AP Bio Unit Reviews

Gene Expression & Regulation

@apbiopenguins

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Daily Review on IG stories

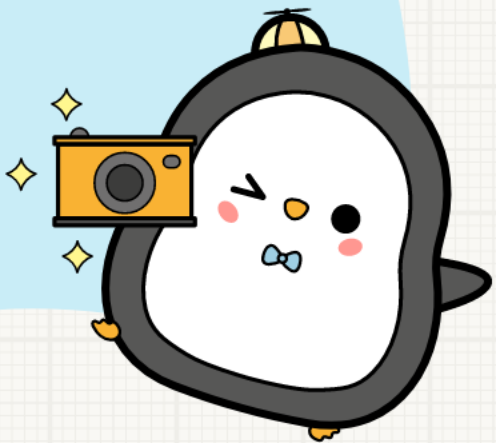
374 page Review Guide on Weebly

Recorded FRQ Fridays on YouTube

120+ Quizizz Games on Weebly

Review PowerPoints on Weebly

Weebly: www.apbiopenguins.weebly.com



Today's Plan

Molecular Genetics
Operons & BioTechnology
Practice Questions
Unit 6 Q&A

Central Dogma

replication

DNA → RNA → Polypeptide

transcription

translation

Retroviruses will use reverse transcriptase to synthesize DNA from their RNA genome

Replication

Location

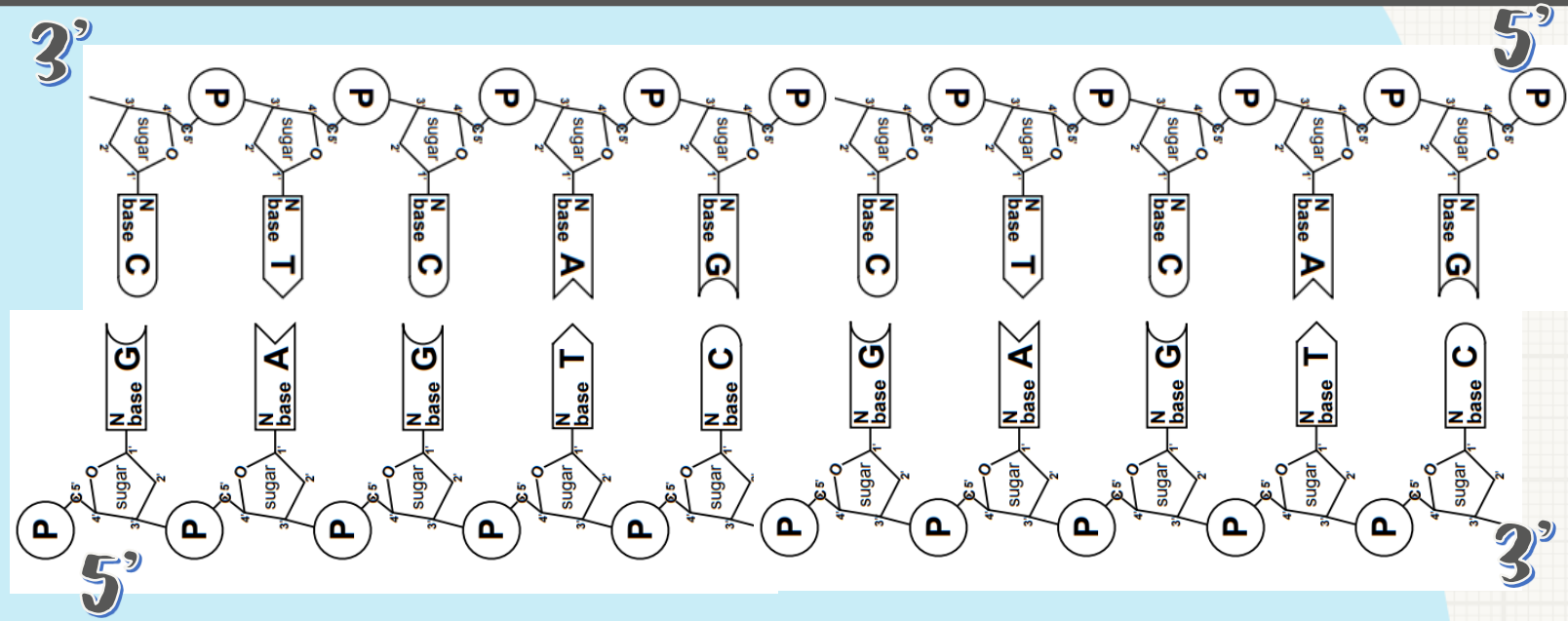
- Eukaryotes: nucleus
- Prokaryotes: nucleoid

Structure

- Eukaryotes: multiple linear
- Prokaryotes: single circular

Reminders about DNA:

- DNA made up of:
  - nitrogenous base (A, T, C, G)
  - pentose sugar (deoxyribose)
  - phosphate group
- Purine (A/G) have a double ring structure
- Pyrimidine (C/T) have a single ring structure
- Base Pair Rules
  - A & T with 2 H bonds
  - C & G with 3 H bonds



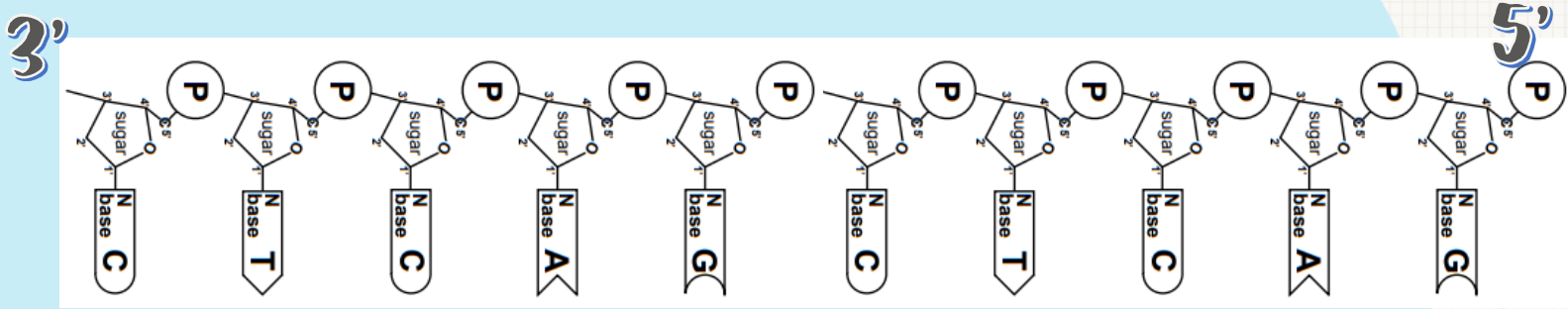
- Sidedness
  - 5' end: phosphate
  - 3' end: hydroxyl group
- Directionality
  - Read 3' to 5'
  - Synthesize 5' to 3'

(Remember ANTIPARALLEL)

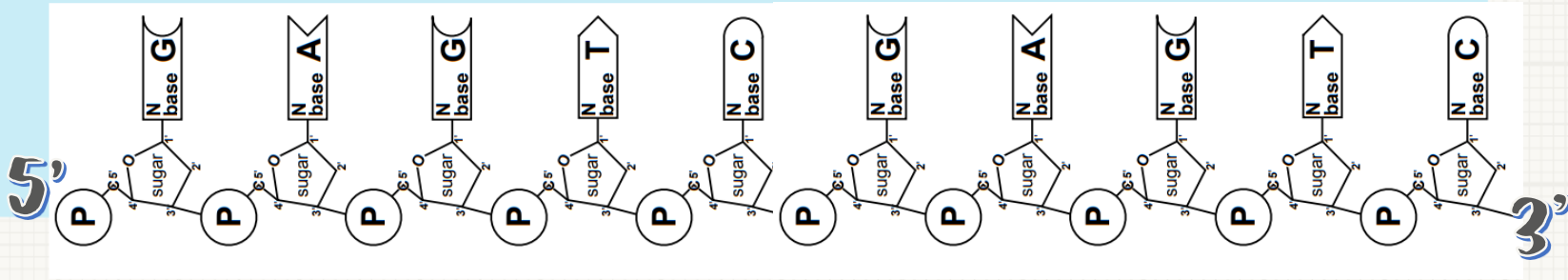
Replication

Important Enzymes

- Helicase unwinds the DNA strands
- Topoisomerase relaxes supercoiling in front of the replication fork.



