val		
IV	Val	His	Leu	Val	Arg	Trp	Ala	Cys	Met	Asp

- (a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III. **(2 points maximum)**

Explanation: **1 point per row**

NOTE: Specific names of mutation types are not required.

Species	Genetic Change in DNA / Bases	Result of Change to Polypeptide / Protein
II	mutation / substitution / point mutation / missense mutation	an amino acid change only at position 4 (Val to Lys)
III	mutation (e.g., substitution / insertion / deletion / point mutation / frameshift mutation / nonsense mutation) that introduces a stop codon after the codon for Val	termination of the polypeptide after the Val at position 8

- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction. **(2 points maximum)**

Predicted Change (1 point maximum)	Justification of Prediction (1 point maximum)
Protein may have a different structure and a change in function.	Change in amino acid sequence of the protein starting at position 5 could alter the overall structure or local structural regions, interfering with function of the protein.
Protein may have a different structure and no change in function.	Change in amino acid sequence alters the shape / conformation / folding / binding region / regulatory region of the protein, but does not affect the critical functional region(s) of the protein.
Protein structure and function may not be affected.	Change in amino acid sequence does not alter the protein shape / conformation / folding and does not alter function.

5A1

5. The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

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- (a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.
- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.

ANSWER PAGE FOR QUESTION 5

a.) In species 2, the most likely genetic change was a point mutation, in which a single nucleotide is altered, which changes the amino acid being coded for. In species 3, the most likely genetic change was a point mutation that coded for a STOP codon, which halted production of the polypeptide prematurely.

b.) The protein produced in species 4 will have a much different structure, and the function will be radically different. The frameshift mutation that resulted in the polypeptide completely altered the polypeptide chain, which in turn will change the interactions between amino acids, so the structure is changed. The altered amino acid sequence will cause the protein's function to shift.

5. The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

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- (a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.
- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.

ANSWER PAGE FOR QUESTION 5

The change in species II at position 4 indicates the ~~mut~~ mutation of a DNA sequence. The mutation, however, did not change anymore the structure of this sequence. The mutation in III caused a stop in this AA sequence.

The mutation in IV caused a change in the sequence of the entire following amino acids. This will change the structure of the protein. And because protein structure determines its function, the mutated protein may either not function properly and cause damage or go unused.

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IV	Val	His	Leu	Val	Arg	Trp	Ala	Cys	Met	Asp

- (a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.
- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.

ANSWER PAGE FOR QUESTION 5

A: In all likelihood, a genetic mutation caused the change of valine to lysine from species I to II, simply by chance or through an environmental factor. To cause the shortening of code from species II to III, it's possible that this was again caused by a mutation, or by a possible error when removing introns during transcription.

B: Well, since the order & content of the amino acids has changed, it is valid to say that the structure & function of the resulting protein will be vastly changed. Perhaps they will be similar, but certainly not the same. The number of effects are many, & could be devastating or harmless.

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2013 SCORING COMMENTARY

Question 5

Question 5 was written to the following Learning Objectives in the AP Biology Curriculum Framework: 3.26, 4.1, and 4.3.

Overview

Question 5 asks students to use models of biological polymers to connect genetic variation with changes in protein structure and function. Students were presented with the amino acid sequences of a conserved polypeptide from four related species. Students were asked to explain how specific genetic changes could have produced the different amino acid sequences shown. Students were then asked to use a model of protein structure and function to predict how a change in the amino acid composition of a polypeptide might affect the structure and function of the resulting protein.

Sample: 5A

Score: 4

The response earned 1 point in part (a) for explaining that the most likely genetic change in species II was a point mutation in which a single nucleotide is altered, and the amino acid being coded for was changed.

The response earned 1 point in part (a) for explaining that the most likely genetic change in species III was a point mutation that coded a STOP codon which halted the production of the polypeptide prematurely.

The response earned 1 point in part (b) for predicting that a frameshift mutation in species IV causes a much different protein structure and a radically different protein function.

The response earned 1 point in part (b) for justifying the prediction by stating that the polypeptide chain was completely altered, which changed the interactions between the amino acids of the protein and caused the protein's function to shift.

Sample: 5B

Score: 3

The response earned 1 point in part (a) for explaining that a mutation in the DNA sequence of species II caused a change only at position 4 of the polypeptide.

The response earned 1 point in part (b) for predicting that the mutation in species IV will change the structure and function of the protein, resulting in a mutant protein that does not function properly or goes unused.

The response earned 1 point in part (b) for justifying the prediction by stating that almost the entire amino acid sequence of the protein was changed and that protein structure determines protein function.

Sample: 5C

Score: 2

The response earned 1 point in part (b) for predicting that the structure and function of the protein in species IV will be vastly changed.

The response earned 1 point in part (b) for justifying the prediction by stating that a structural and functional change in the protein is due to changes in the order and content of its amino acids.