

# FRQ Friday – 4/2

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2017 #6

2016 #4

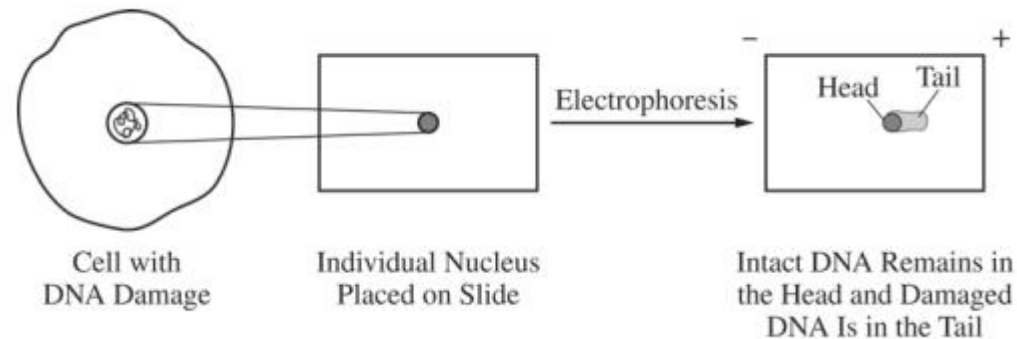
2013 #5



# FRQ 2017 #6

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A comet assay is a technique used to determine the amount of double-strand breaks in DNA (DNA damage) in cells. The nucleus of an individual cell is placed on a microscope slide coated with an agarose gel. An electric current is applied to the gel that causes DNA to move (electrophoresis), and the DNA is stained with a fluorescent dye. When viewed using a microscope, undamaged DNA from the nucleus appears as a round shape (the head), and the fragments of damaged DNA extend out from the head (the tail). The length of the tail corresponds to the amount of the damage in the DNA (see Figure 1).

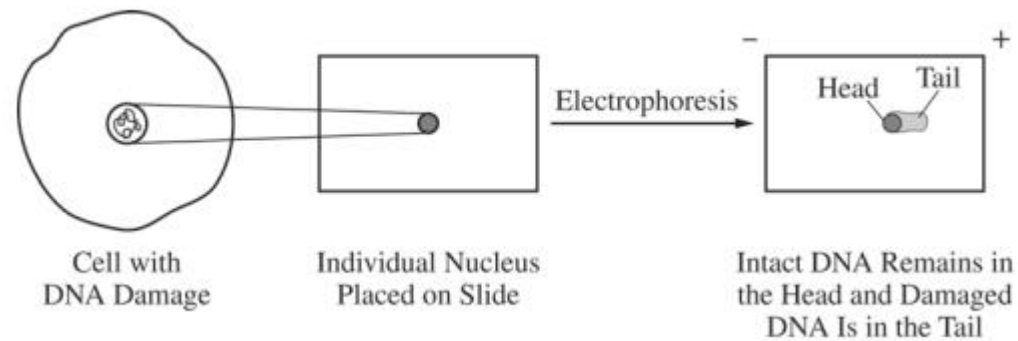




# FRQ 2017 #6

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(a) To explain the movement of DNA fragments in the comet assay, **identify** one property of DNA and **provide reasoning** to support how the property contributes to the movement during the comet assay technique.



Identification (1 point)	Reasoning (1 point)
DNA has a (negative) charge.	DNA moves toward the positive/oppositely charged pole.
DNA can be different sizes.	(Different size DNA fragments) move at different rates.



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(b) In a different experiment, cells are treated with a chemical mutagen that causes only nucleotide substitutions in DNA. **Predict** the likely results of a comet assay for this treatment.