Helicase



Replication

Important Enzymes

- Helicase unwinds the DNA strands
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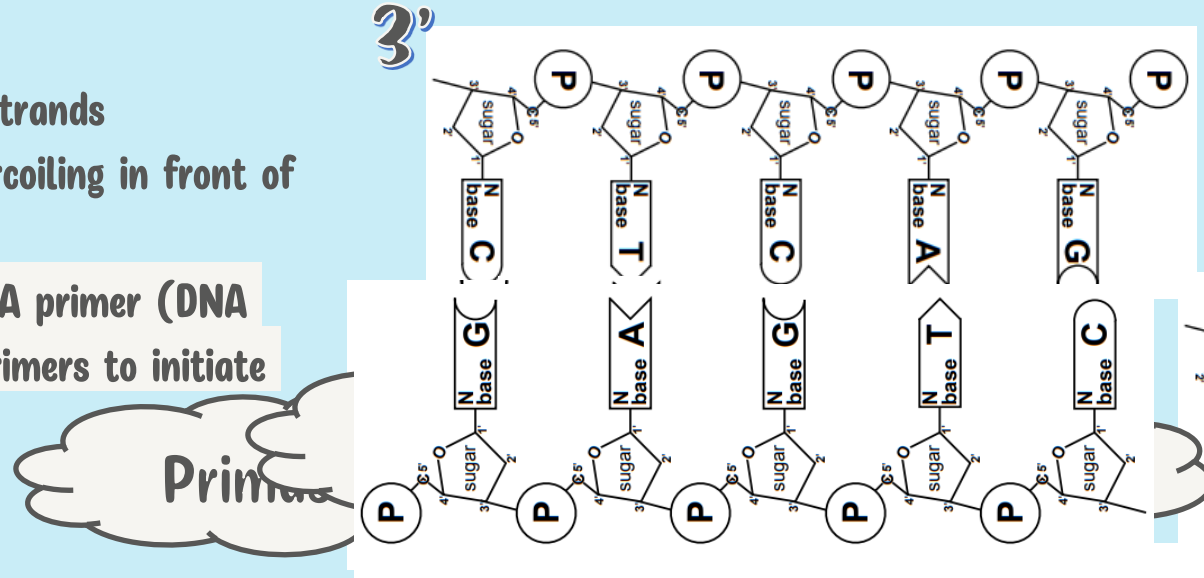
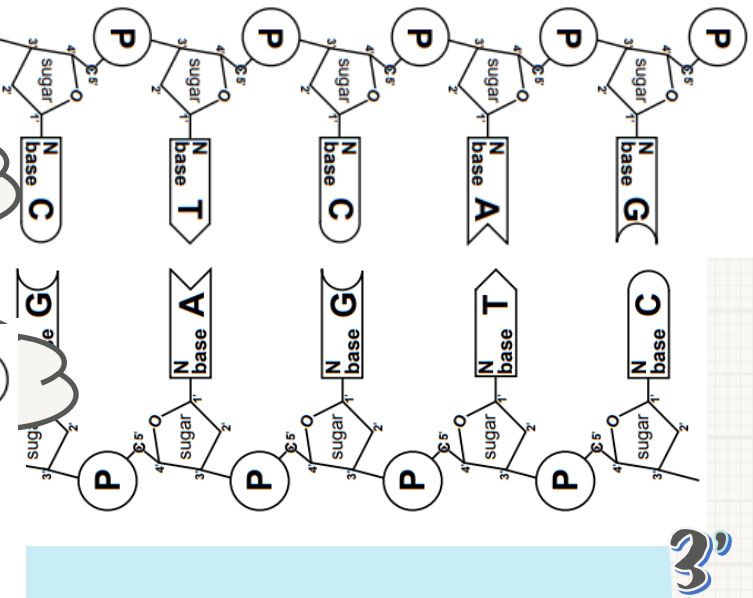
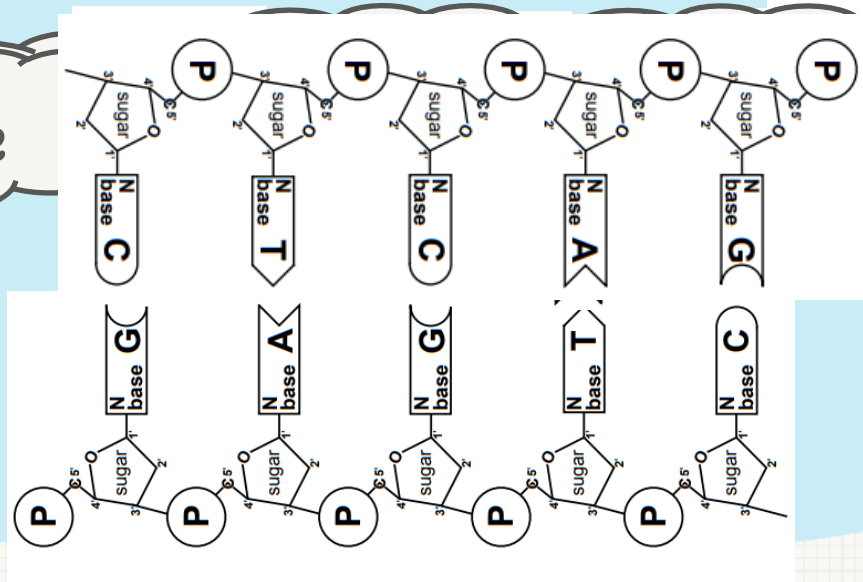
- Primase synthesizes the RNA primer (DNA polymerase requires RNA primers to initiate DNA synthesis).







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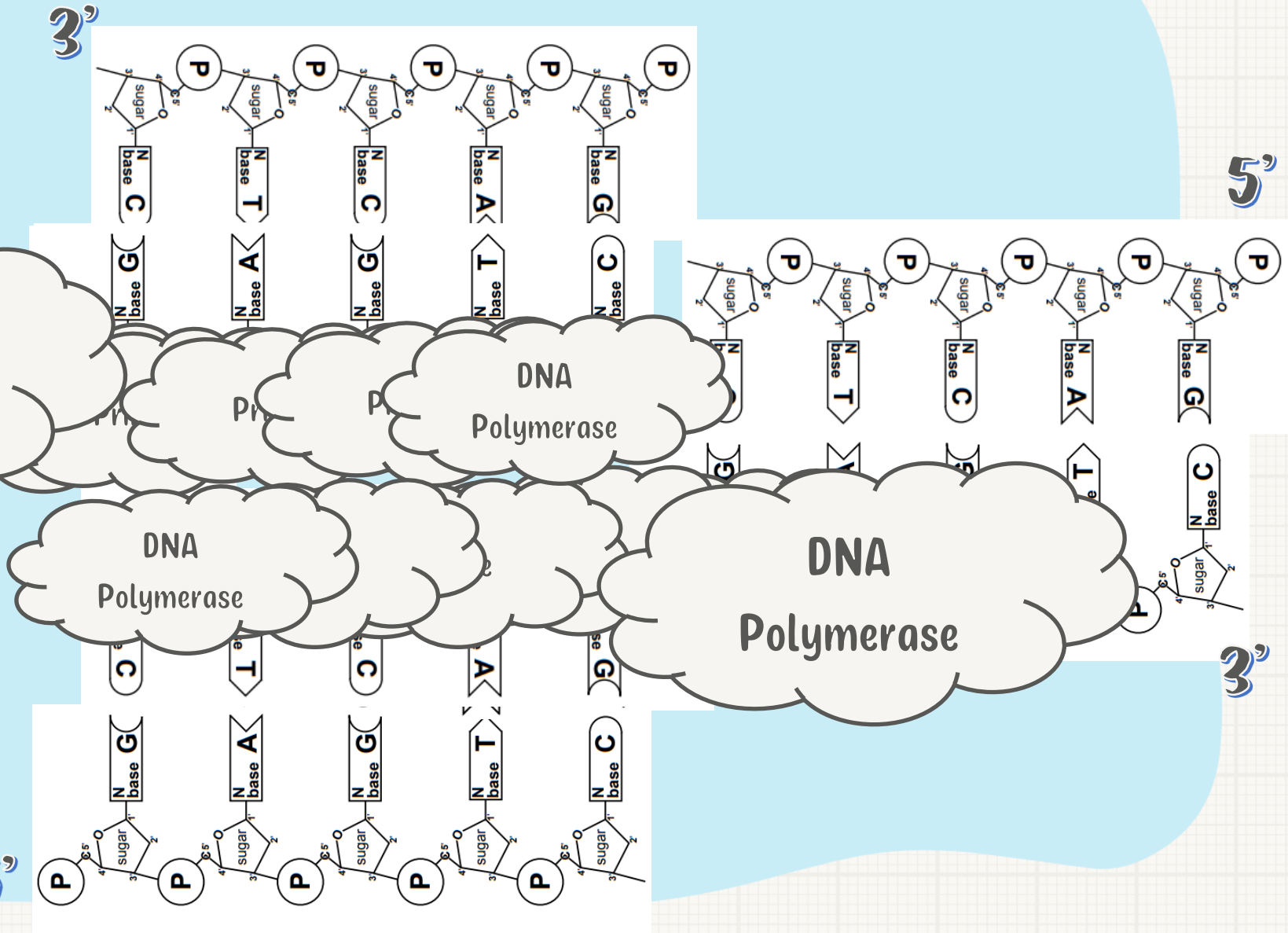

Replication

Important Enzymes

- Helicase unwinds the DNA strands
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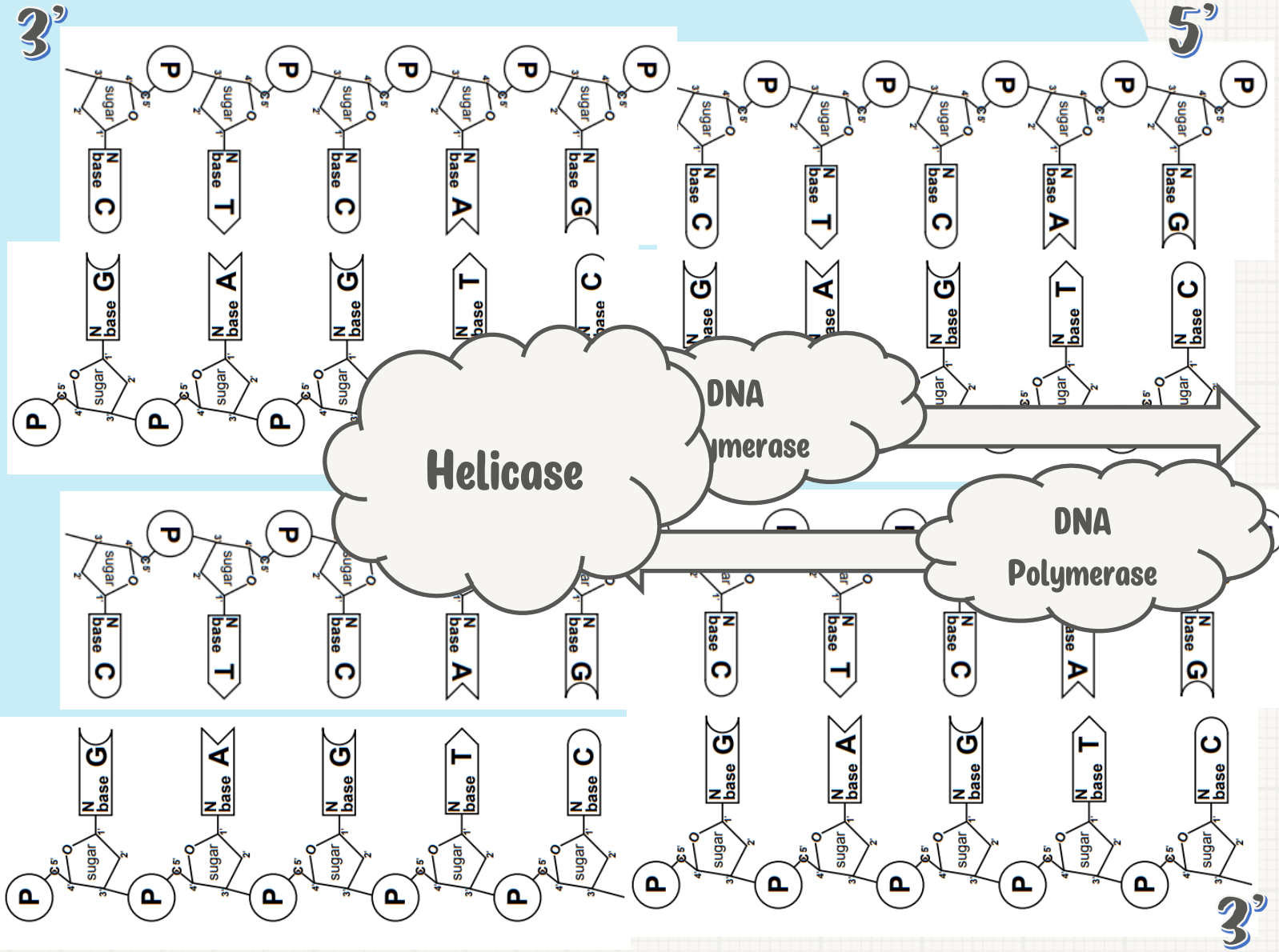
- Primase synthesizes the RNA primer (DNA polymerase requires RNA primers to initiate DNA synthesis).
- DNA polymerase synthesizes new strands of DNA continuously on the leading strand and discontinuously on the lagging strand.



