

2013 AP® BIOLOGY FREE-RESPONSE QUESTIONS

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.
- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.
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6. The following data were collected by observing subcellular structures of three different types of eukaryotic cells.

RELATIVE AMOUNTS OF ORGANELLES IN THREE CELL TYPES

Cell Type	Smooth ER	Rough ER	Mitochondria	Cilia	Golgi Bodies
X	Small amount	Small amount	Large number	Present	Small amount
Y	Large amount	Large amount	Moderate number	Absent	Large amount
Z	Absent	Absent	Absent	Absent	Absent

Based on an analysis of the data, **identify** a likely primary function of each cell type and **explain** how the data support the identification.

**AP[®] BIOLOGY
2013 SCORING GUIDELINES**

Question 5

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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. (**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.