Insta-Review: Unit 4B

AP Biology Insta-Review @apbiopenguins

DNA Replication

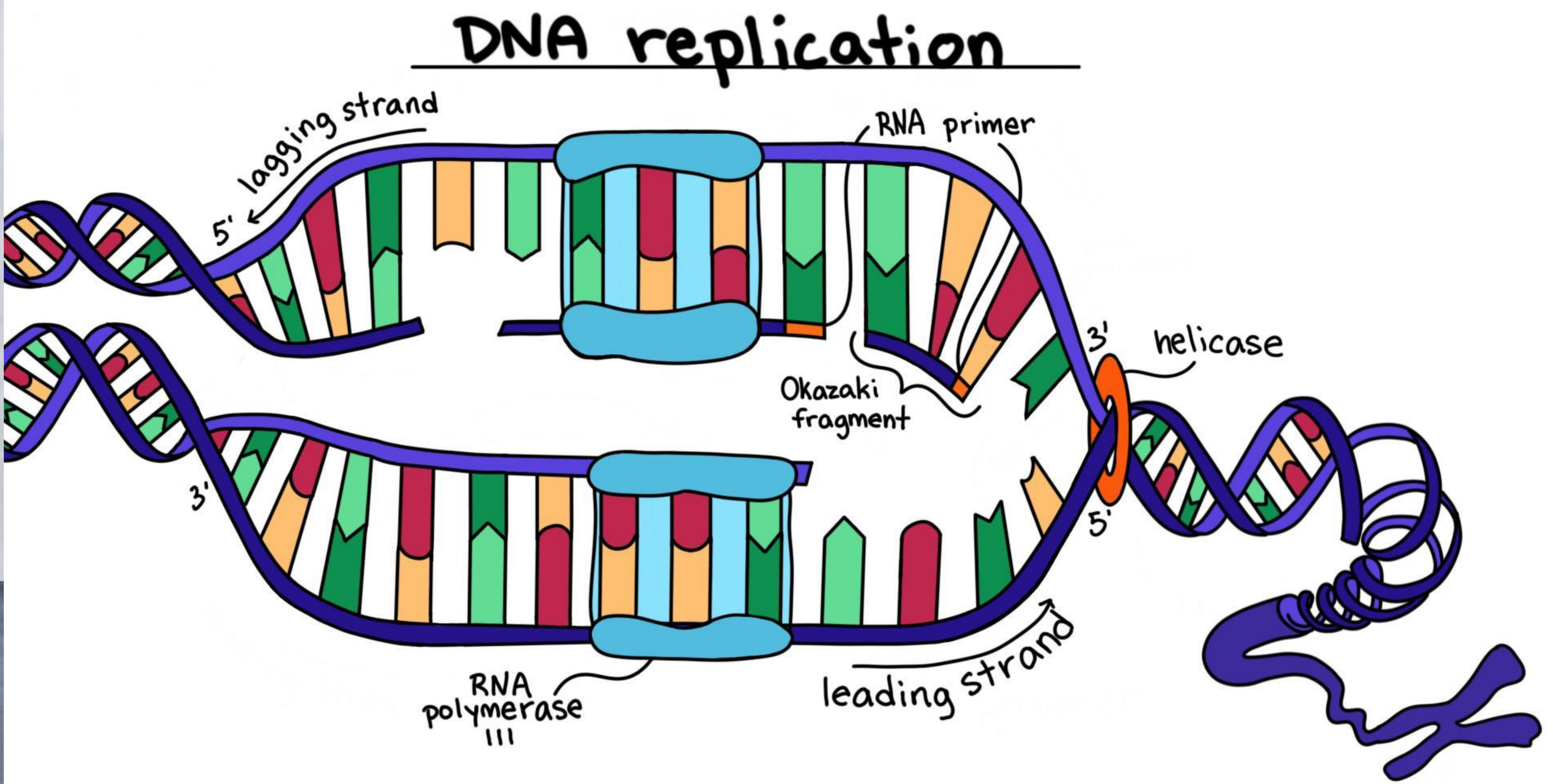
Transcription & Translation

Operons

DNA Technology

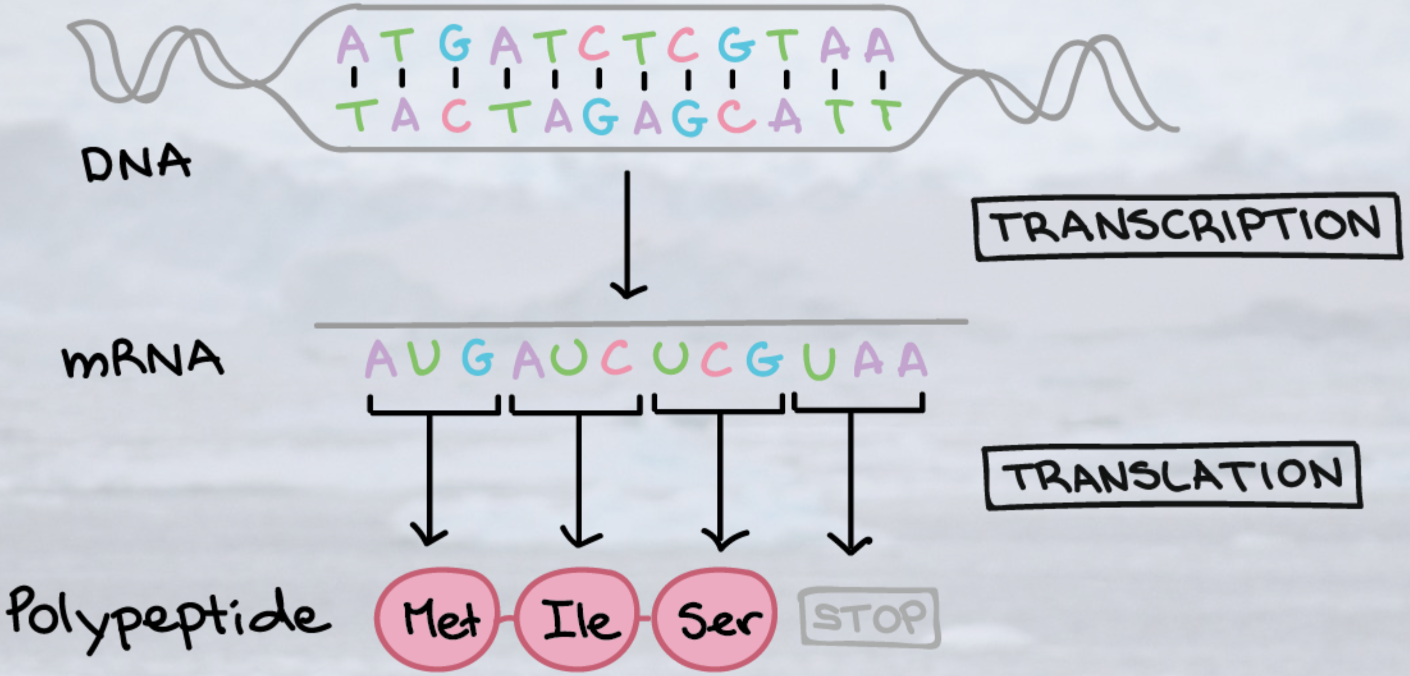
DNA Replication

AP Biology Insta-Review @apbiopenguins



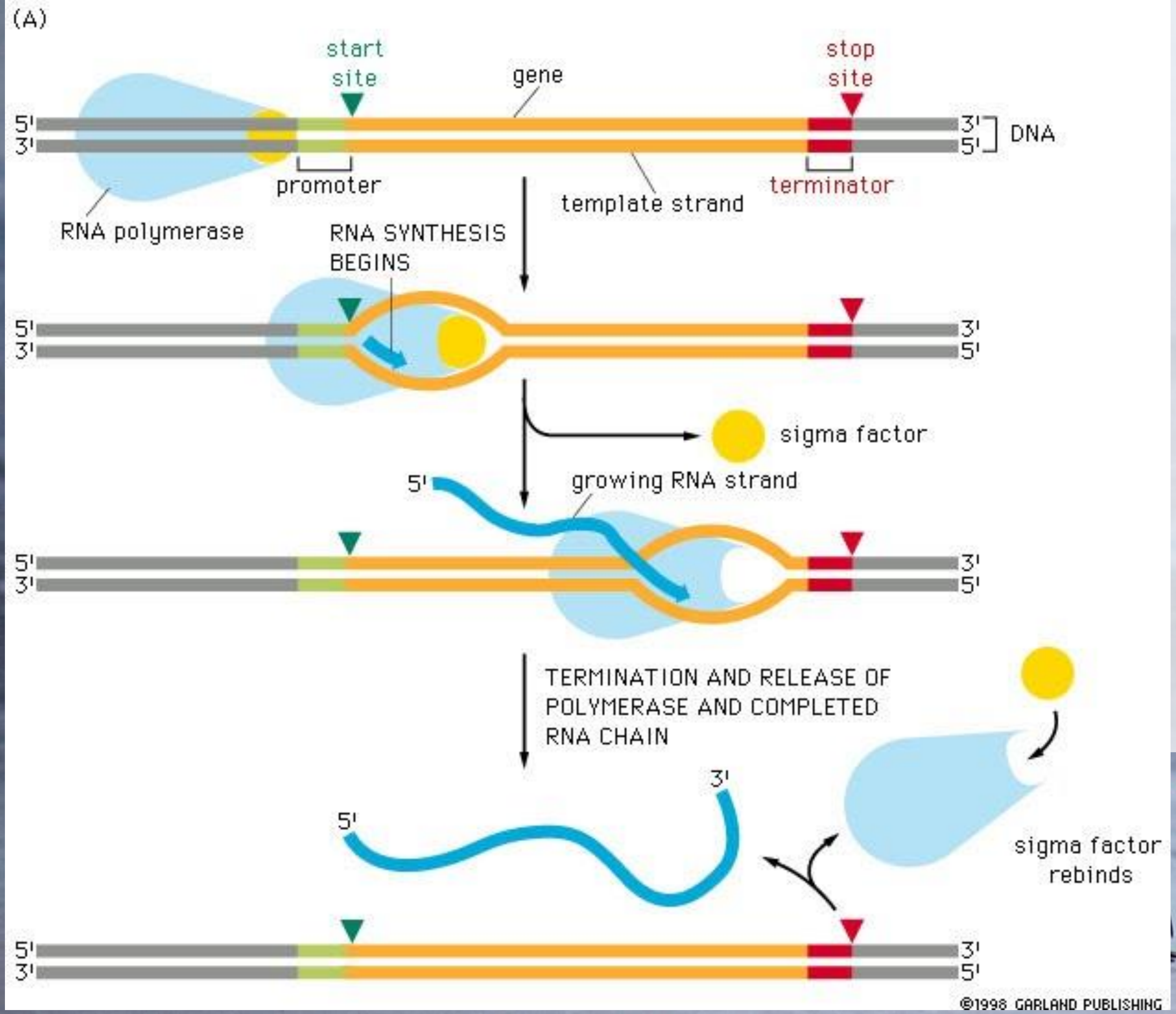