Replication

Important Enzymes

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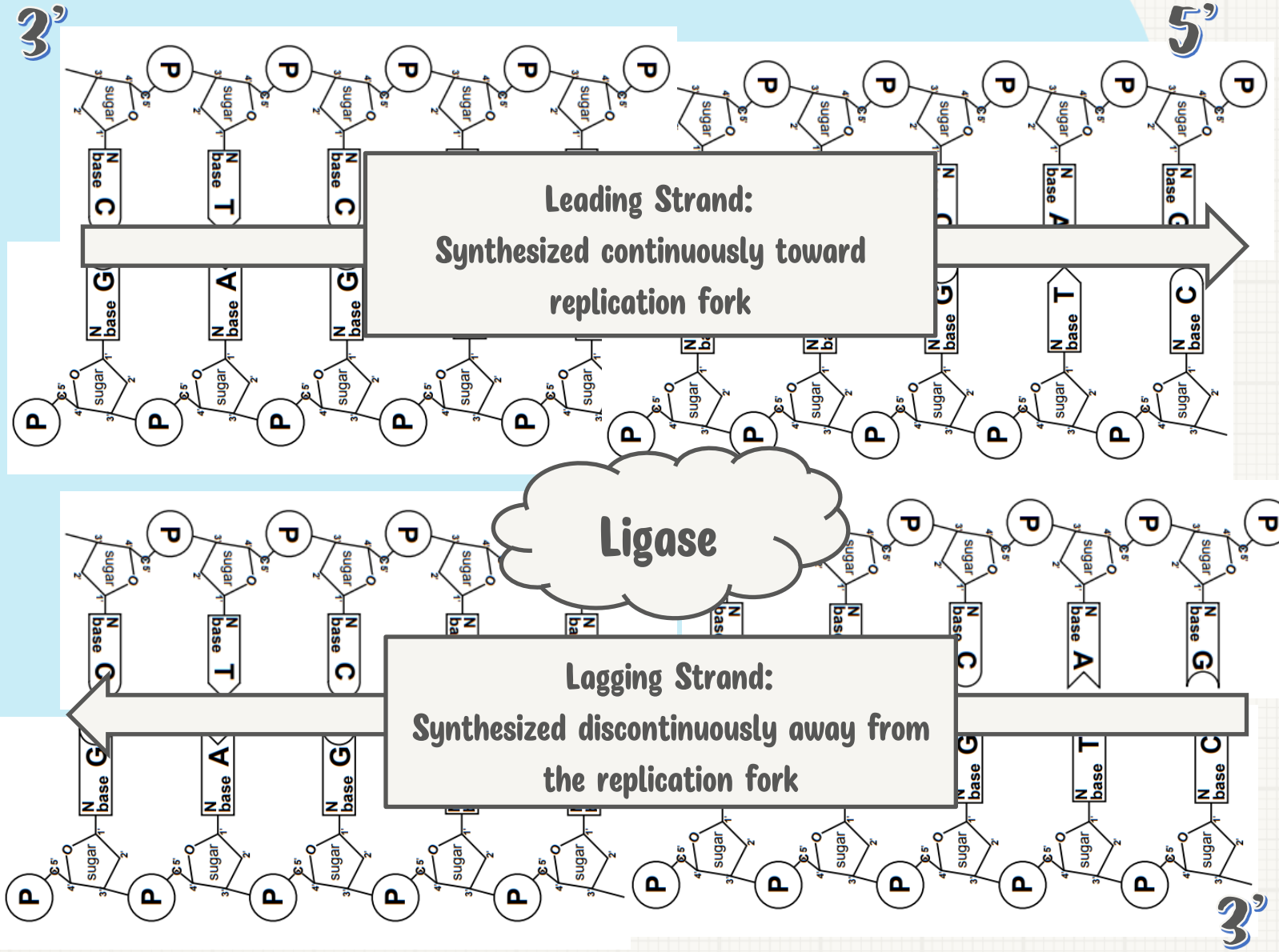
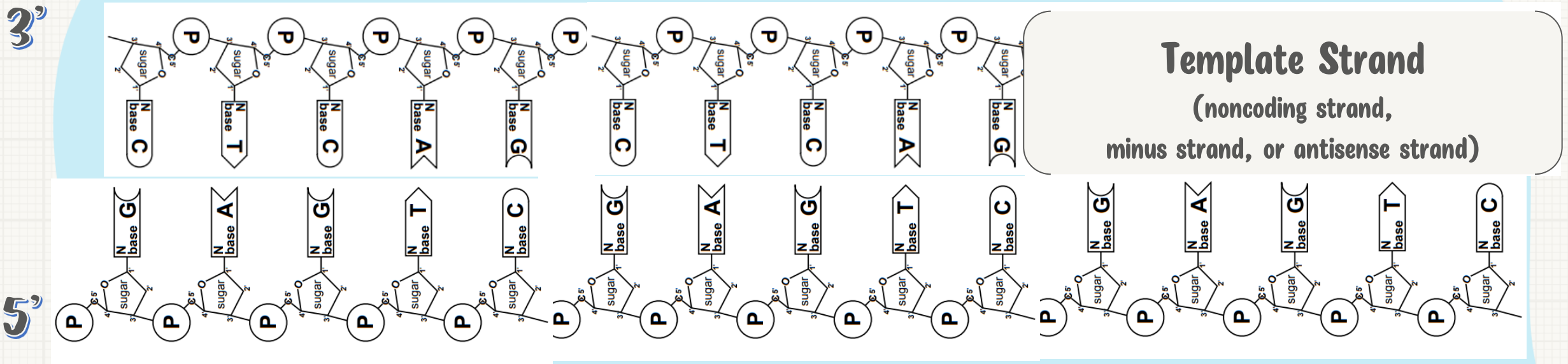
- Topoisomerase relaxes supercoiling in front of the replication fork.
- Primase synthesizes the RNA primer (DNA polymerase requires RNA primers to initiate DNA synthesis).
- DNA polymerase synthesizes new strands of DNA continuously on the leading strand and discontinuously on the lagging strand.
- Ligase joins the fragments on the lagging strand.



Transcription



Location

- Eukaryotes: nucleus
- Prokaryotes: nucleoid (cytosol)

Reminders about RNA:

- DNA made up of:
  - nitrogenous base (A, U, C, G)
  - pentose sugar (ribose)
  - phosphate group
- Purine (A/G) have a double ring structure
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- Base Pair Rules
  - A & T(DNA)/U(RNA) with 2 H bonds
  - C & G with 3 H bonds
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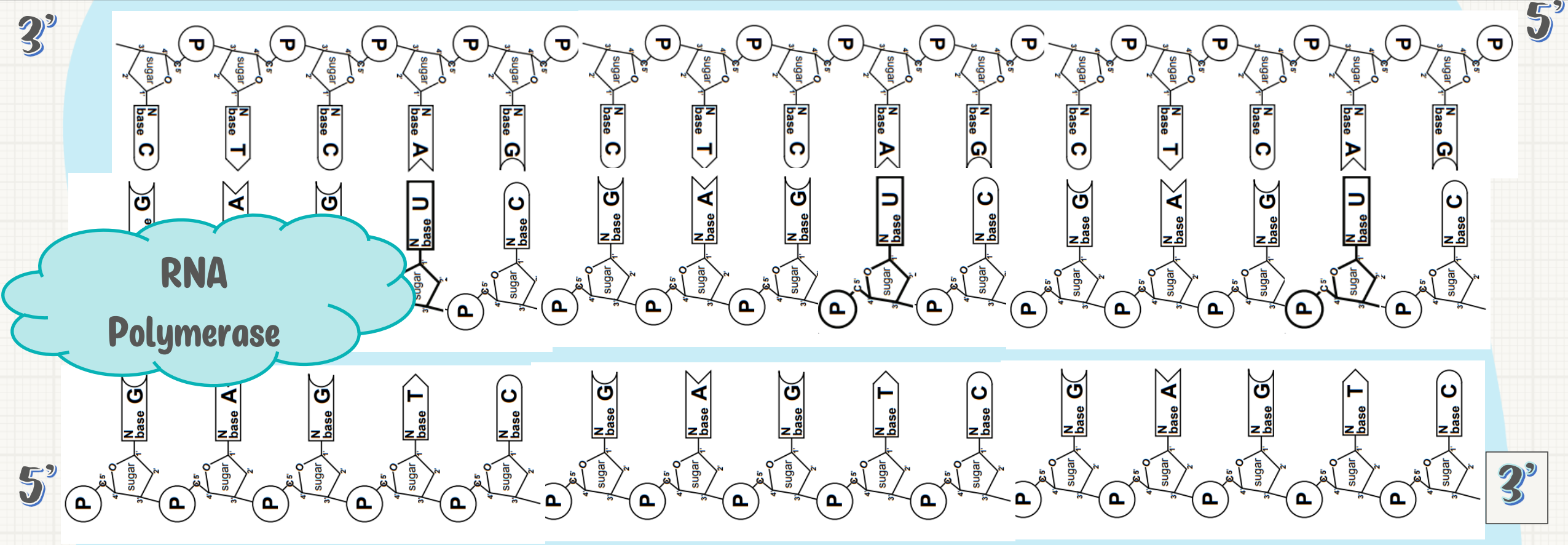
Transcription



Important Enzyme & Components

- RNA polymerase synthesizes mRNA molecules in the 5' to 3' direction by reading the template DNA strand in the 3' to 5' direction.
- Promoter: site where RNA polymerase binds to start transcription
- Transcription Factors: activators/inhibitors to turn on/off gene expression

