

Unit 9: DNA, RNA, and Proteins



Pig and elephant DNA just don't splice, but why?

• **Structure of DNA**

- 3.3.1 - Outline DNA nucleotide structure in terms of sugar (deoxyribose), base and phosphate. [2]
- 3.3.2 - State the names of the four bases in DNA. [1]
- 3.3.3 - Outline how DNA nucleotides are linked together by covalent bonds into a single strand. [2]
- 3.3.4 - Explain how a DNA double helix is formed using complementary base pairing and hydrogen bonds. [3]
- 3.3.5 - Draw and label a simple diagram of the molecular structure of DNA. [1]
- 7.1.1 - Describe the structure of DNA, including the antiparallel strands, 3'-5' linkages and hydrogen bonding between purines and pyrimidines. [2]
- 4.1.1 - State that eukaryote chromosomes are made of DNA and proteins. [1]
- 7.1.2 - Outline the structure of nucleosomes. [2]
- 7.1.3 - State that nucleosomes help to supercoil chromosomes and help to regulate transcription. [1]

• **DNA Replication**

- 3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]
- 7.2.1 - State that DNA replication occurs in a 5' → 3' direction. [1]
- 3.4.2 - Explain the significance of complementary base pairing in the conservation of the base sequence of DNA. [3]
- 3.4.3 - State that DNA replication is semi-conservative. [1]
- 3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]
- 7.2.1 - State that DNA replication occurs in a 5' → 3' direction. [1]
- 7.2.3 - State that DNA replication is initiated at many points in eukaryotic chromosomes. [1]
- 7.2.2 - Explain the process of DNA replication in prokaryotes, including the role of enzymes (helicase, DNA polymerase, RNA primase and DNA ligase), Okazaki fragments and deoxynucleoside triphosphates. [3]

• **Transcription**

- 3.5.1 - Compare the structure of RNA and DNA. [3]
- 3.5.2 - Outline DNA transcription in terms of the formation of an RNA strand complementary to the DNA strand by RNA polymerase. [2]
- 7.3.2 - Distinguish between the sense and antisense strands of DNA. [2]
- 7.3.1 - State that transcription is carried out in a 5' 3' direction. [1]
- 7.3.3 - Explain the process of transcription in prokaryotes, including the role of the promoter region, RNA polymerase, nucleoside triphosphates and the terminator. [3]
- 7.1.5 - State that eukaryotic genes can contain exons and introns. [1]
- 7.3.4 - State that eukaryotic RNA needs the removal of introns to form mature mRNA. [1]
- 3.5.5 - Discuss the relationship between one gene and one polypeptide. [3]

- 3.5.3 - Describe the genetic code in terms of codons composed of triplets of bases. [2]
- 3.5.4 - Explain the process of translation, leading to polypeptide formation. [3]
- 7.4.6 - Explain the process of translation, including ribosomes, polysomes, start codons and stop codons. [3]
- 7.4.1 - Explain that each tRNA molecule is recognized by a tRNA-activating enzyme that binds a specific amino acid to the tRNA, using ATP for energy. [3]
- 7.4.2 - Outline the structure of ribosomes, including protein and RNA composition, large and small subunits, three tRNA binding sites and mRNA binding sites. [2]
- 7.4.4 - State that translation occurs in a 5' → 3' direction. [1]
- 7.4.3 - State that translation consists of initiation, elongation, translocation and termination. [1]
- 7.4.5 - Draw and label a diagram showing the structure of a peptide bond between two amino acids. [1]
- 7.4.7 - State that free ribosomes synthesize proteins for use primarily within the cell, and that bound ribosomes synthesize proteins primarily for secretion or for lysosomes. [1]

• **Genes and Mutations**

- 4.1.2 - Define gene, allele and genome. [1]
- 7.1.4 - Distinguish between unique or single-copy genes and highly repetitive sequences in nuclear DNA. [2]
- 4.1.3 - Define gene mutation. [1]
- 4.1.4 - Explain the consequence of a base substitution mutation in relation to the processes of transcription and translation, using the example of sickle-cell anemia. [3]

Bonus - History of DNA

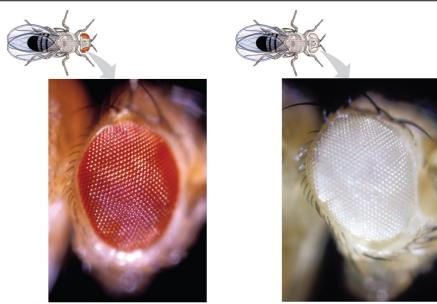
- The march to understanding that DNA is the genetic material:
 - Gregor Mendel (1857) – Laws of Heredity
 - Friedrich Miescher (1869) – Nucleic Acids
 - T.H. Morgan (1908) - Chromosomes and Genes
 - Frederick Griffith (1928) – Transforming Factor
 - Avery, McCarty & MacLeod (1944) - = DNA
 - Hershey & Chase (1952) – Confirm DNA
 - Watson & Crick (1953) – SHAPE of DNA
 - Meselson & Stahl (1958) – DNA Replication



Bonus - History of DNA (cont.)