Central Dogma

AP Biology Insta-Review @apbiopenguins

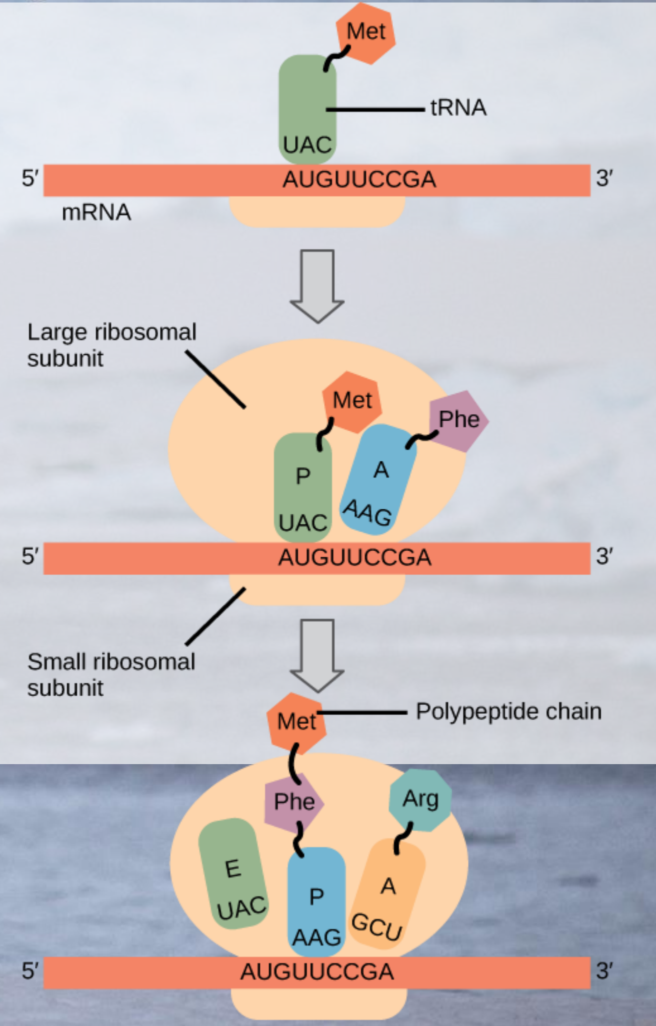


Transcription & Translation

AP Biology Insta-Review @apbiopenguins

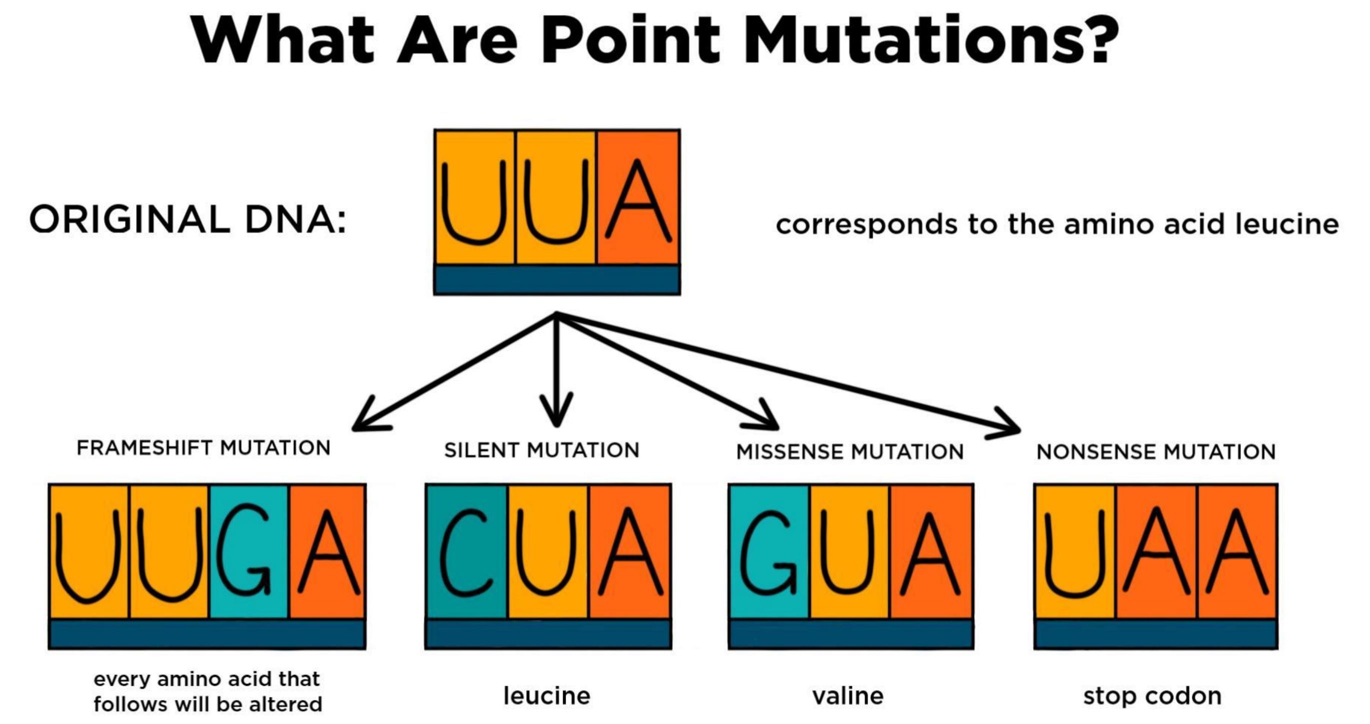


©1998 GARLAND PUBLISHING



Mutations

AP Biology Insta-Review @apbiopenguins



What Are Point Mutations?