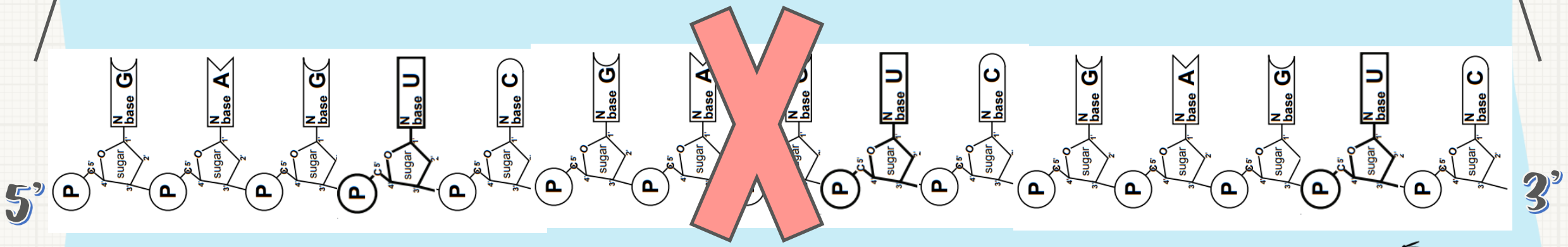
Post-Transcriptional Modifications

5' Guanine Cap

- Signals the "start" of the mRNA transcript for ribosome to bind
- Facilitates export from nucleus

Poly-A Tail

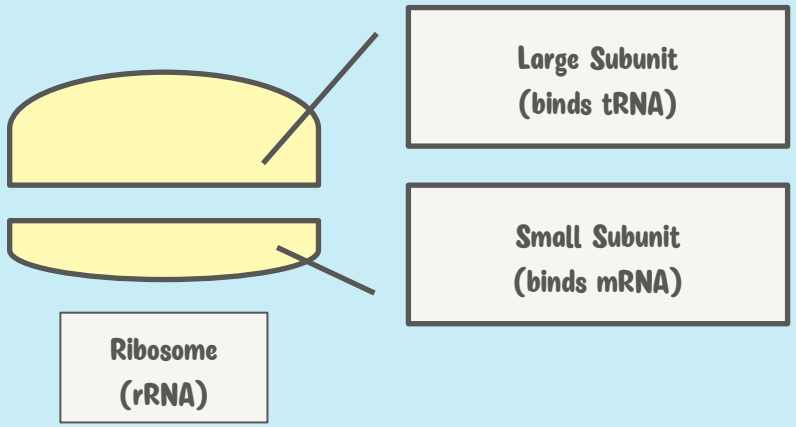
- Inhibits degradation from hydrolytic enzymes in cytosol



Splicing

- Removal of introns from pre-mRNA transcript

Translation



Location

- Eukaryotes: cytosol/rough ER
- Prokaryotes: cytosol

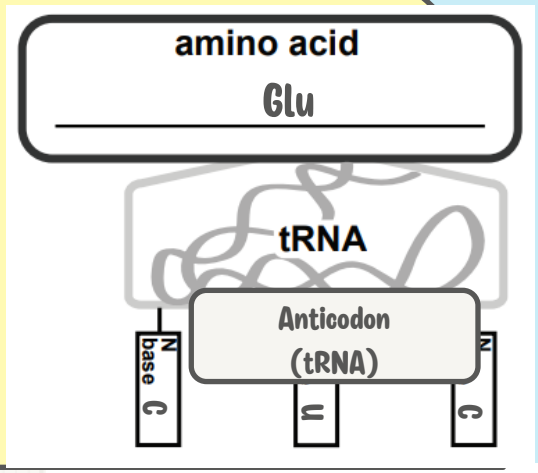
Steps of Translation

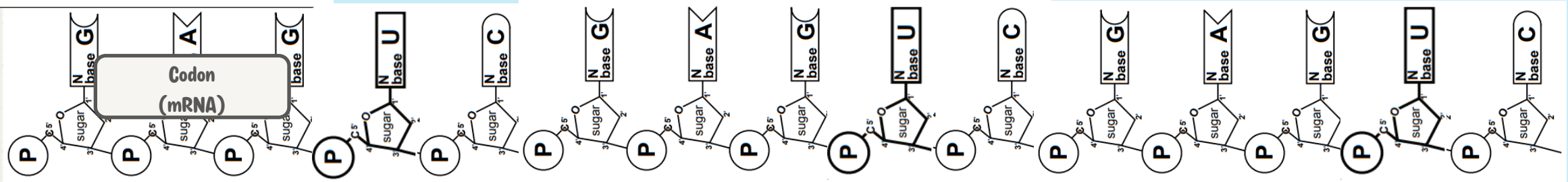
- Initiation: start codon (AUG)
- Elongation: base pair between tRNA/mRNA with amino acid added
- Termination: stop codon (UAG, UAA, UGA)

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

Translation





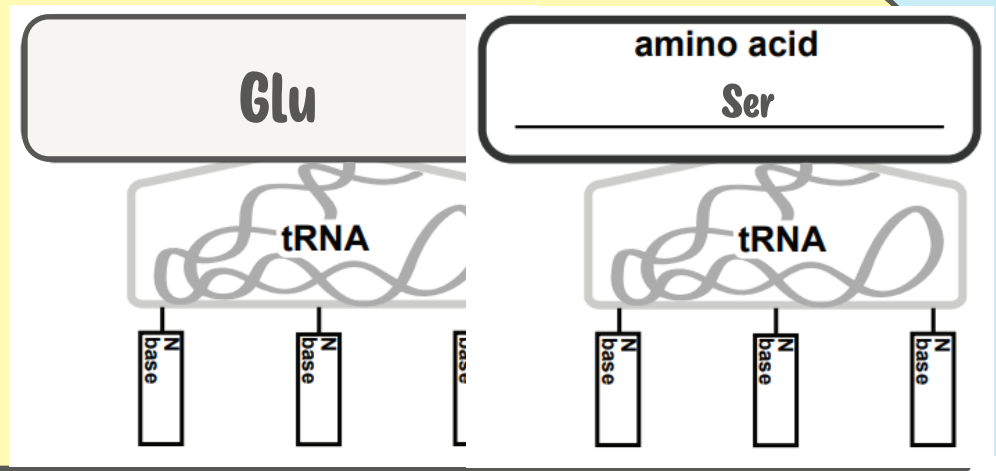
Second Base in Codon

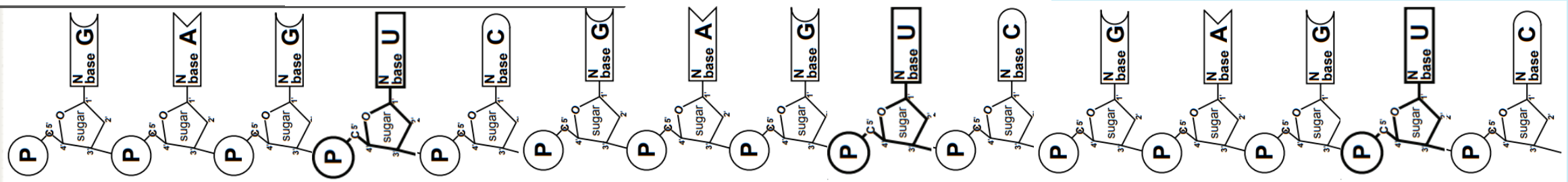
First Base in Codon	U	C	A	G	Third Base in Codon
U	UUU Phe UUC UUA Leu UUG	UCU UCC UCA Ser UCG	UAU Tyr UAC UAA Stop UAG Stop	UGU Cys UGC UGA Stop UGG Trp	U C A G
C	CUU CUC CUA Leu CUG	CCU CCC CCA Pro CCG	CAU His CAC CAA Gln CAG	CGU CGC CGA Arg CGG	U C A G
A	AUU AUC Ile AUA AUG Met or Start	ACU ACC ACA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

Translation

Second Base in Codon

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





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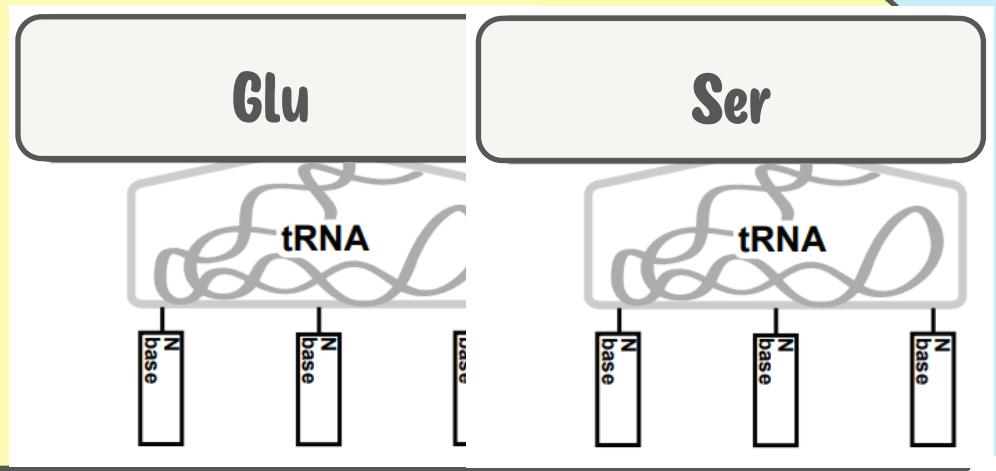