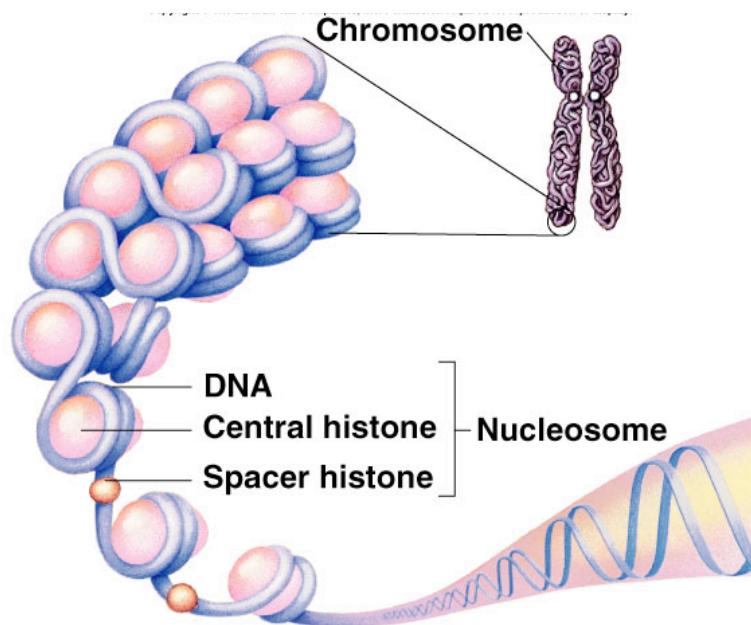
- T.H. Morgan
 - Working with Drosophila (Fruit Flies)
 - Genes are on chromosomes, but is it the protein or the DNA of the chromosomes that are the genes?
- Through 1940 proteins were thought to be genetic material... Why?





Bonus - History of DNA (cont.)

- Thomas Hunt Morgan
 - Working with Drosophila (Fruit Flies)
 - Genes are on chromosomes, but is it the protein or the DNA of the chromosomes that are the genes?
- Through 1940 proteins were thought to be genetic material... Why?



Next 



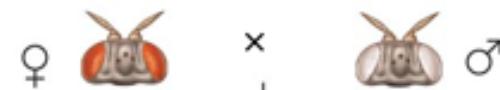
1908 | 1933

Bonus - History of DNA (cont.)

- Thomas Hunt Morgan (cont.)

EXPERIMENT

P Generation



F₁ Generation

All offspring had red eyes

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RESULTS

F₂ Generation



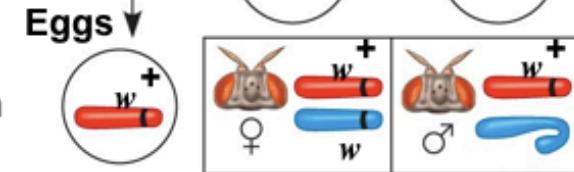
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CONCLUSION

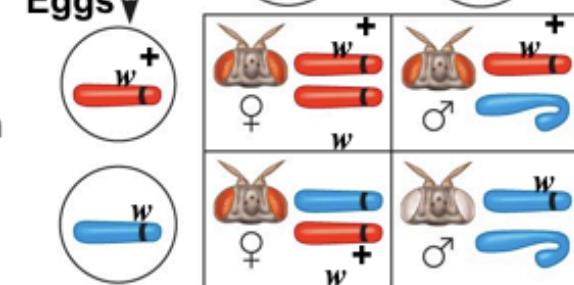
P Generation



F₁ Generation



F₂ Generation



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Bonus - History of DNA (cont.)

- Frederick Griffith

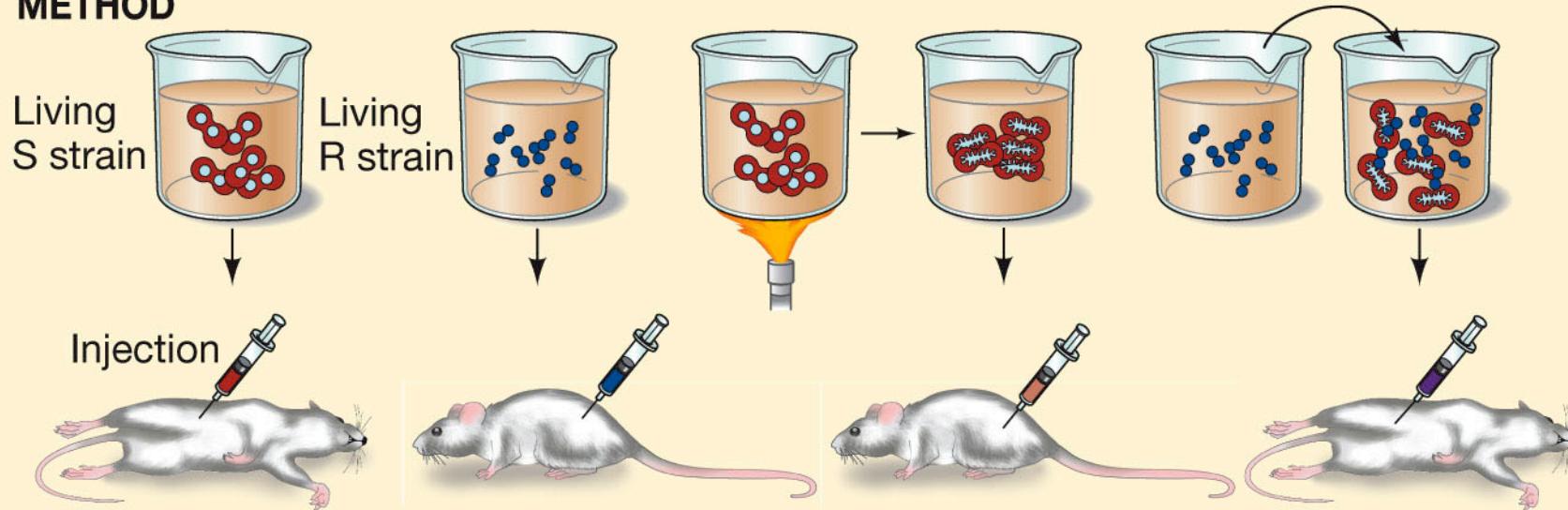
- Studied Streptococcus pneumoniae bacteria
 - Was working to find cure for pneumonia
- Two strains in experiment with mice:
 - Harmless “rough” bacteria 
 - Pneumonia causing “smooth” bacteria 
- Led to the discovery of *transformation*
 - A change in the genotype and phenotype due to the assimilation of external DNA by a cell.