ORIGINAL DNA: UUA corresponds to the amino acid leucine

FRAMESHIFT MUTATION: UUGA — every amino acid that follows will be altered

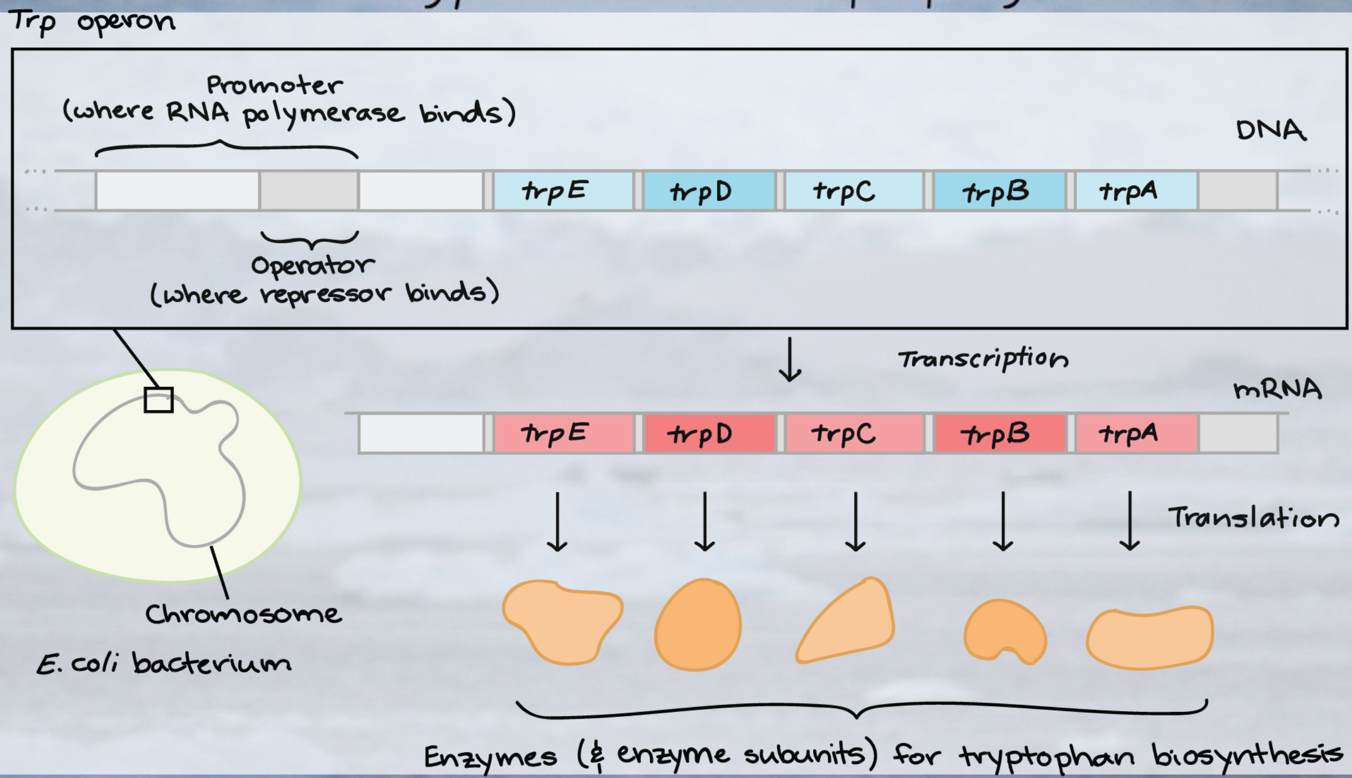
SILENT MUTATION: CUA — leucine

MISSENSE MUTATION: GUA — valine

NONSENSE MUTATION: UAA — stop codon

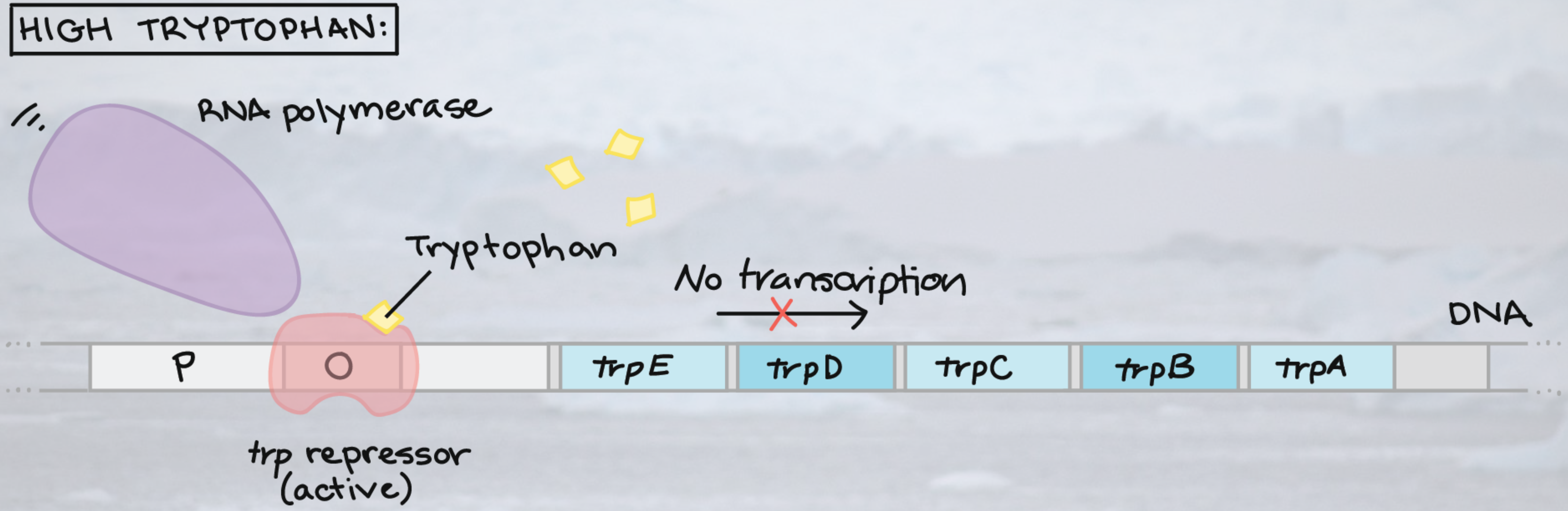
Trp Operon

AP Biology Insta-Review @apbiopenguins



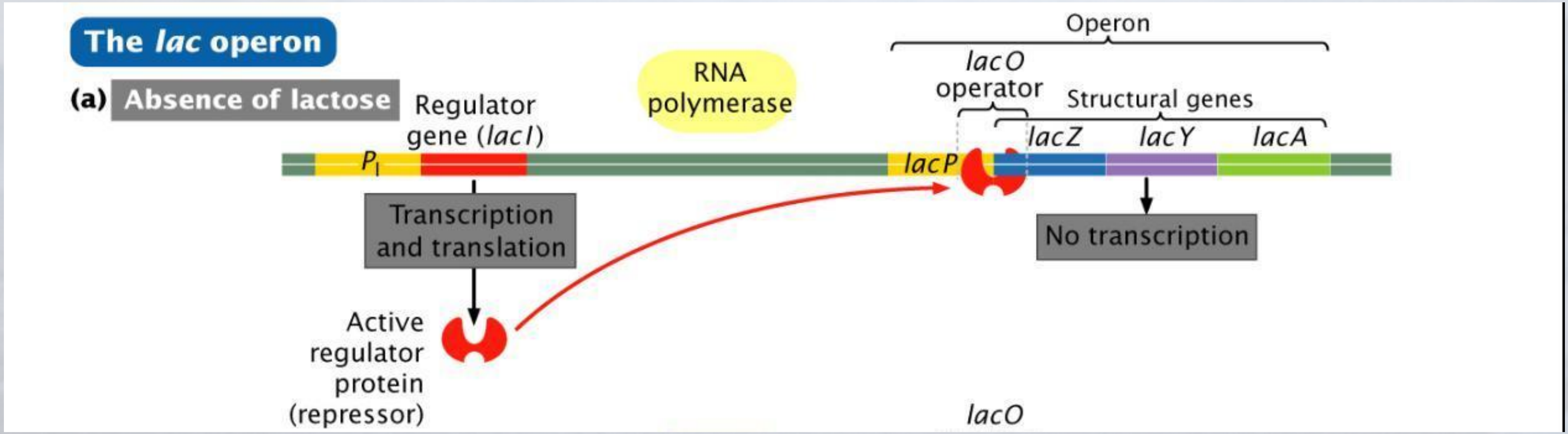
Trp Operon

AP Biology Insta-Review @apbiopenguins



Lac Operon

AP Biology Insta-Review @apbiopenguins