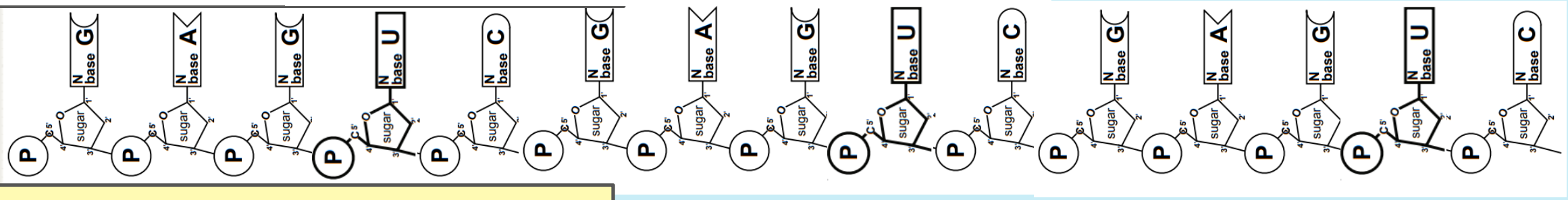

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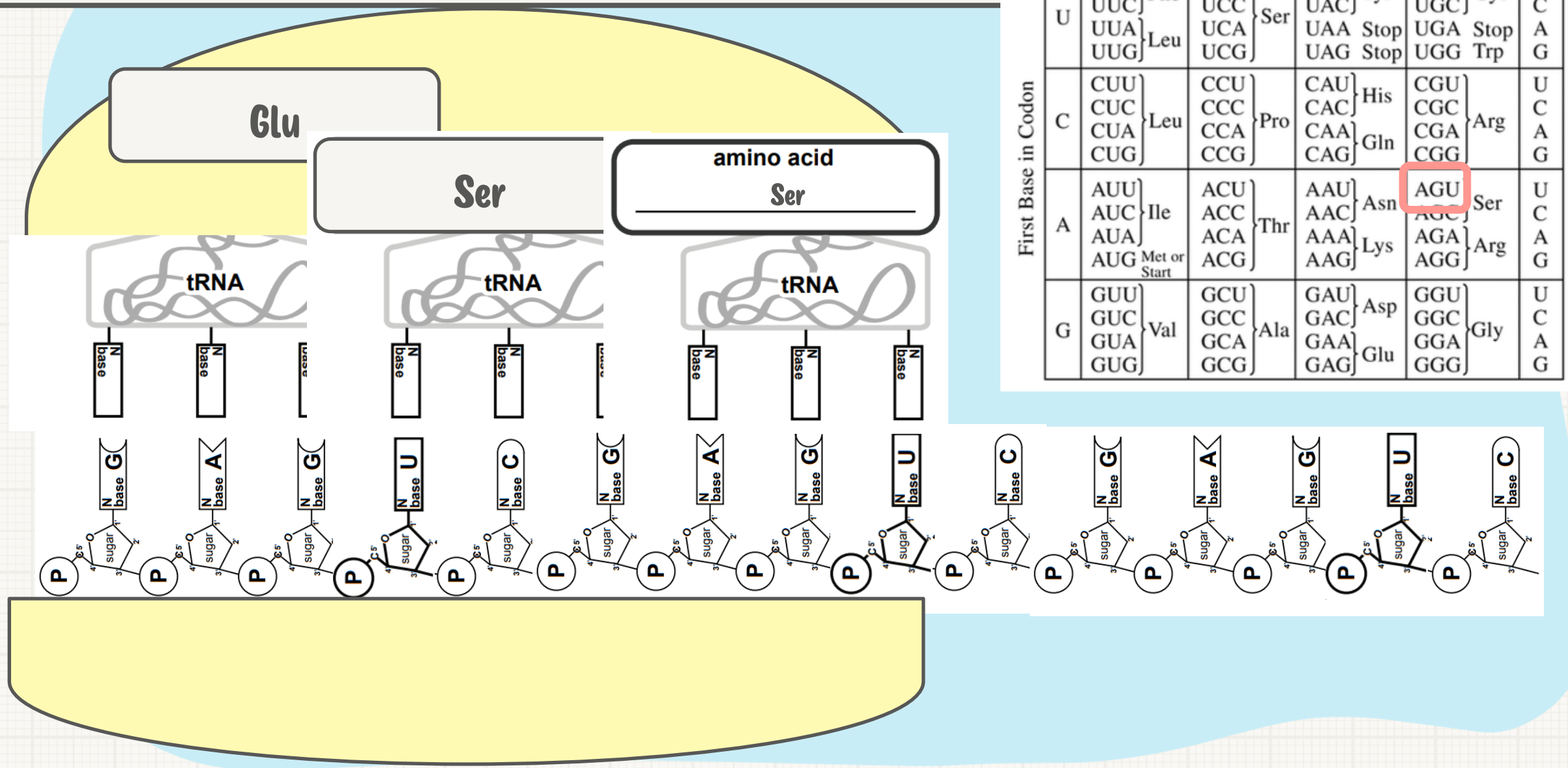
A	AUU AUC Ile AUA AUG Met or Start	ACU ACC ACA ACG Thr	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G
G	GUU GUC GUA Val GUG	GCU GCC GCA Ala GCG	GAU Asp GAC GAA Glu GAG	GGU GGC GGA Gly GGG	U C A G

Translation



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A	AUU AUC Ile AUA AUG Met or Start	ACU ACC ACA Thr ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G
G	GUU GUC GUA Val GUG	GCU GCC GCA Ala GCG	GAU Asp GAC GAA Glu GAG	GGU GGC GGA Gly GGG	U C A G

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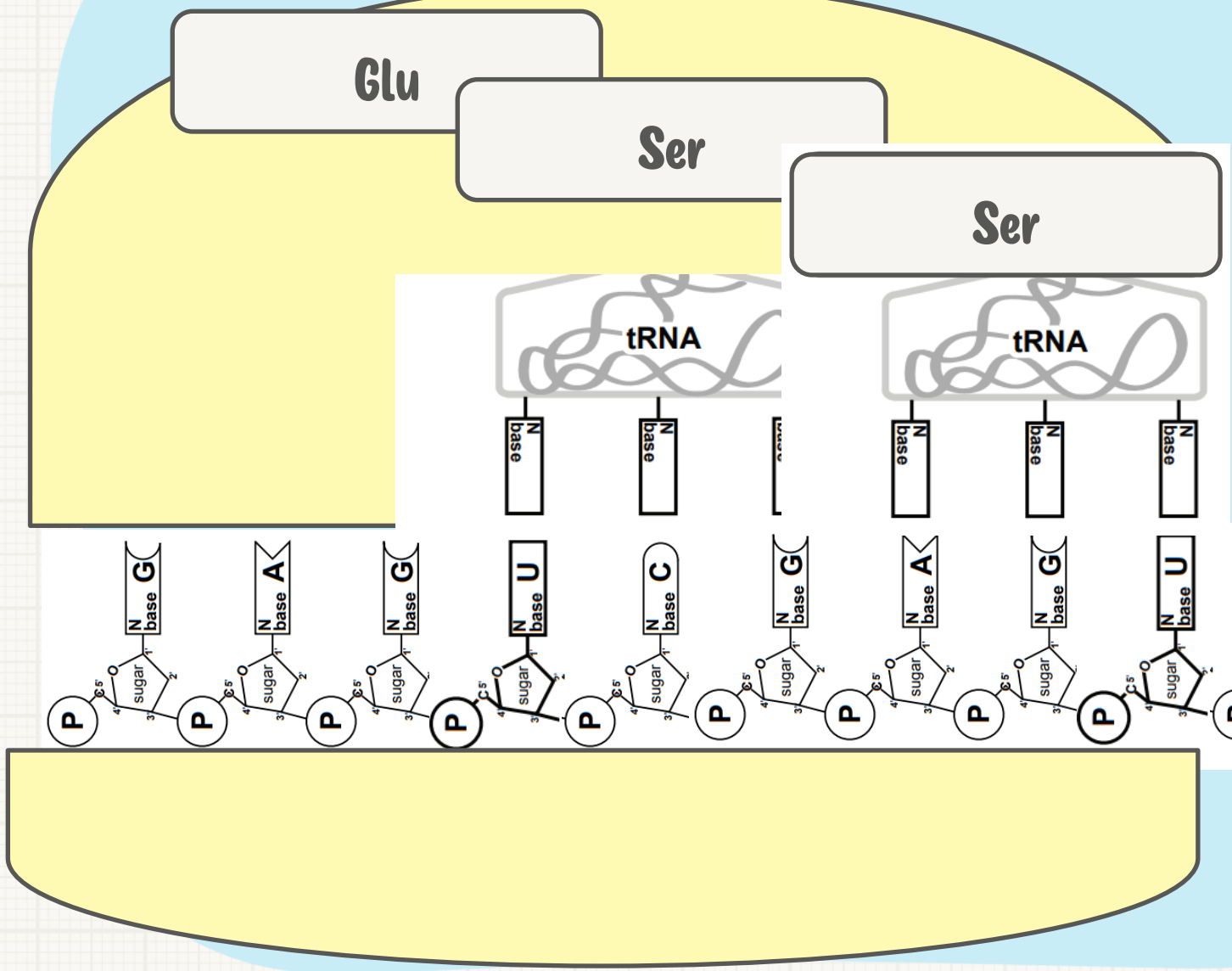

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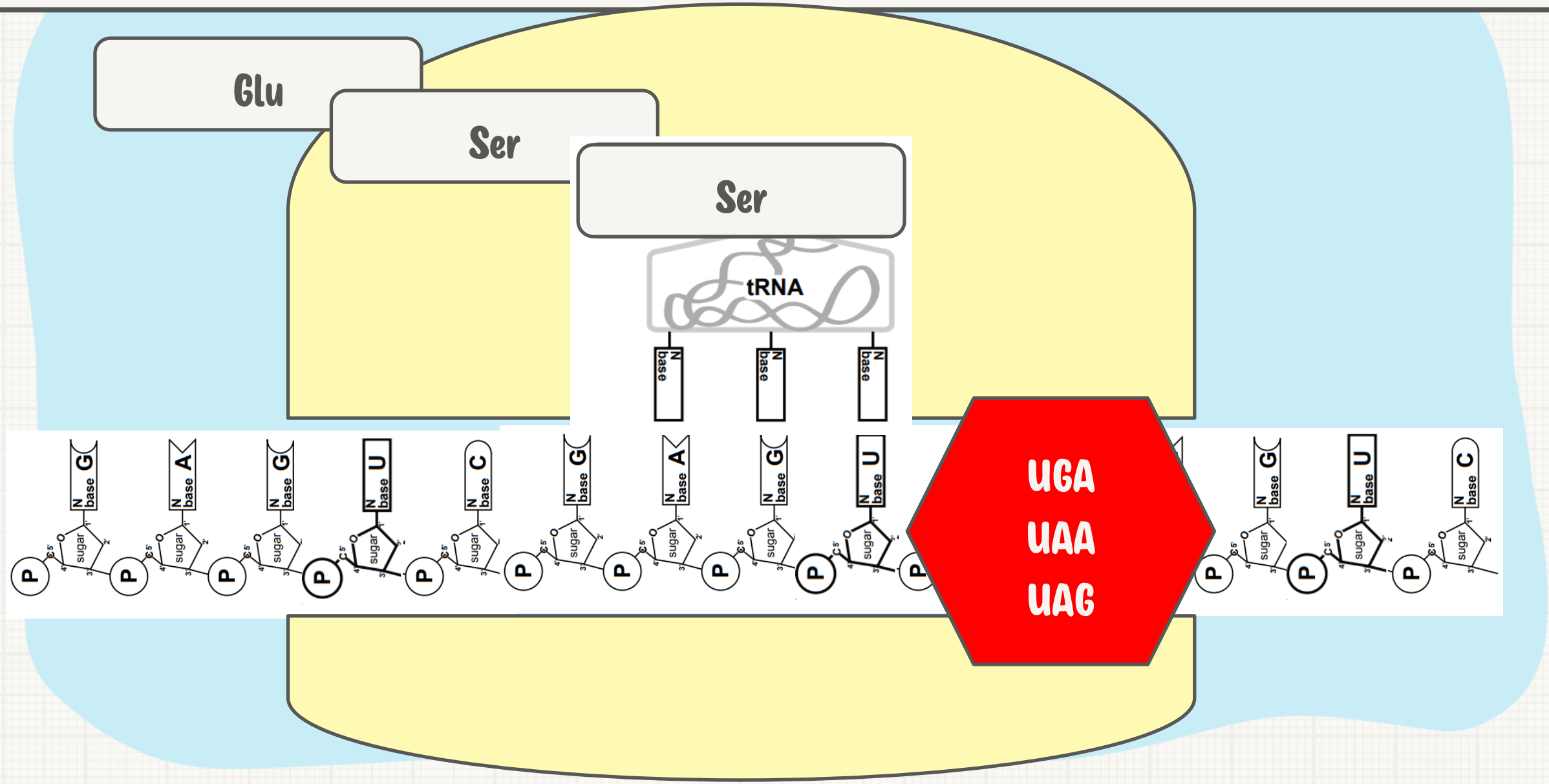
A	AUU AUC Ile AUA AUG Met or Start	ACU ACC ACA Thr ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G
G	GUU GUC GUA Val GUG	GCU GCC GCA Ala GCG	GAU Asp GAC GAA Glu GAG	GGU GGC GGA Gly GGG	U C A G