EXPERIMENT

HYPOTHESIS: Material in dead bacterial cells can genetically transform living bacterial cells.

METHOD



RESULTS

Mouse dies
Living S strain
cells found in
heart

Mouse healthy
No bacterial cells
found in heart

Mouse healthy
No bacterial cells
found in heart

Mouse dies
Living S strain
cells found in
heart

CONCLUSION: A chemical substance from one cell is capable of genetically transforming another cell.

LIFE 8e, Figure 11.1

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Additional related
resource in wiki.

Next

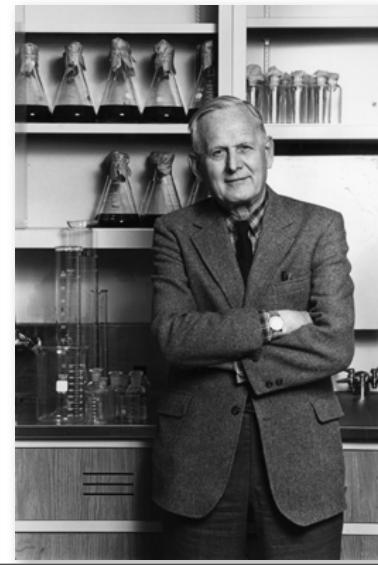
Bonus - History of DNA (cont.)

- Oswald Avery, Maclyn McCarty, and Colin McLeod
 - Took mixture of heat killed smooth and live rough and destroyed lipids, RNA, proteins, etc. – still led to transformation
 - Only when they destroyed *DNA* did transformation **NOT** occur
 - Conclusion that DNA was the transforming agent was met with much skepticism.

Oswald Avery



Maclyn McCarty



Colin McLeod



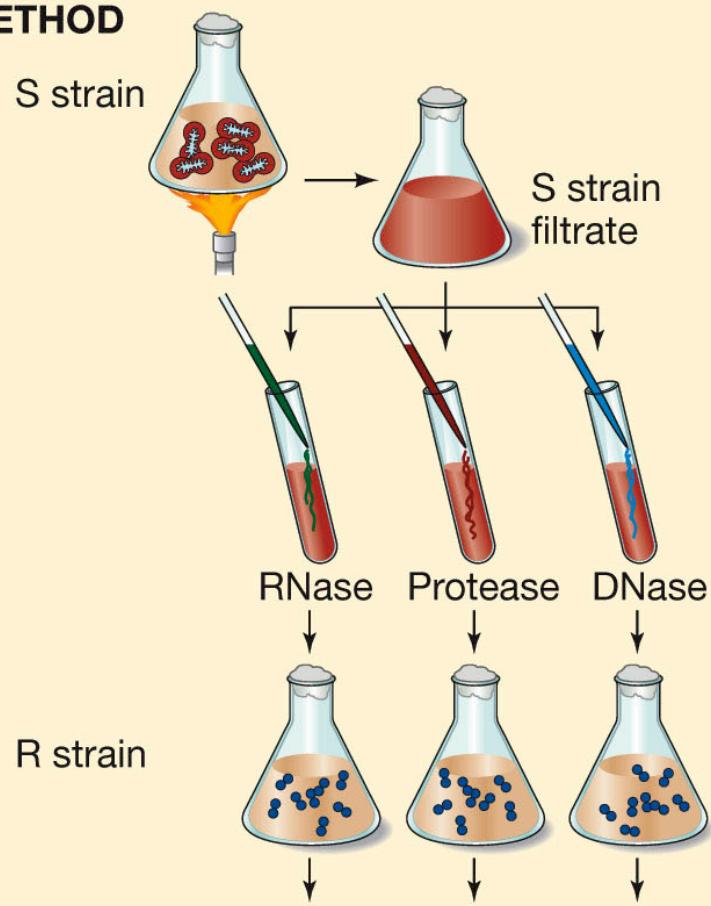
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Bonus - History of DNA (cont.)

EXPERIMENT

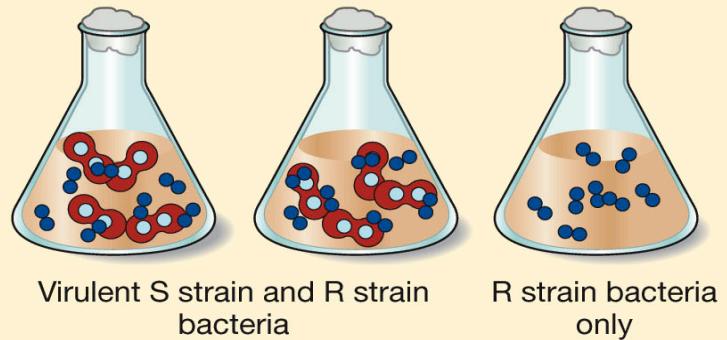
HYPOTHESIS: The chemical nature of the transforming substance from pneumococcus is DNA.