Lac Operon

AP Biology Insta-Review @apbiopenguins

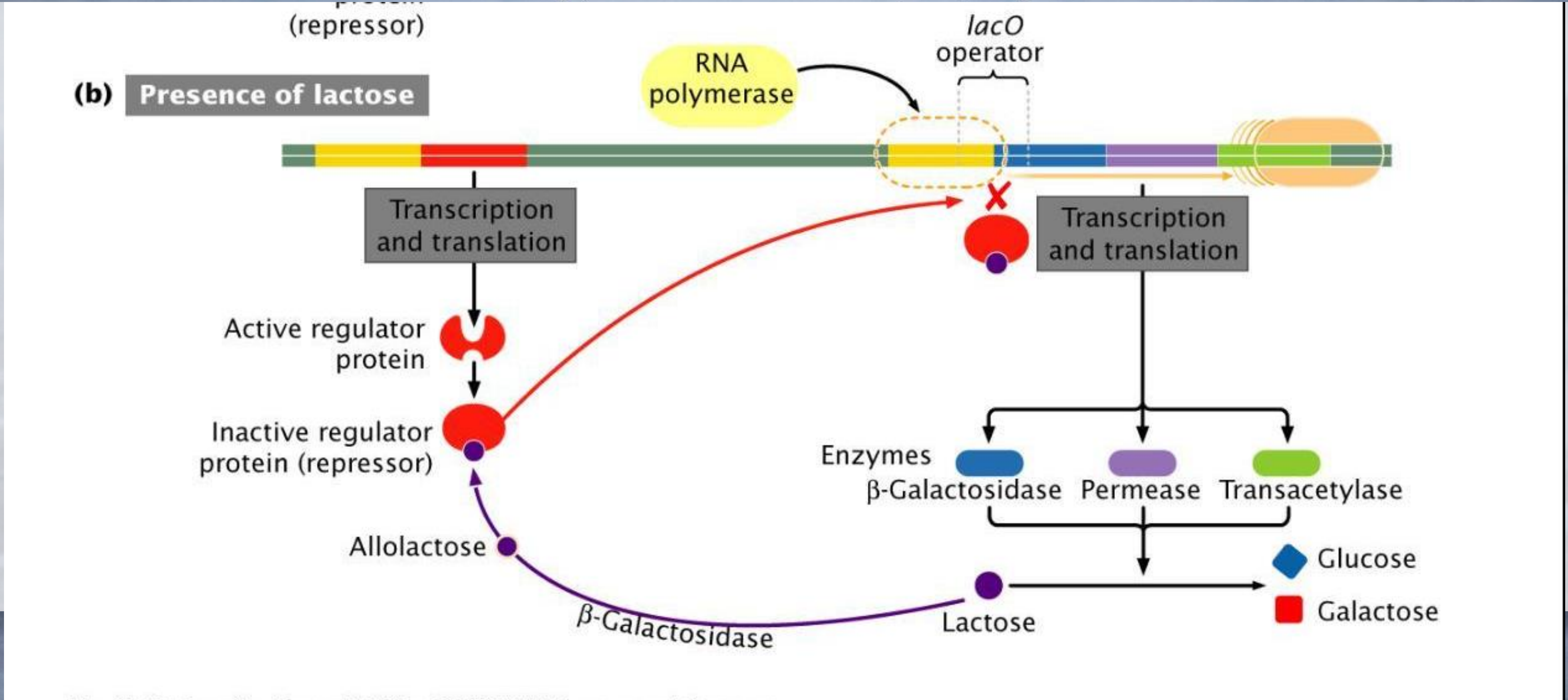
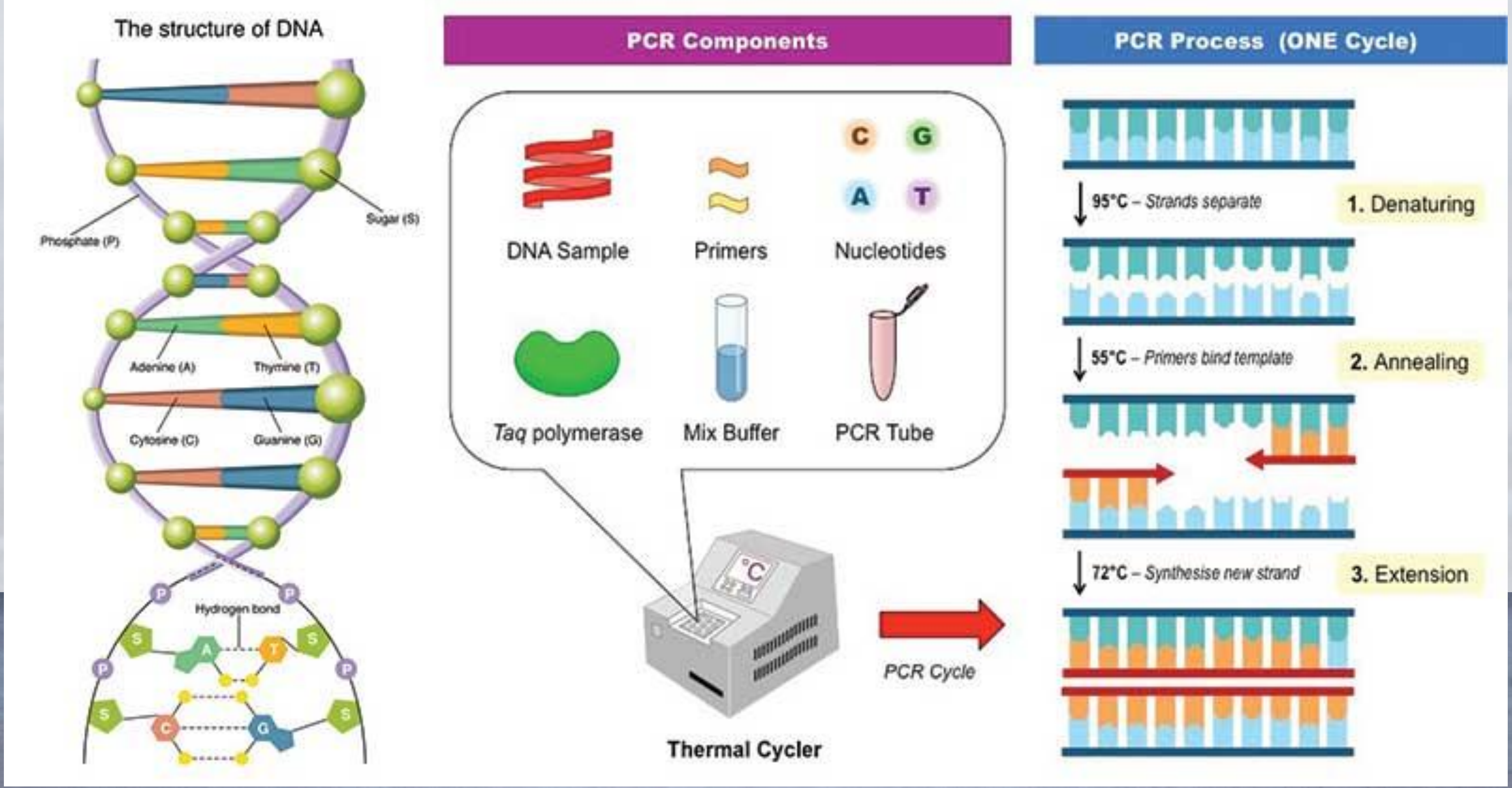


Fig_16-08 *Genetics, Second Edition* © 2005 W.H. Freeman and Company

DNA Technology: PCR

AP Biology Insta-Review @apbiopenguins



DNA Technology: Gel Electrophoresis

AP Biology Insta-Review @apbiopenguins

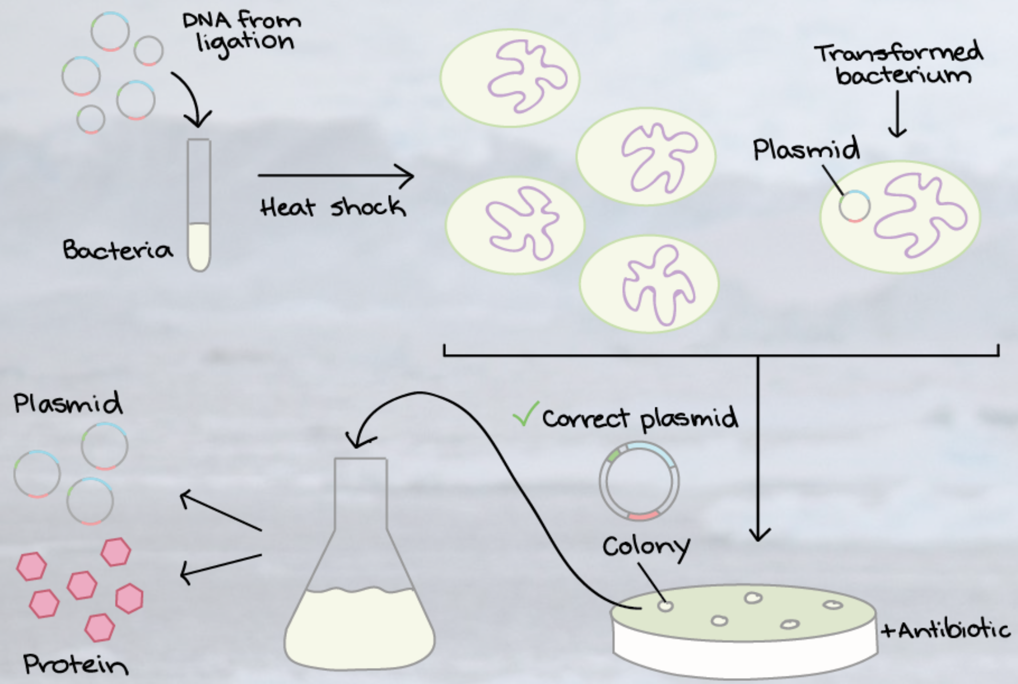
DNA samples loaded into wells

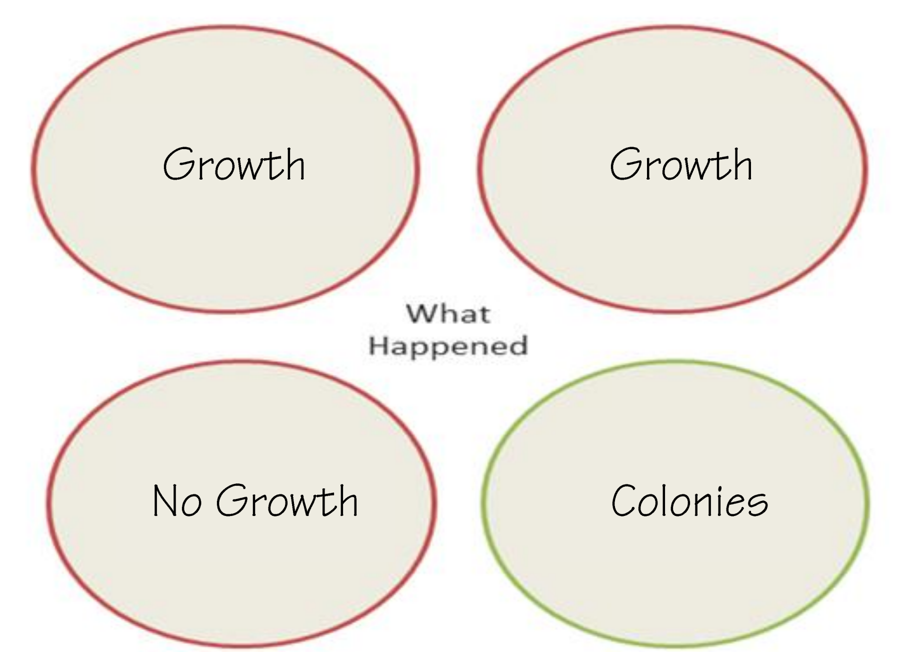
Power is turned on and DNA fragments migrate through gel.