Translation



Mutations

Point Mutations

Mutation at one nucleotide base pair

Silent

no change in amino acid (AA)

Missense

change from one AA to another AA

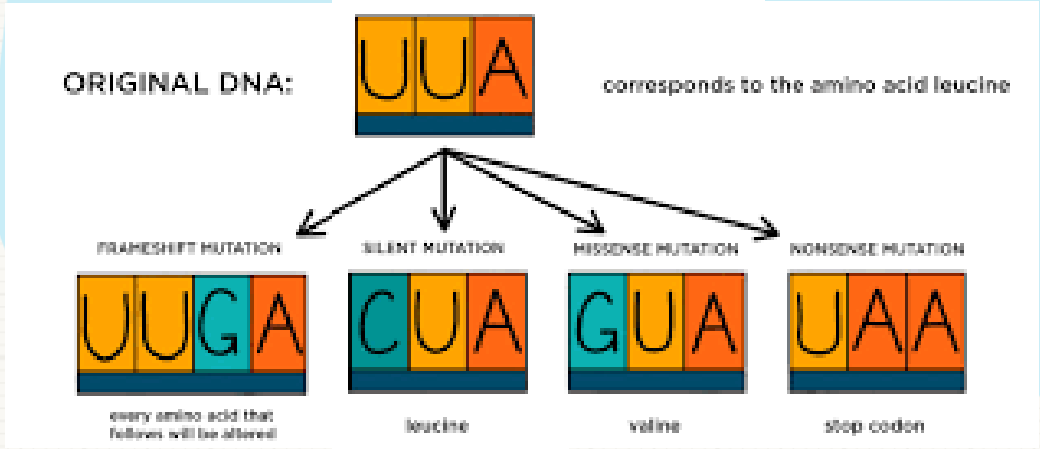
Nonsense

change from AA to STOP codon

Frameshift

insertion/deletion of 1 or 2 nucleotide base pairs

shifts the reading frame for codons



Chromosomal Mutations

Rearrangement of chromosome parts or changes in chromosome numbers

Rearrangement

Insertion

Deletion

Duplication

Inversion

Translocation

Changes in Chromosome Number

Nondisjunction

Polyploidy

Operons

Gene Regulation found in prokaryotes

Promoter
Site when RNA polymerase binds

Operator
Site when repressor binds

Genes
DNA

Repressible Operon

Example: Trp Operon
synthesizes tryptophan

Starts: ON
Repressor: INACTIVE

If trp is present...
Trp binds to repressor to ACTIVATE
Repressor binds to operator to turn the operon OFF

Inducible Operon

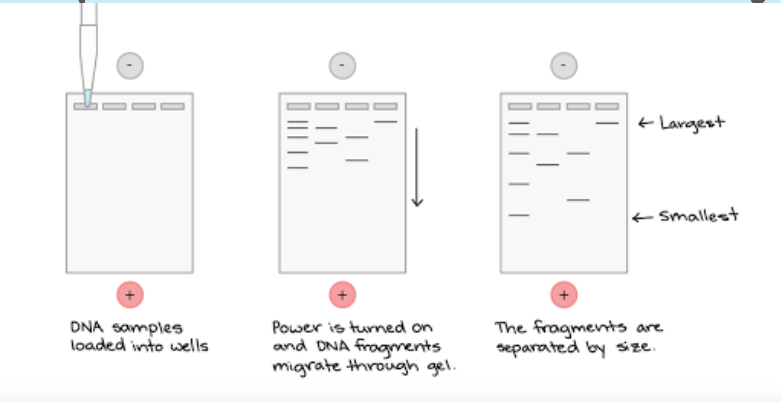
Example: Lac Operon
synthesizes enzymes to break down lactose

Starts: OFF
Repressor: ACTIVE

If lactose is present...
lactose binds to repressor to INACTIVATE
Repressor no longer binds to operator to turn the operon ON

Gel Electrophoresis

Separate molecules based on size and charge

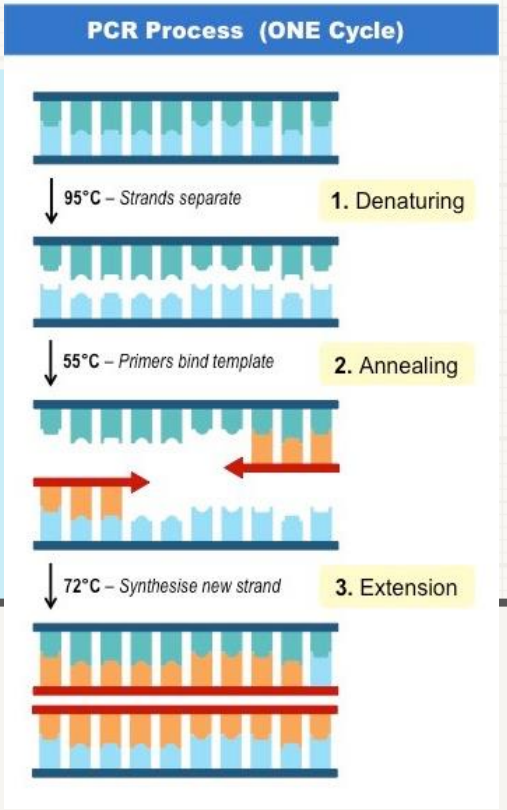


Polymerase Chain Reaction (PCR)

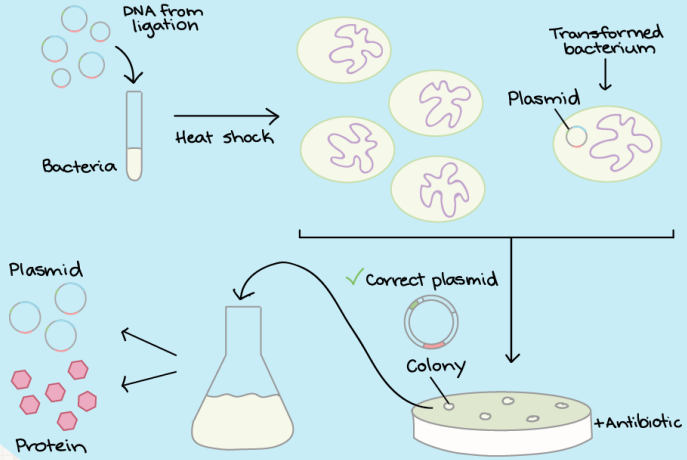
Makes multiple copies of DNA fragments

Steps

1. Heating
2. Cooling
3. Annealing



BioTechnology

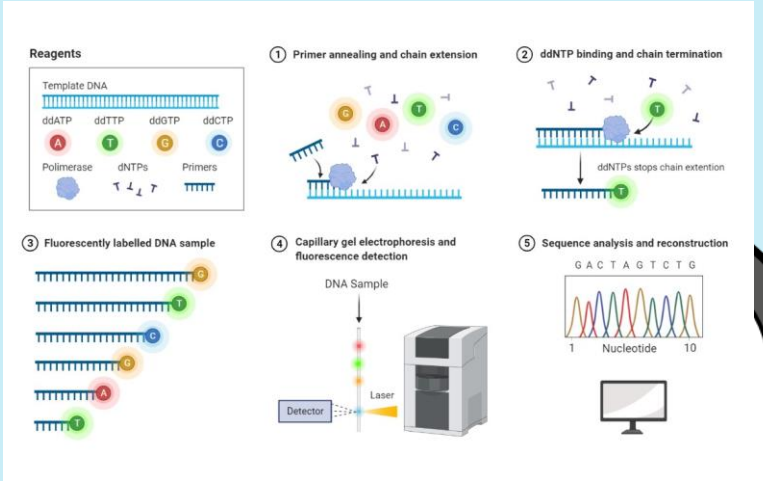


Bacterial Transformation

Introduce genetic material (plasmid) to bacteria

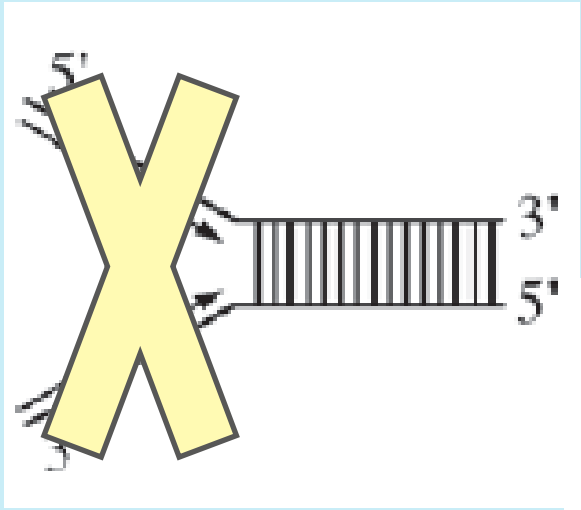
DNA Sequencing

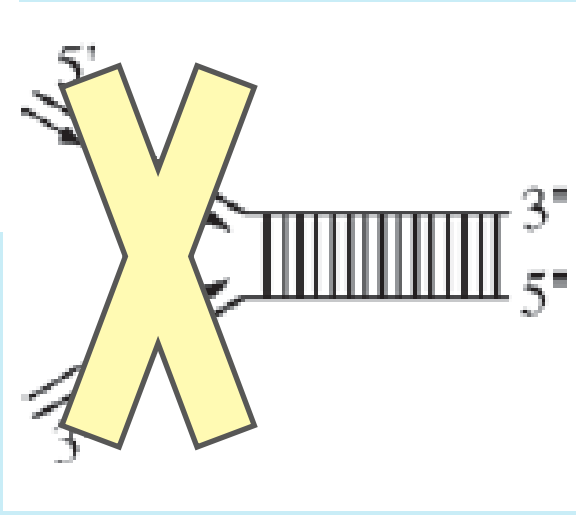
Use radioactive nucleotides to determine the sequence of a DNA strand