METHOD



EXPERIMENT

RESULTS



CONCLUSION: Because only DNase destroyed the transforming substance, the transforming substance is DNA.

Next

Bonus - History of DNA (cont.)

- Alfred Hershey and Martha Chase

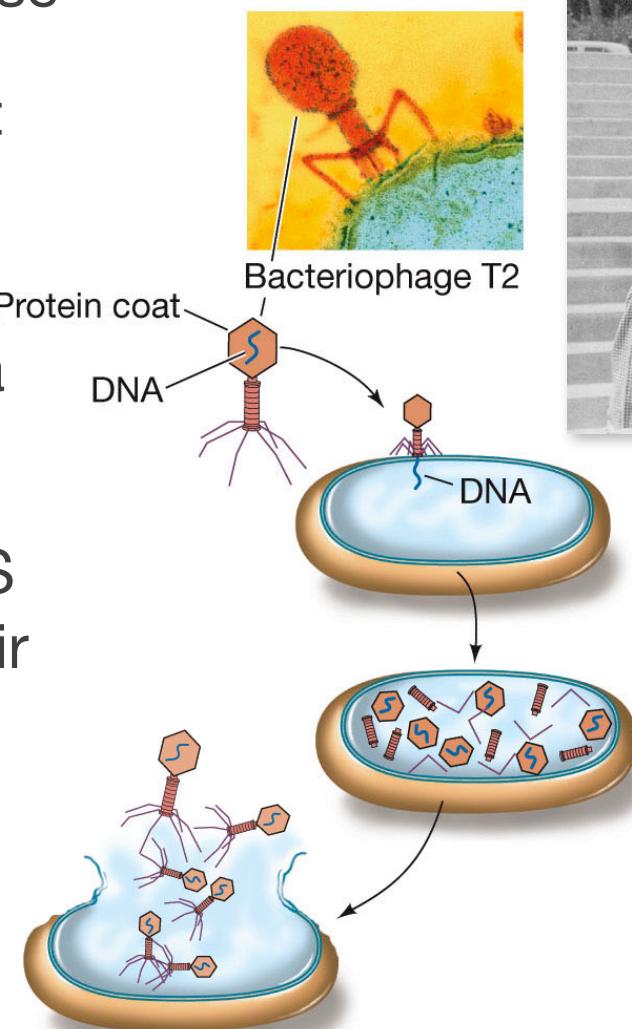
- Classic “blender” experiment

- Worked with bacteriophage

- Viruses that infect bacteria

- Grew viruses in radioactively labeled media with either ^{35}S in their proteins or ^{32}P in their DNA

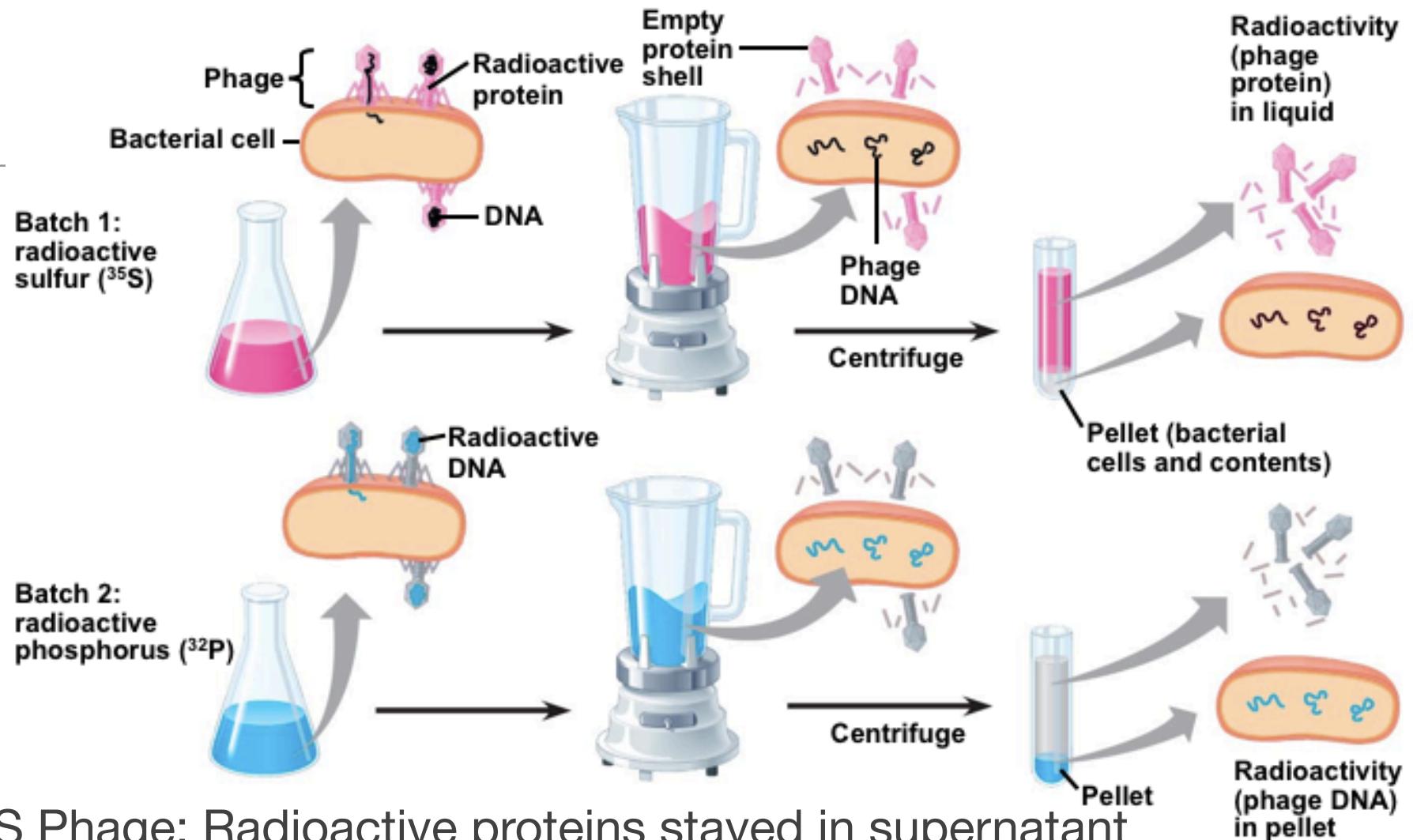
- Confirmed that DNA is the “transforming factor”



