

The image is a colorful, hand-drawn style graphic on a light gray grid background. A large, light green, rounded rectangular shape is the central focus, containing the main text. The text 'AP Bio' is in a large, dark green, bubbly font with a pink shadow. Below it, 'FRQ Fridays' is in a large, purple, bubbly font with a pink shadow. Underneath that, '2013 #5' is in a smaller, black, sans-serif font, followed by 'Point & Frameshift Mutations' in a black, sans-serif font. To the right of the text is a small, cute penguin character with a black body, white belly, and a small black bow tie. The penguin has a speech bubble above it that says 'Hi!'. The background is decorated with various colorful elements: a DNA double helix in red and blue on the top left and bottom right; a yellow pencil with a pink eraser on the left; a purple spiral notebook with 'NOTES' written on it on the bottom left; several yellow paper clips scattered around; and some teal and orange squiggly lines and shapes. The overall style is playful and educational.

2013 #5
Point & Frameshift Mutations



FRQ Friday #15

2013 #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.

	Relative Amino Acid Position									
Species	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



FRQ Friday #15

2013 #5

(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.

	Relative Amino Acid Position									
Species	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

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)



FRQ Friday #15

2013 #5

(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.

	Relative Amino Acid Position									
Species	1	2	3	4	5	6	7	8	9	10
I	Val	His	Leu	Val	Glu	Glu	His	Val	Glu	His
III	Val	His	Leu	Val	Glu	Glu	His	Val		

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
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



FRQ Friday #15

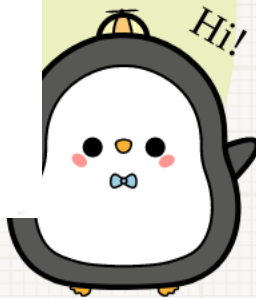
2013 #5

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

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.



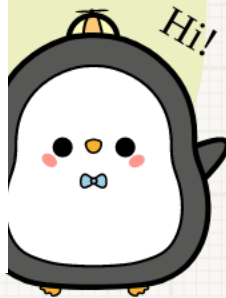
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2013 #5

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

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

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.



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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.

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.