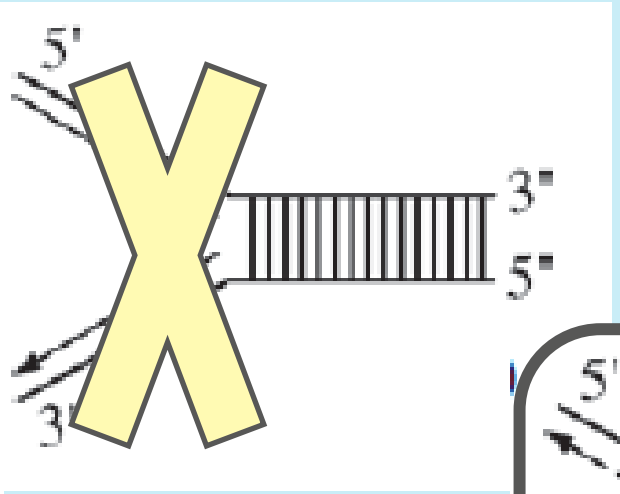


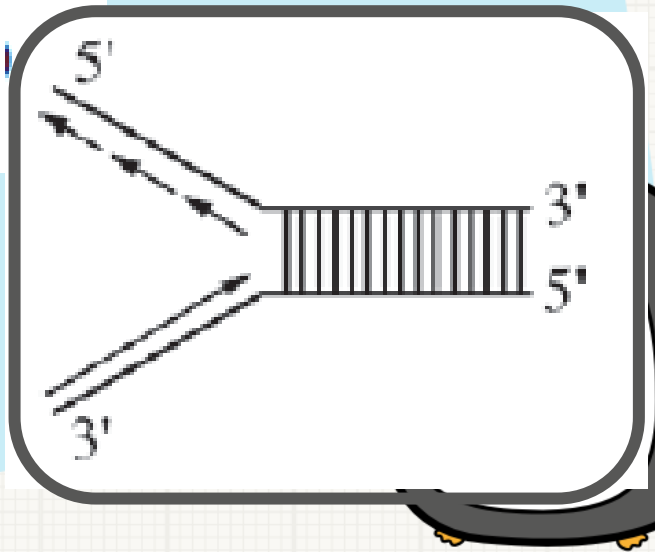
Multiple Choice Practice:

When DNA replicates, each strand of the original DNA molecule is used as a template for the synthesis of a second, complementary strand. Which of the following figures most accurately illustrates enzyme-mediated synthesis of new DNA at a replication fork?









Multiple Choice Practice:

Sickle-cell anemia results from a point mutation in the HBB gene. The mutation results in the replacement of an amino acid that has a hydrophilic R-group with an amino acid that has a hydrophobic R-group on the exterior of the hemoglobin protein. Such a mutation would most likely result in altered

a. properties of the molecule as a result of abnormal interactions between adjacent hemoglobin molecules

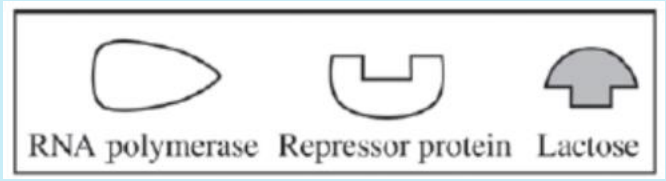
b. DNA structure as a result of abnormal hydrogen bonding between nitrogenous bases

c. fatty acid structure as a result of changes in ionic interactions between adjacent fatty acid chains

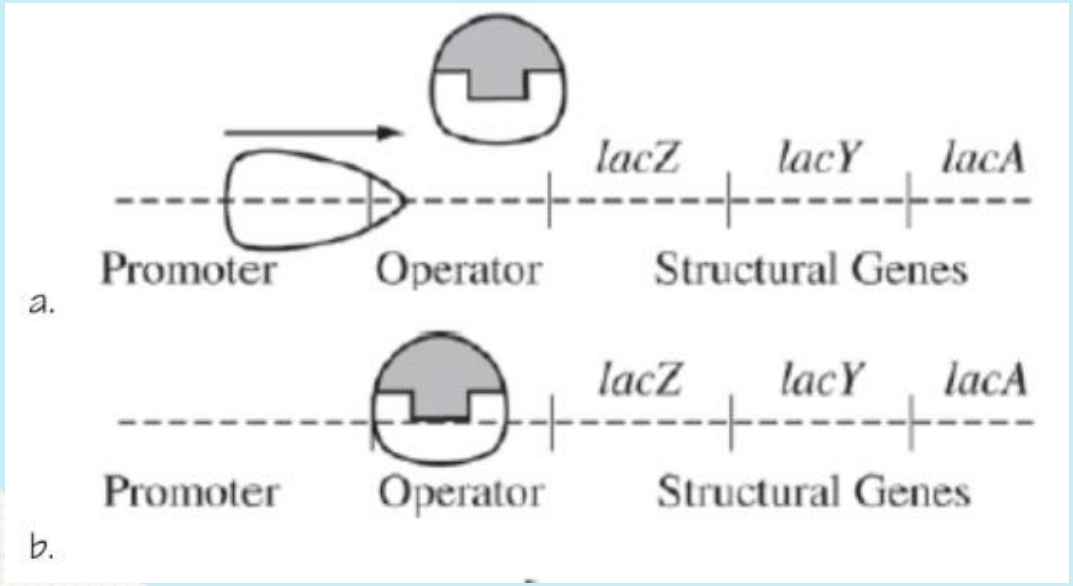
d. protein secondary structure as a result of abnormal hydrophobic interactions between R-groups in the backbone of the protein

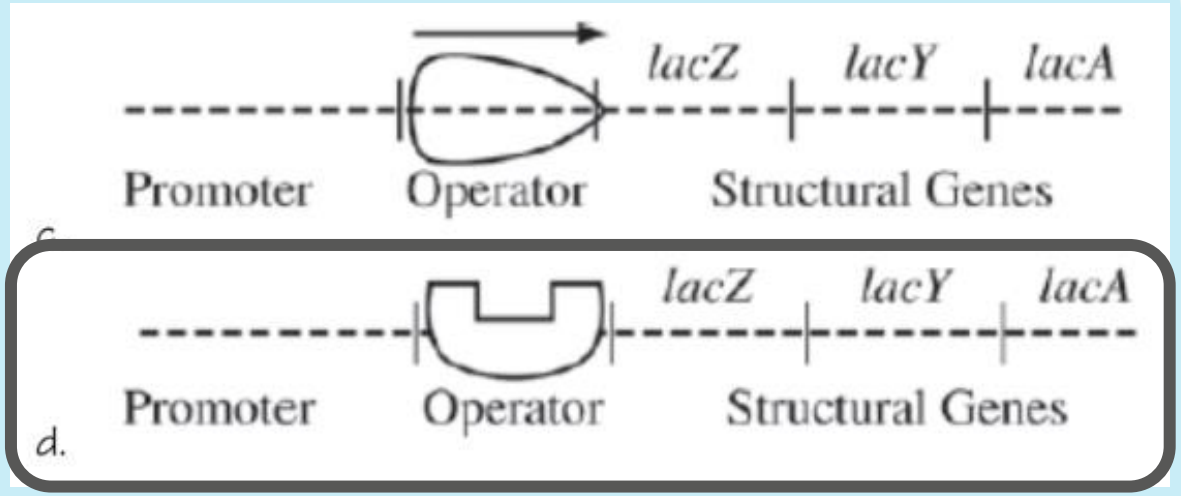
Multiple Choice Practice:

Lactose digestion in E. coli begins with its hydrolysis by the enzyme b-galactosidase. The gene encoding b-galactosidase, lacZ, is part of a coordinately regulated operon containing other genes required for lactose utilization.



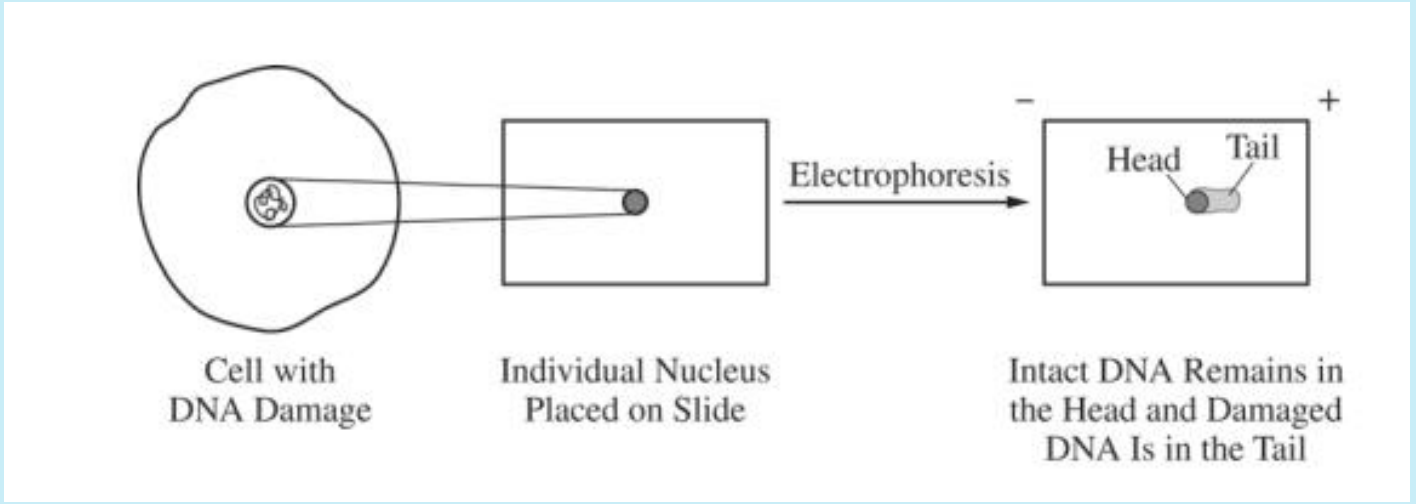
Which of the following figures correctly depicts the interactions at the lac operon when lactose is NOT being utilized? (The legend above defines the shapes of the molecules illustrated in the options.)