Additional related resources in wiki.

Next

EXPERIMENT

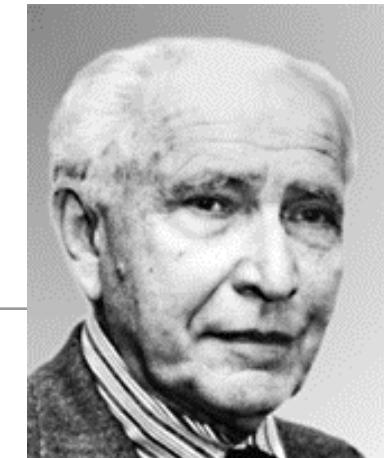


- 35S Phage: Radioactive proteins stayed in supernatant
 - Therefore protein did NOT enter bacteria
- 32P Phage: Radioactive DNA stayed in pellet
 - Therefore DNA did enter bacteria

Which molecule carries viral genetic info?

Next

Bonus - History of DNA (cont.)



Erwin Chargaff

- Erwin Chargaff
 - DNA composition: “Chargaff’s rules”
 - Varies from species to species
 - All 4 bases not in equal quantity
 - Bases present in characteristic ratio
 - Humans:
 - A = 30.9%
 - T = 29.4%
 - G = 19.9%
 - C = 19.8%

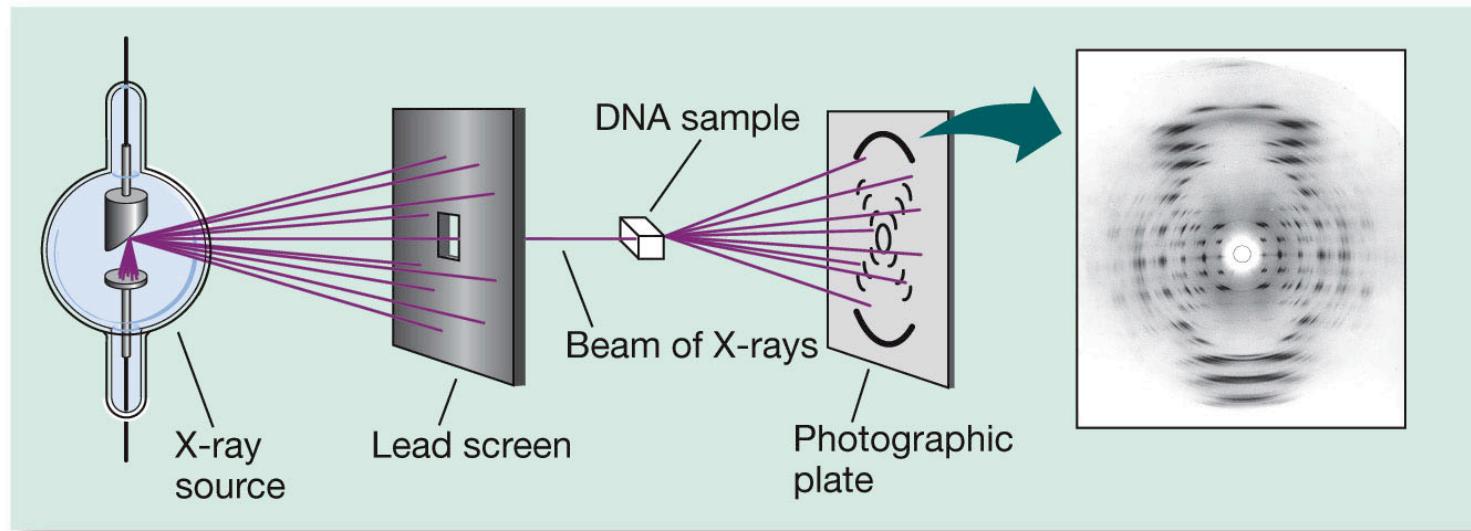
Chargaff's Data				
	Base Composition (Mole Percent)			
Organism	A	T	G	C
<i>Escherichia coli</i>	26.0	23.9	24.9	25.2
Yeast	31.3	32.9	18.7	17.1
Herring	27.8	27.5	22.2	22.6
Rat	28.6	28.4	21.4	21.5
Human	30.9	29.4	19.9	19.8



Bonus - History of DNA (cont.)