The fragments are separated by size.

DNA Technology: Bacterial Transformation

AP Biology Insta-Review @apbiopenguins



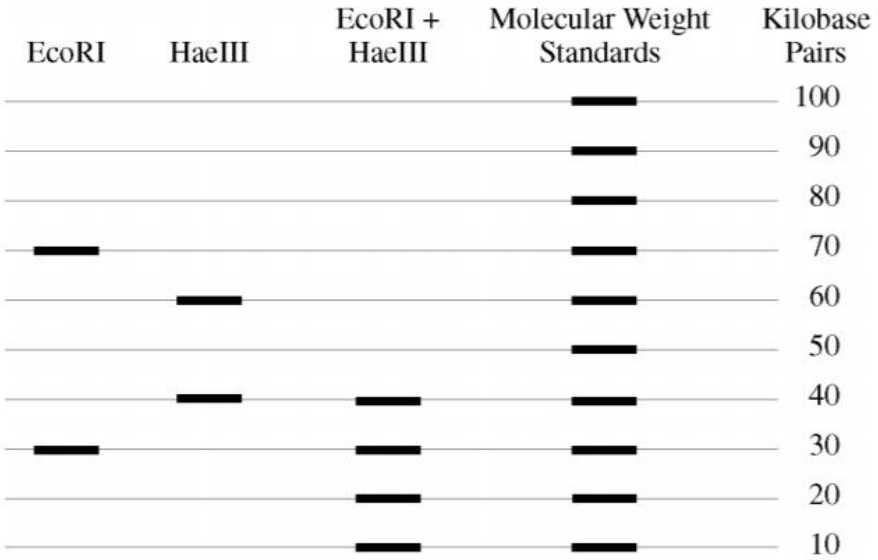


FRQ 2007 #4

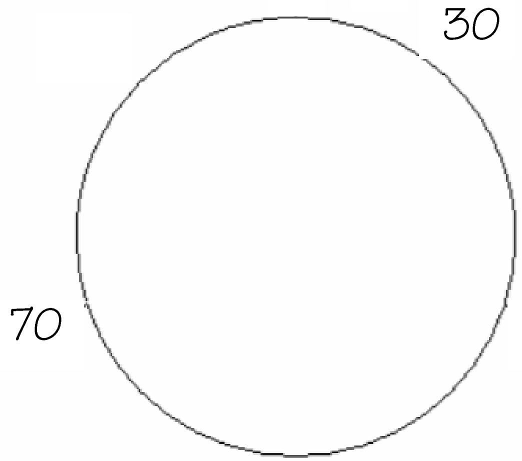
AP Biology Insta-Review @apbiopenguins

A bacterial plasmid is 100 kb in length. The plasmid DNA was digested to completion with two restriction enzymes in three separate treatments: EcoRI, HaeIII, and EcoRI + HaeIII (double digest). The fragments were then separated with electrophoresis, as shown.

RESULTS OF GEL ELECTROPHORESIS

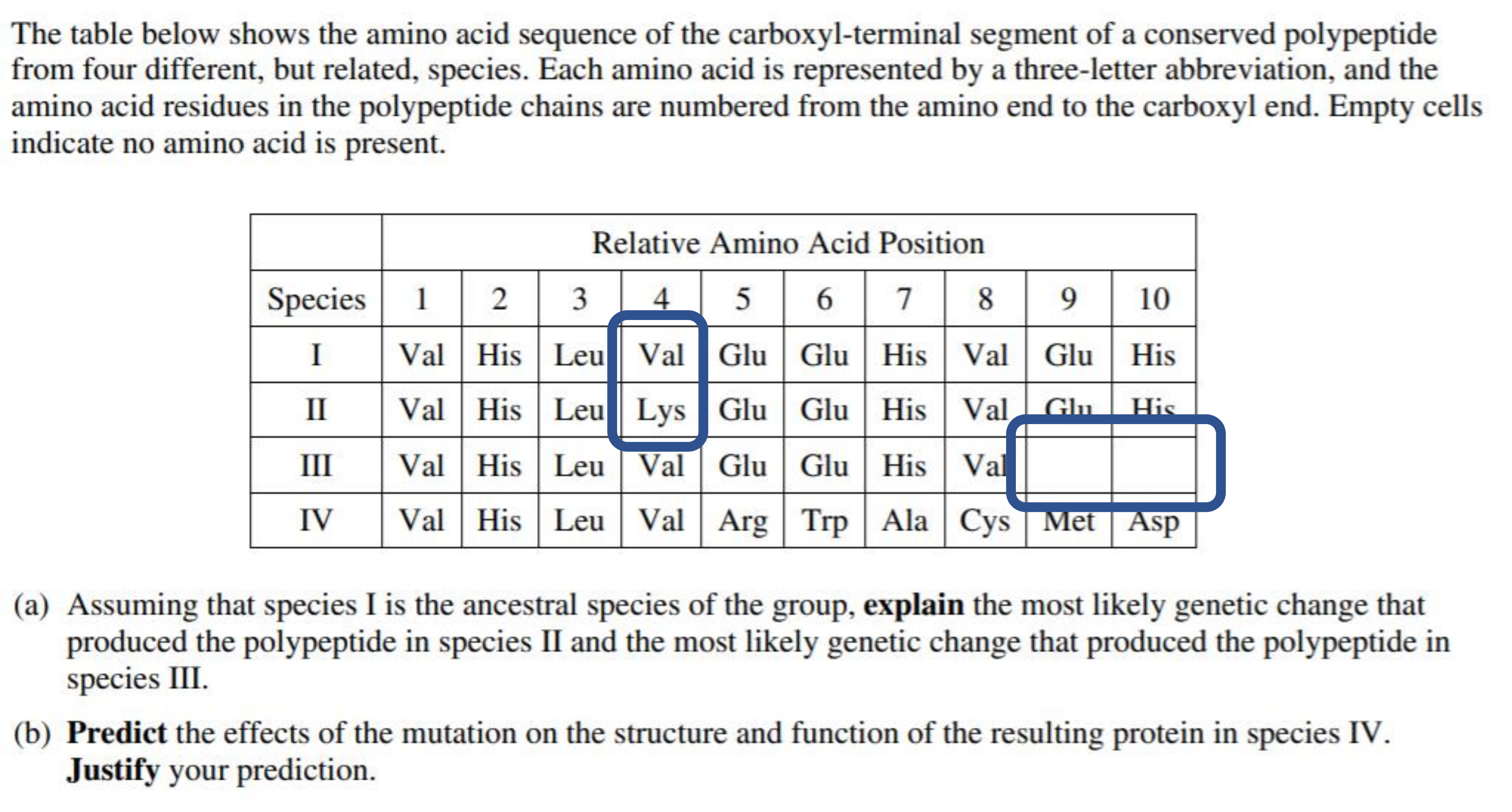


(a) Using the circle provided, **construct** a labeled diagram of the restriction map of the plasmid. **Explain** how you developed your map.



FRQ 2013 #5

AP Biology Insta-Review @apbiopenguins



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

(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.

FRQ 2016 #4

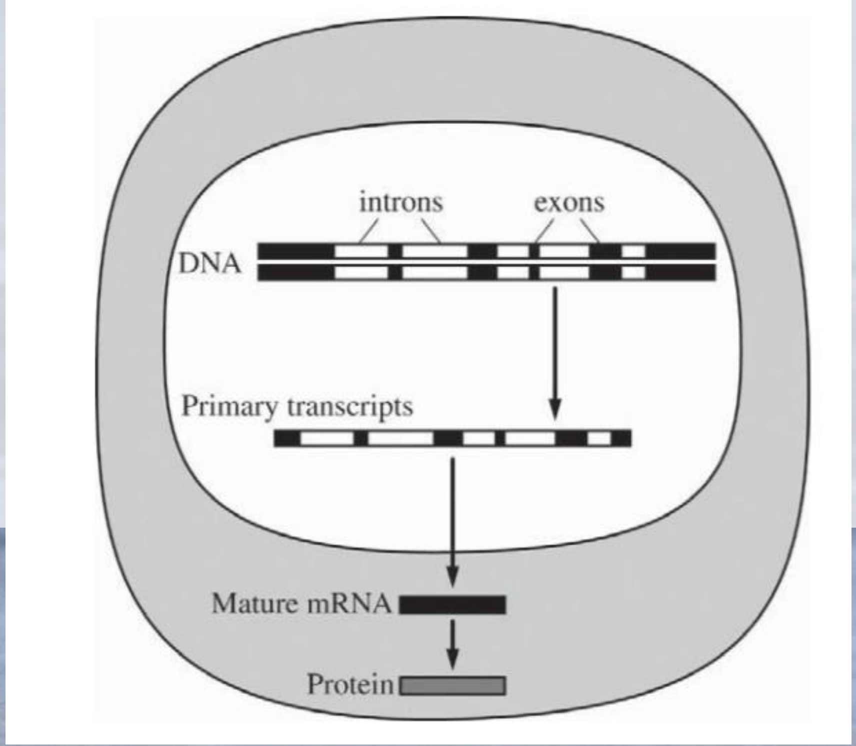
AP Biology Insta-Review @apbiopenguins

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

(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.