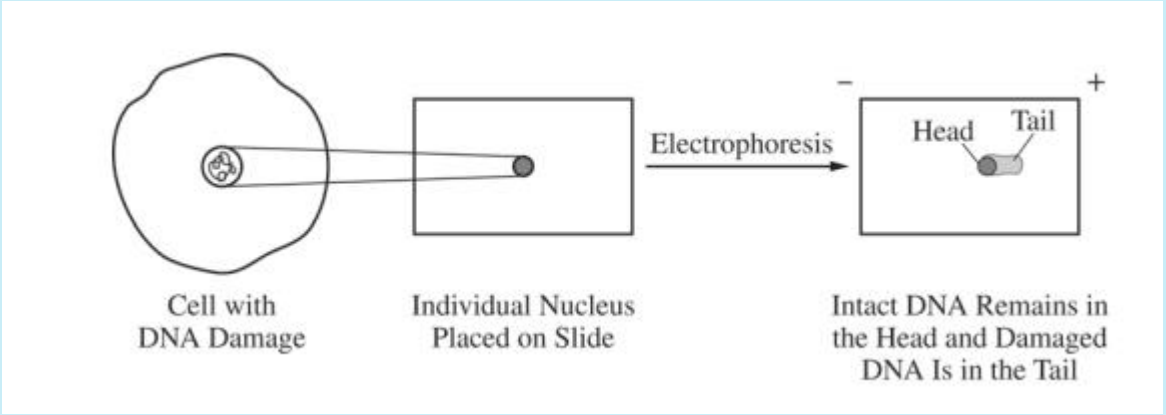
Free Response Practice (2017 #6):

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)



Free Response Practice (2017 #6):

(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.

Free Response Practice (2017 #6):

(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.

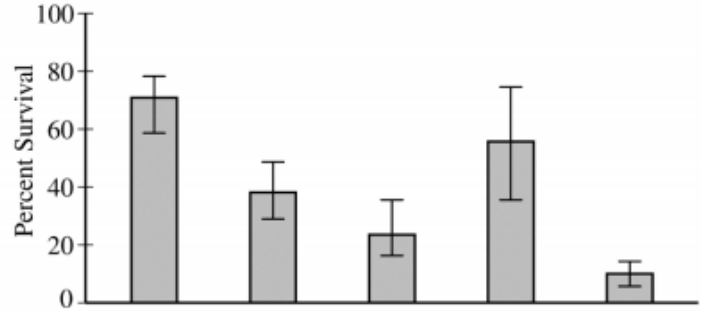
When viewed using a microscope, undamaged DNA from the nucleus appears as a round shape (the head), and the fragments of damaged DNA extend out from the head (the tail).

Prediction (1 point)

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

Free Response Practice (2018 #4):

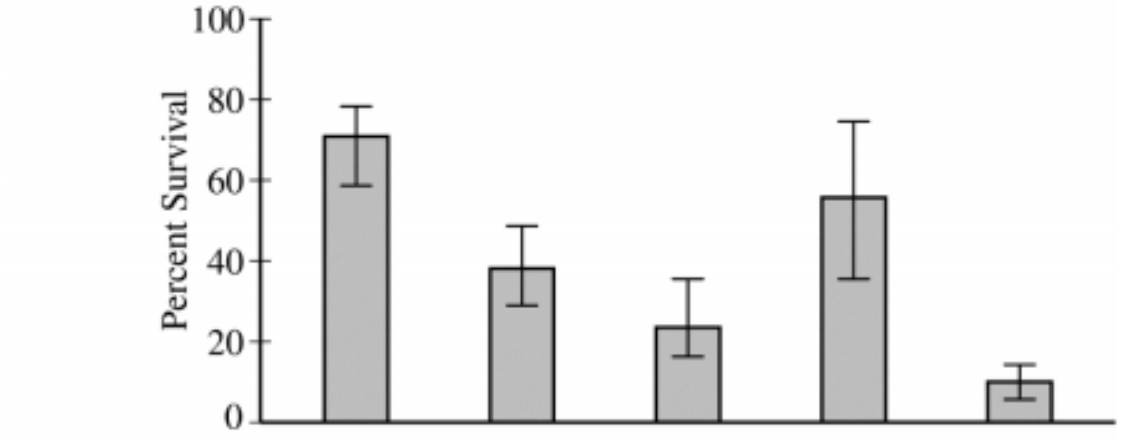
The common bedbug (*Cimex lectularius*) is a species of insect that is becomingly increasingly resistant to insecticides. Bedbugs possess several genes suspected of contributing to the resistance, including P450, Abc8, and Cps. To investigate the role of these genes in insecticide resistance, researchers deleted one or more of these genes in different strains of bedbugs, as indicated in Figure 1, and treated the strains with the insecticide beta-cyfluthrin. Each strain was genetically identical except for the deleted gene(s) and was equally fit in the absence of beta-cyfluthrin. The percent survival of each strain following beta-cyfluthrin treatment is shown in Figure 1.



Strain	I	II	III	IV	V
P450	+	–	+	+	–
Abc8	+	+	–	+	–
Cps	+	+	+	–	+

+ = Wildtype
– = Deletion

Free Response Practice (2018 #4):



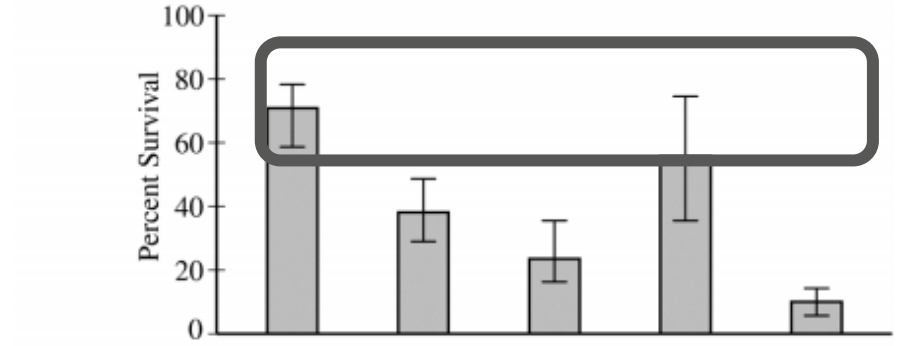
Strain	I	II	III	IV	V
P450	+	–	+	+	–
Abc8	+	+	–	+	–
Cps	+	+	+	–	+

+ = Wildtype
– = Deletion

Figure 1. Percent survival of five strains of bedbugs treated with beta-cyfluthrin. A (+) indicates the gene is present; a (–) indicates the gene is deleted. Error bars represent the 95% confidence interval.

Free Response Practice (2018 #4):

(a) Identify the control strain in the experiment. Use the means and confidence intervals in Figure 1 to justify the claim that Abc8 is effective at providing resistance to beta-cyfluthrin.



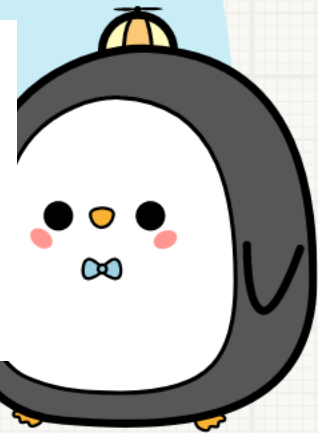
Strain	I	II	III	IV	V
P450	+	–	+	+	–
Abc8	+	+	–	+	–

Identification (1 point)

- Strain I

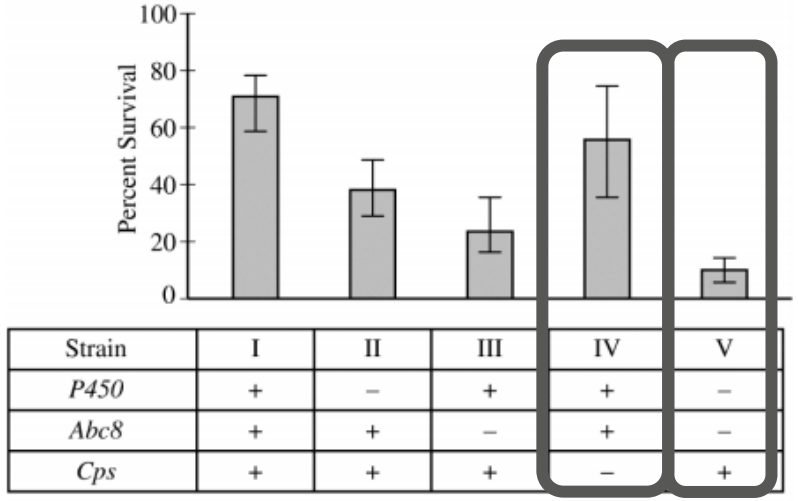
Justification (1 point)

- Error bars/CIs from strain I/control/WT do not overlap with strain III/*Abc8* deleted strain.
- Mean % survival of strain III/*Abc8* deletion falls outside the 95% confidence interval of strain I/control/WT.
- Strain III/*Abc8* deletion shows a statistically significant difference from strain I/control.



Free Response Practice (2018 #4):

(b) P450 encodes an enzyme that detoxifies insecticides. Abc8 encodes a transporter protein that pumps insecticides out of cells. Cps encodes an external structural protein located in the exoskeleton that greatly reduces the absorption of insecticides. Based on this information and the data in Figure 1, explain how a deletion of both P450 and Abc8 results in lower survival in bedbugs compared with a deletion of Cps only.



Strain	I	II	III	IV	V
P450	+	–	+	+	–
Abc8	+	+	–	+	–
Cps	+	+	+	–	+

+ = Wildtype
– = Deletion

Explanation (1 point per row; 2 points maximum)

Strain	*P450* and *Abc8*	*Cps* only	Explanation
V	Deleted	Present	Bedbugs can neither detoxify nor pump out insecticide, which results in a lower chance of bedbug survival.
IV	Present	Deleted	Bedbugs can detoxify and pump out insecticide, which results in a higher chance of bedbug survival.

Q & A

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