- Rosalind Franklin and Maurice Wilkins
 - Developed X-ray diffraction images of DNA
 - Suggested that DNA resembled a tightly coiled helix
 - Wilkins shared their results to two other scientists, Watson and Crick, without Franklin's knowledge.

Maurice Wilkins

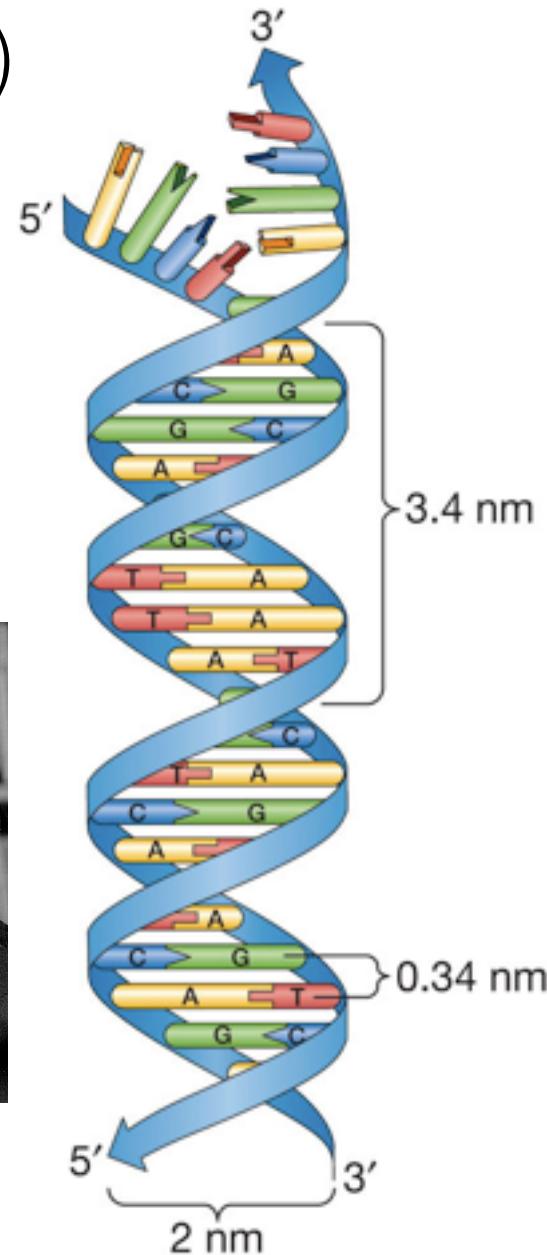
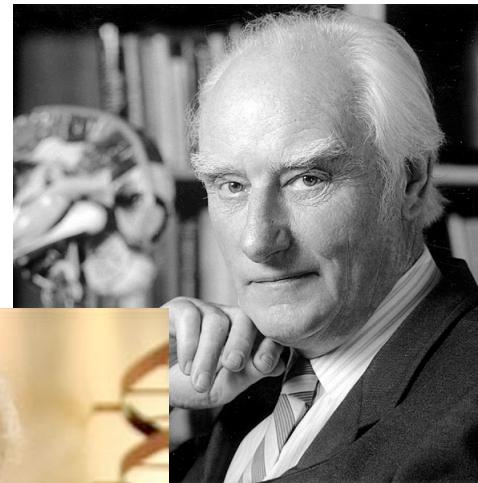
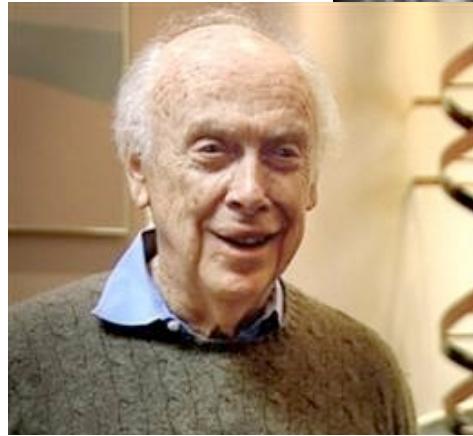
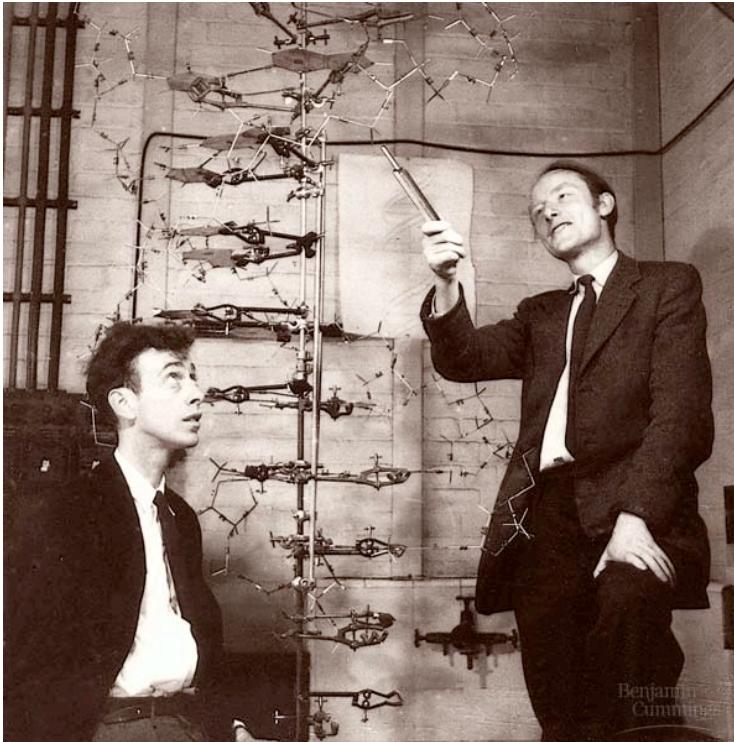


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1953 | 1962

Bonus - History of DNA (cont.)