Describe process (1 point)

- Removal of introns
- RNA processing

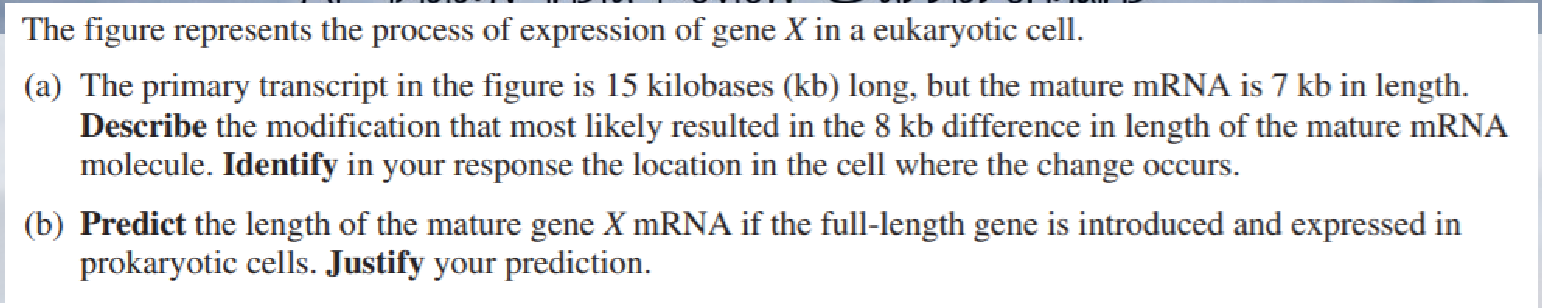


Identification (1 point)

- Nucleus

FRQ 2016 #4

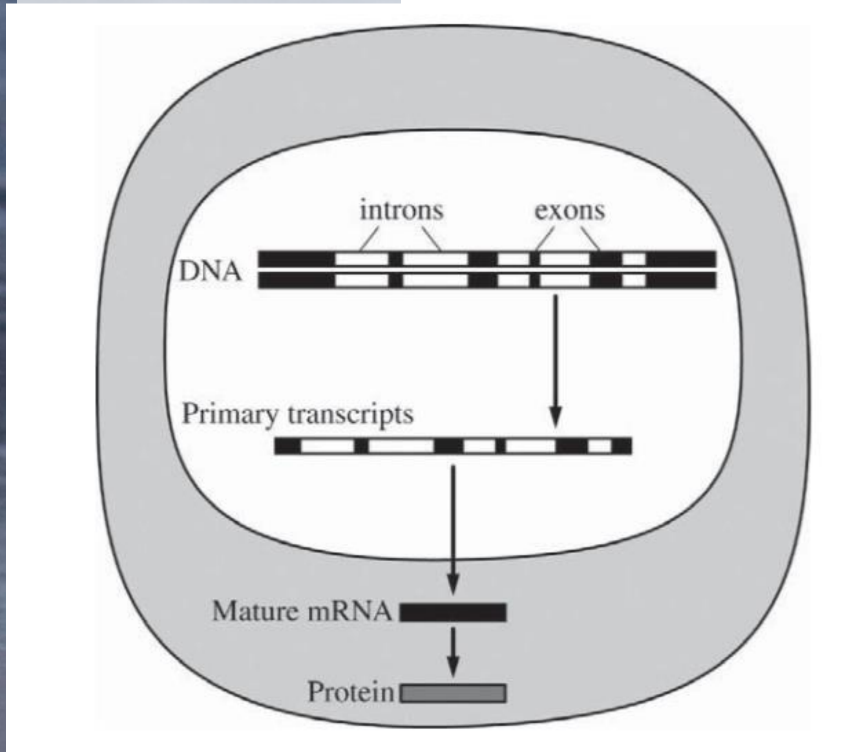
AP Biology Insta-Review @apbiopenguins

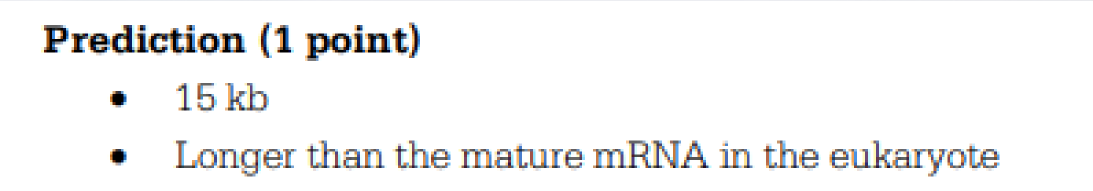


The figure represents the process of expression of gene *X* in a eukaryotic cell.

(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.

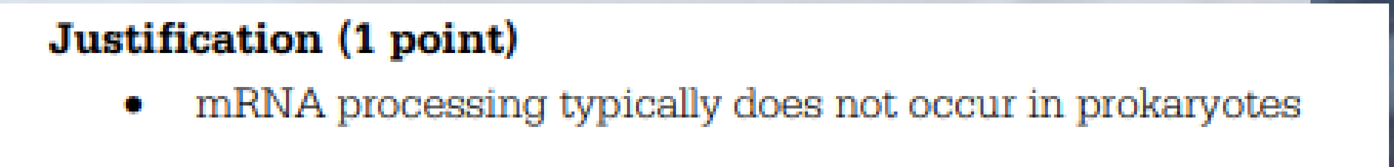
(b) **Predict** the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction.





Prediction (1 point)

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

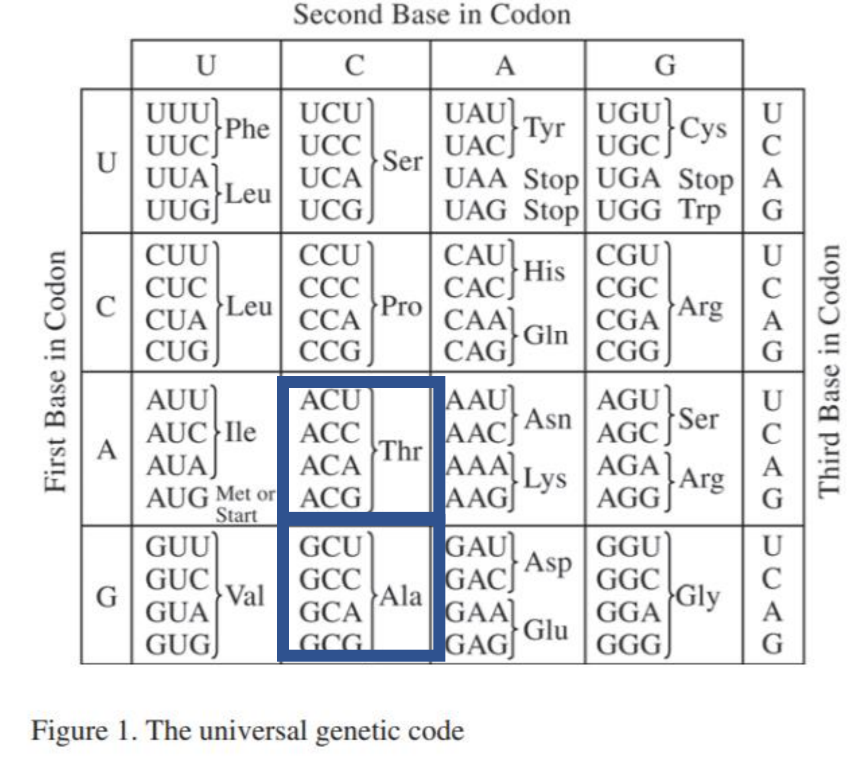


Justification (1 point)

- mRNA processing typically does not occur in prokaryotes

FRQ 2017 #3

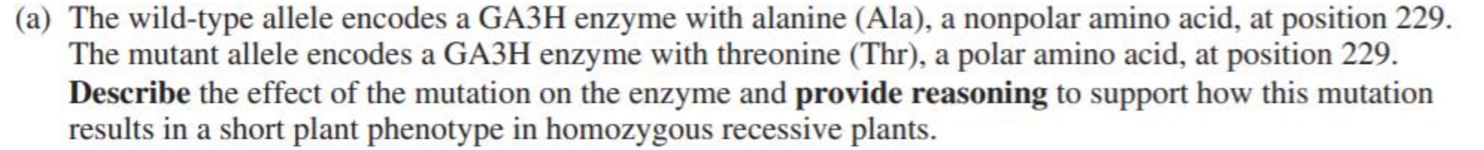
AP Biology Insta-Review @apbiopenguins



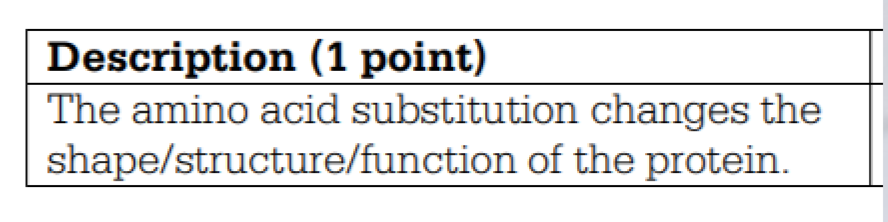
Second Base in Codon

First Base in Codon	U	C	A	G	Third Base in Codon
U	UUU UUC } Phe UUA UUG } Leu	UCU UCC UCA UCG } Ser	UAU UAC } Tyr UAA Stop UAG Stop	UGU UGC } Cys UGA Stop UGG Trp	U C A G
C	CUU CUC CUA CUG } Leu	CCU CCC CCA CCG } Pro	CAU CAC } His CAA CAG } Gln	CGU CGC CGA CGG } Arg	U C A G
A	AUU AUC AUA } Ile AUG Met or Start	ACU ACC ACA ACG } Thr	AAU AAC } Asn AAA AAG } Lys	AGU AGC } Ser AGA AGG } Arg	U C A G
G	GUU GUC GUA GUG } Val	GCU GCC GCA GCG } Ala	GAU GAC } Asp GAA GAG } Glu	GGU GGC GGA GGG } Gly	U C A G