## **Prediction (1 point)**

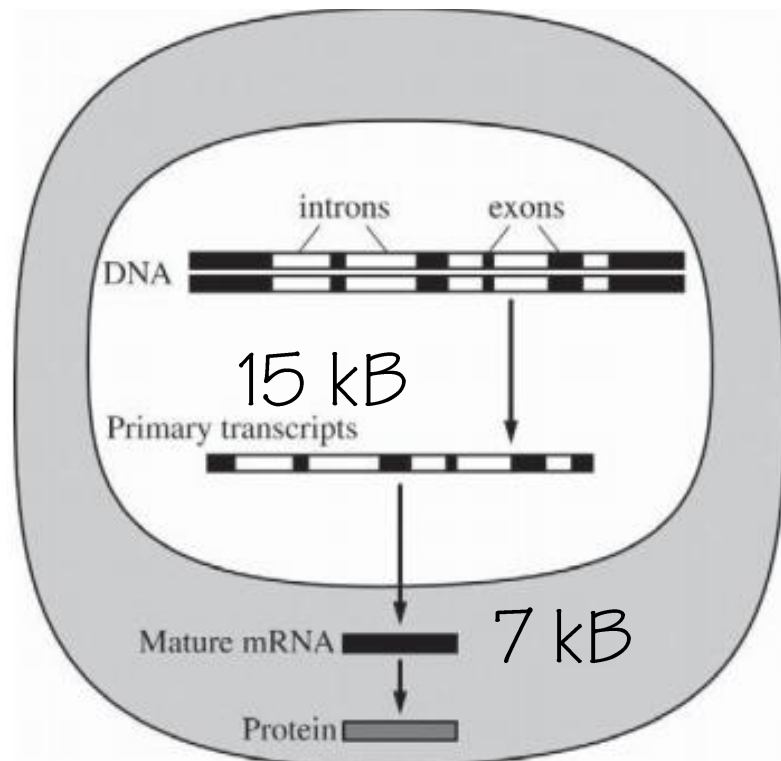
- Head (only) OR (head with) no tail.
- Tail will be shorter than a cell with double-stranded breaks in DNA.



# FRQ 2016 #4

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- (a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length. Describe the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. Identify in your response the location in the cell where the change occurs.



The figure represents the process of expression of gene X in a eukaryotic cell.

## Describe process (1 point)

- Removal of introns
- RNA processing

## Identification (1 point)

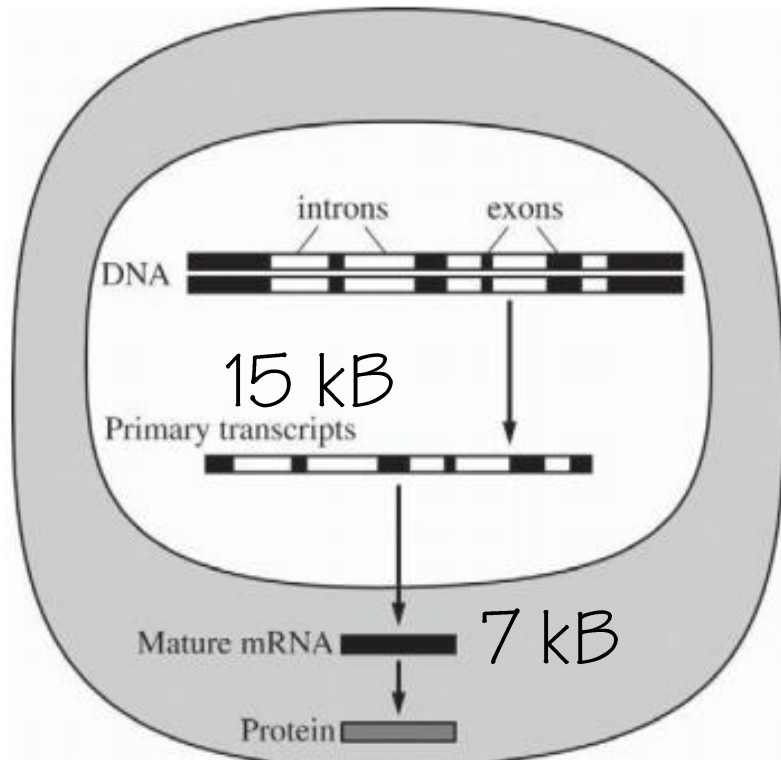
- Nucleus



# FRQ 2016 #4

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(b) **Predict** the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction.



The figure represents the process of expression of gene *X* in a eukaryotic cell.

## Prediction (1 point)

- 15 kb
- Longer than the mature mRNA in the eukaryote

## Justification (1 point)

- mRNA processing typically does not occur in prokaryotes



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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





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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.

	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)





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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.

	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 mutation (e.g., substitution / insertion / deletion / point mutation / frameshift mutation / nonsense mutation) that introduces a stop codon after the codon for Val	Result of Change to Polypeptide / Protein
III		termination of the polypeptide after the Val at position 8

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(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.



Next FRQ Friday (4/9)

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2016 #1

2015 #3