- James Watson and Francis Crick
 - First to develop the double helix structure of DNA
 - Watson, Crick, and Wilkins were awarded the nobel prize in 1962 for discovering the structure of DNA.



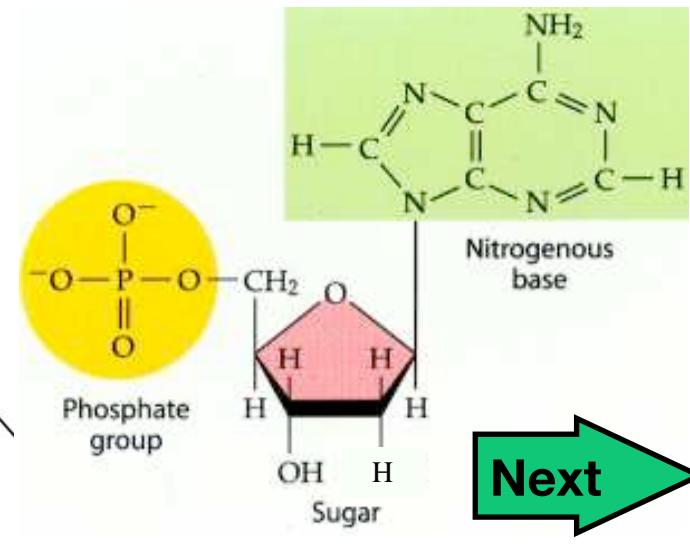
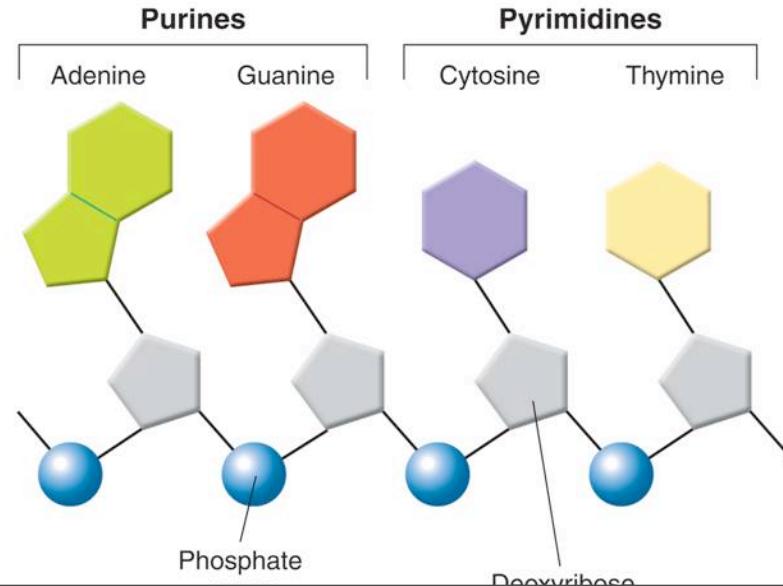
Objectives

3.3.1 - Outline DNA nucleotide structure in terms of sugar (deoxyribose), base and phosphate. [2]

3.3.2 - State the names of the four bases in DNA. [1]

- DNA (Deoxyribonucleic acid) is made up of nucleotides, which contain 3 parts: A **phosphate group**, a **deoxyribose sugar**, and a **nitrogenous base**.
- There are four different kinds of nitrogenous bases: **Adenine (A)**, **guanine (G)**, **cytosine (C)**, and **thymine (T)**.

IB Note: Chemical formulas and the purine/pyrimidine subdivision are not required. Simple shapes can be used to represent the component parts. Only the relative positions are required.



3.3.1 - Outline DNA nucleotide structure in terms of sugar (deoxyribose), base and phosphate. [2]