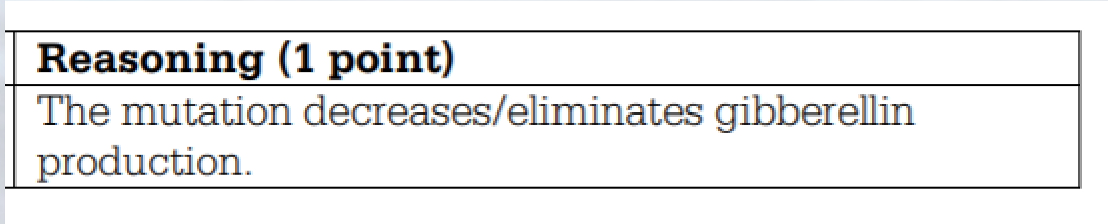
Figure 1. The universal genetic code



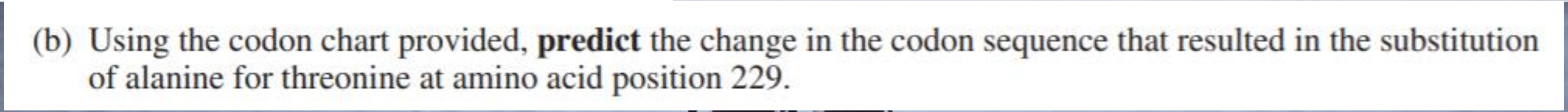
(a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.



Description (1 point)
The amino acid substitution changes the shape/structure/function of the protein.



Reasoning (1 point)
The mutation decreases/eliminates gibberellin production.



(b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.

FRQ 2019 #1

AP Biology Insta-Review @apbiopenguins

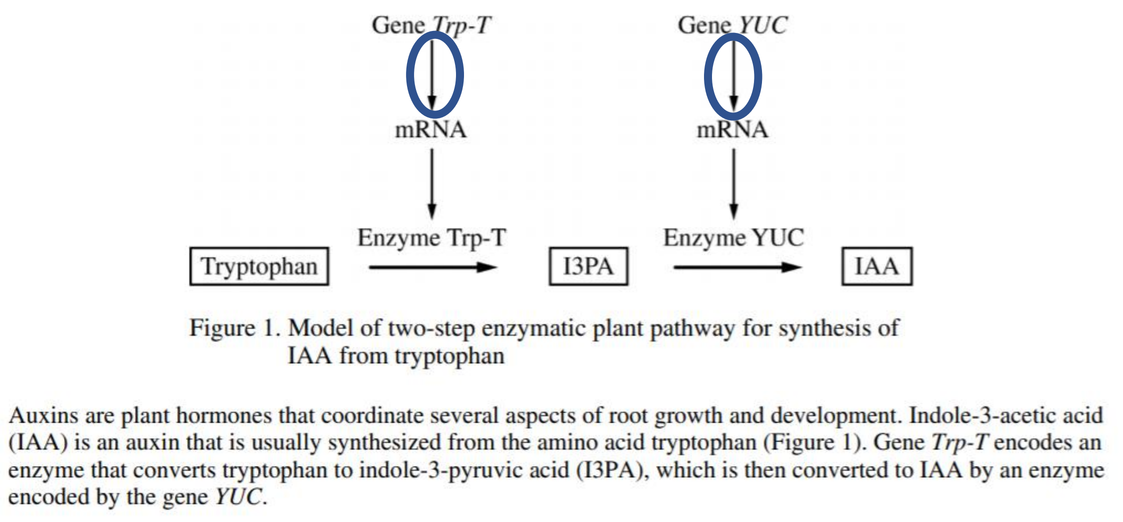
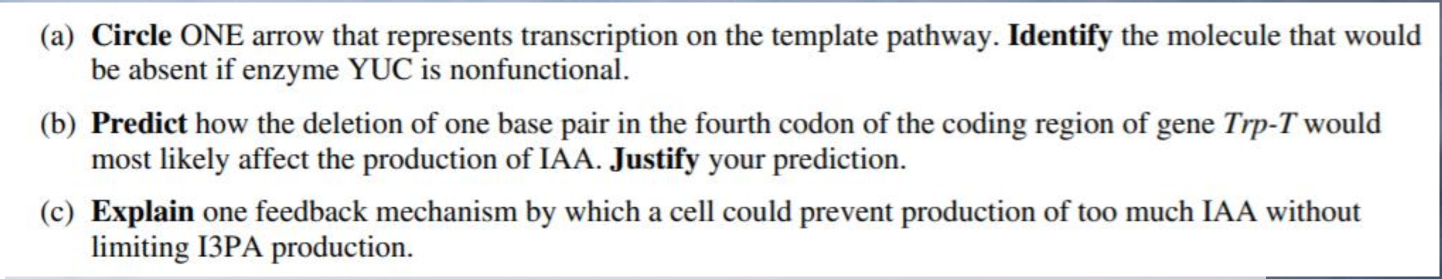


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

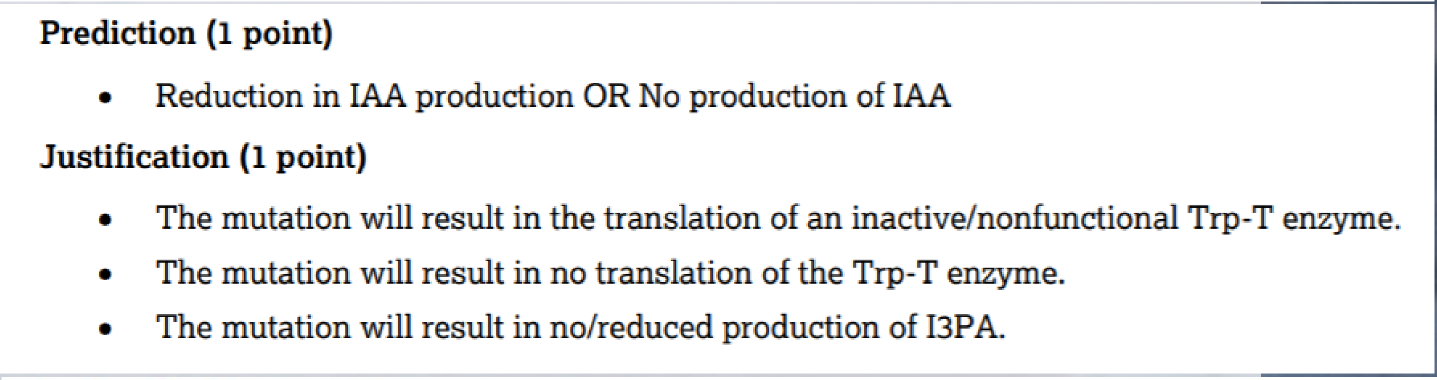
Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*.



(a) **Circle** ONE arrow that represents transcription on the template pathway. **Identify** the molecule that would be absent if enzyme YUC is nonfunctional.

(b) **Predict** how the deletion of one base pair in the fourth codon of the coding region of gene *Trp-T* would most likely affect the production of IAA. **Justify** your prediction.

(c) **Explain** one feedback mechanism by which a cell could prevent production of too much IAA without limiting I3PA production.

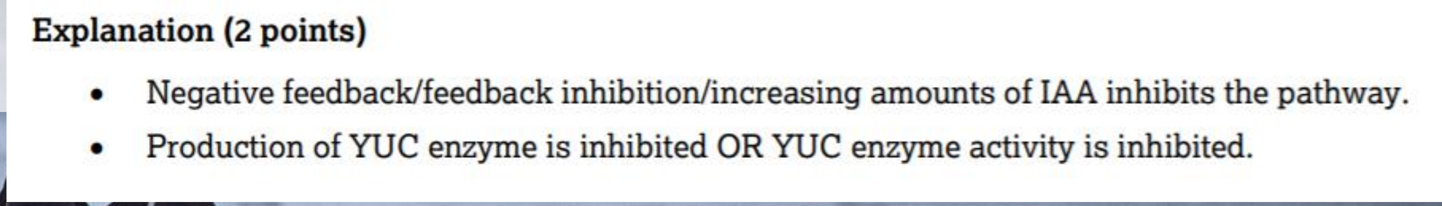


Prediction (1 point)

- Reduction in IAA production OR No production of IAA

Justification (1 point)

- The mutation will result in the translation of an inactive/nonfunctional Trp-T enzyme.
- The mutation will result in no translation of the Trp-T enzyme.
- The mutation will result in no/reduced production of I3PA.

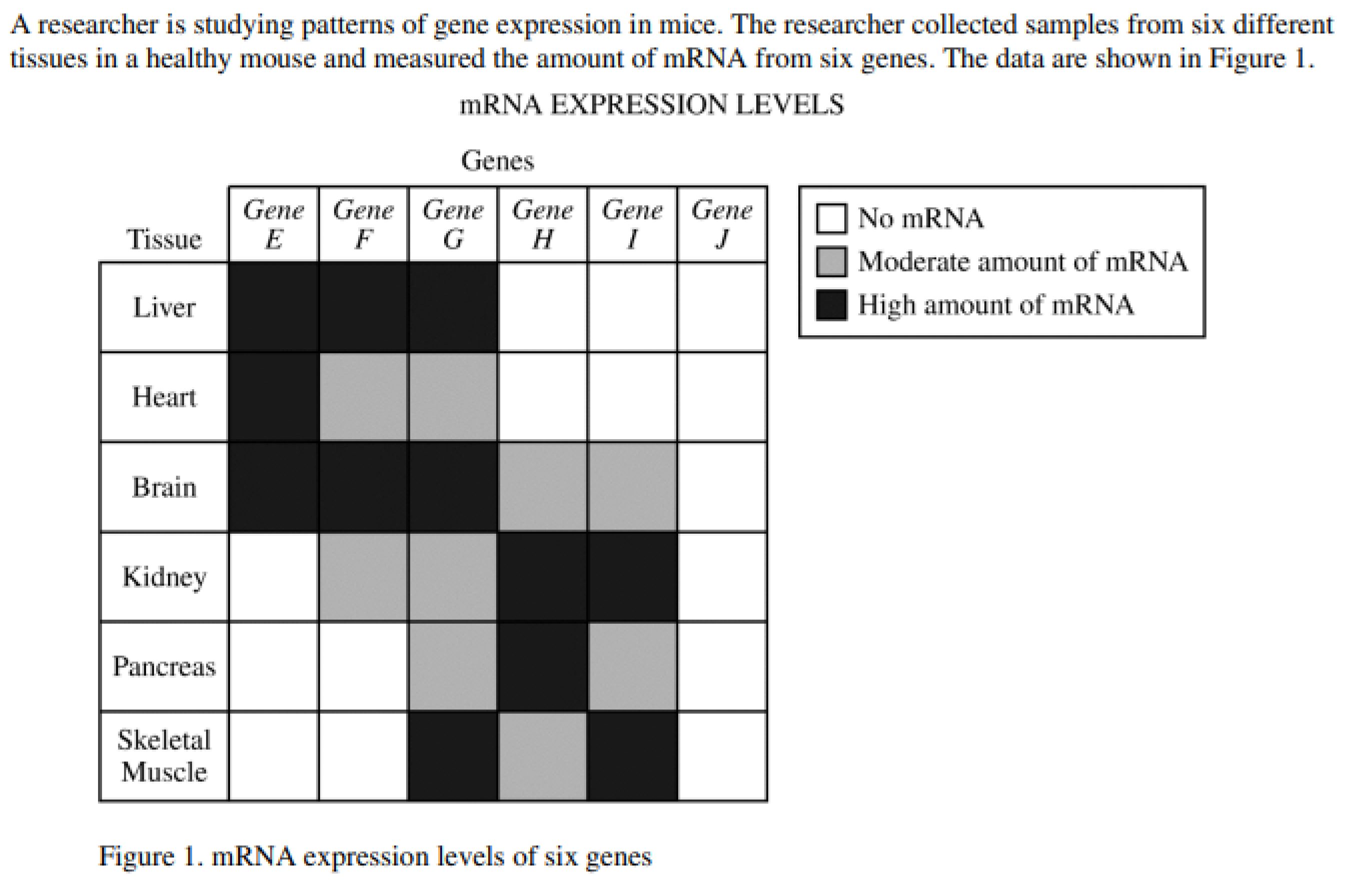


Explanation (2 points)

- Negative feedback/feedback inhibition/increasing amounts of IAA inhibits the pathway.
- Production of YUC enzyme is inhibited OR YUC enzyme activity is inhibited.

FRQ 2019 #7

AP Biology Insta-Review @apbiopenguins



A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

mRNA EXPRESSION LEVELS

	Genes					
Tissue	*Gene E*	*Gene F*	*Gene G*	*Gene H*	*Gene I*	*Gene J*
Liver	■	■	■	□	□	□
Heart	■	▨	▨	□	□	□
Brain	■	■	■	▨	▨	□
Kidney	□	▨	▨	■	■	□
Pancreas	□	□	▨	■	▨	□
Skeletal Muscle	□	□	■	▨	■	□

□	No mRNA
▨	Moderate amount of mRNA
■	High amount of mRNA

Figure 1. mRNA expression levels of six genes

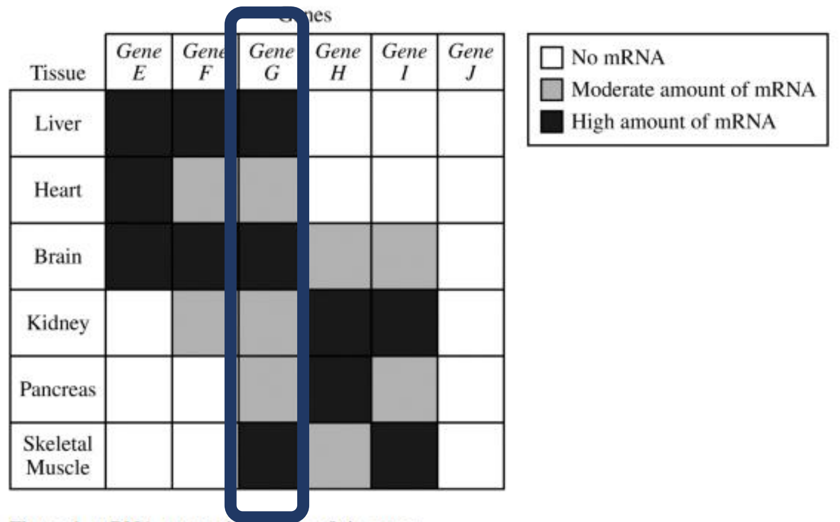
FRQ 2019 #7

AP Biology Insta-Review @apbiopenguins

(a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.

Identification (1 point)

- *Gene G*



Tissue	Gene E	Gene F	Gene G	Gene H	Gene I	Gene J
Liver	■	■	■	□	□	□
Heart	■	▨	▨	□	□	□
Brain	■	■	■	▨	▨	□
Kidney	□	▨	▨	■	■	□
Pancreas	□	□	▨	■	▨	□
Skeletal Muscle	□	□	■	▨	■	□

□ No mRNA
▨ Moderate amount of mRNA
■ High amount of mRNA

Figure 1. mRNA expression levels of six genes

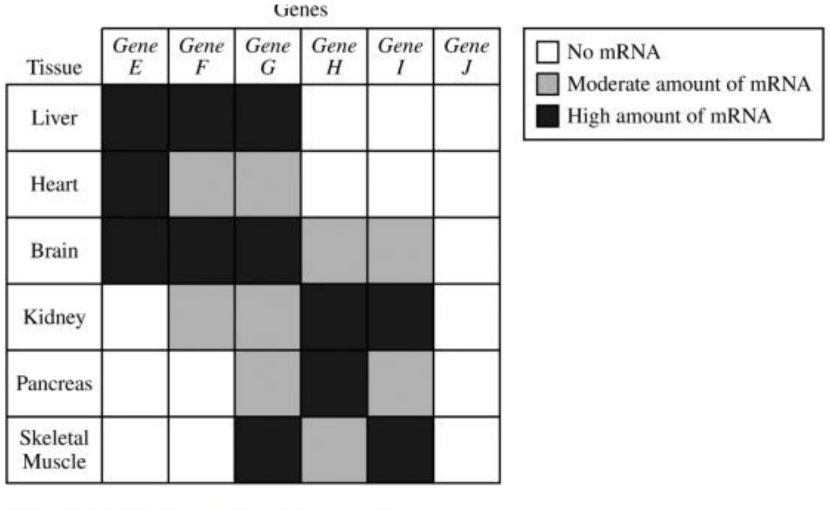
Reasoning (1 point)

- (*Gene G*) is the only gene expressed in all (six) tissues, AND glycolysis occurs in all (six) tissues.
- (*Gene G*) mRNA is the only mRNA present in all (six) tissues, AND glycolysis occurs in all (six) tissues.

FRQ 2019 #7

AP Biology Insta-Review @apbiopenguins

(b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.



Genes

Tissue	*Gene E*	*Gene F*	*Gene G*	*Gene H*	*Gene I*	*Gene J*
Liver	■	■	■	☐	☐	☐
Heart	■	▨	▨	☐	☐	☐
Brain	■	■	■	▨	▨	☐
Kidney	☐	▨	▨	■	■	☐
Pancreas	☐	☐	▨	■	▨	☐
Skeletal Muscle	☐	☐	■	▨	■	☐

☐ No mRNA
▨ Moderate amount of mRNA
■ High amount of mRNA

Figure 1. mRNA expression levels of six genes

Reasoning (1 point)

- The mRNA is not exported from the nucleus.
- *Gene H* mRNA is not translated/RNA interference prevent(s) translation.
- Post-transcriptional modifications.