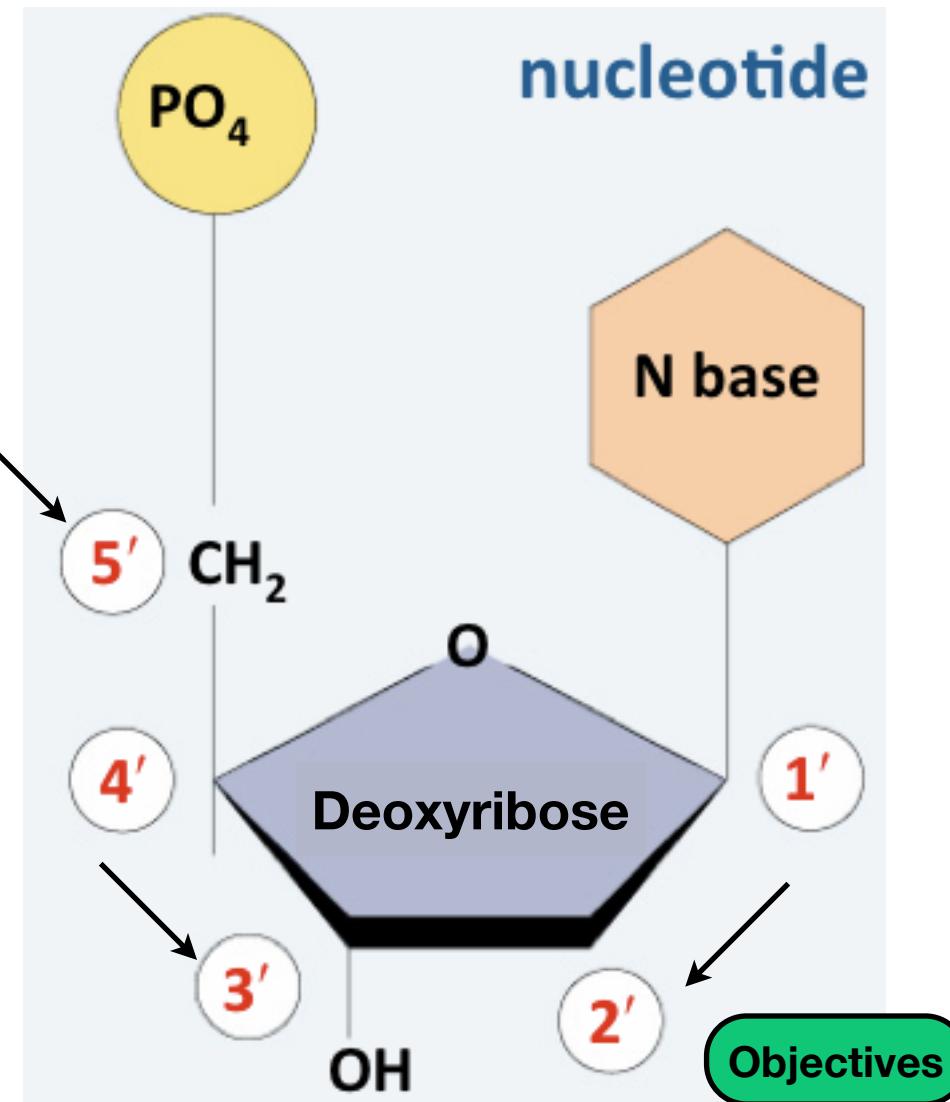
3.3.2 - State the names of the four bases in DNA. [1]

- In both types of nucleic acids, the nucleotides contain a 5-carbon sugar.

- DNA → Deoxyribose Sugar

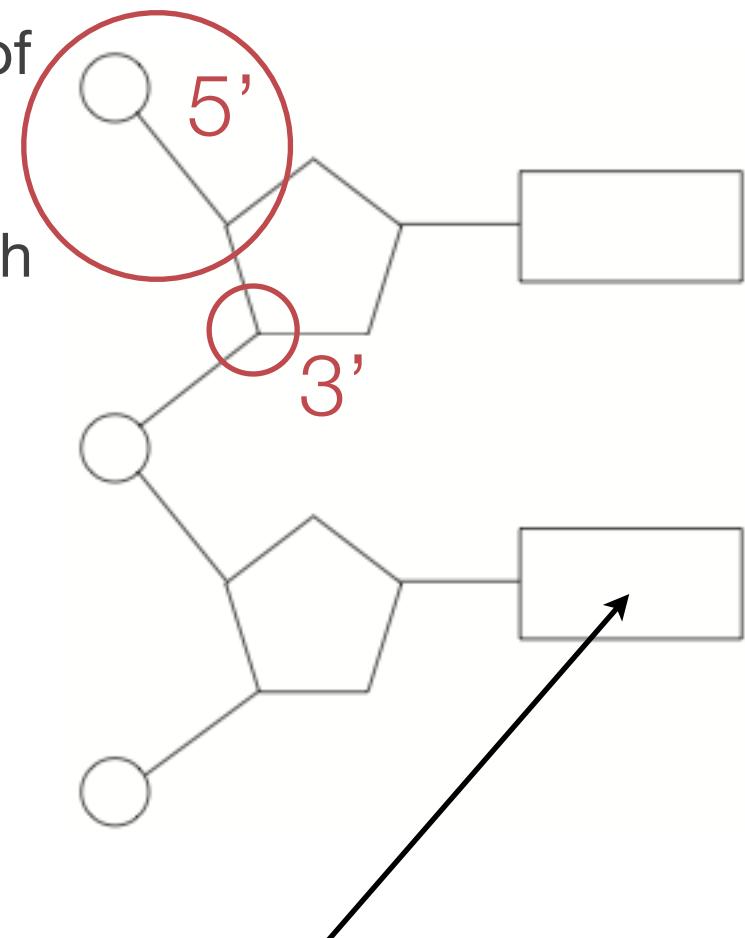
- RNA → Ribose Sugar

- In a nucleotide, the nitrogenous base is connected to the first carbon and the phosphate group is connected to the fifth carbon.



3.3.3 - Outline how DNA nucleotides are linked together by covalent bonds into a single strand. [2]

- Covalent bonds connect the 5' and 3' ends of each nucleotide.
 - Phosphodiester bonds link each sugar with a phosphate group in between.
 - Creates a sugar-phosphate backbone
 - Alternates between sugar and phosphate groups



Does this part matter when forming a polynucleotide?

IB Note: Only the relative positions are required.

Objectives

3.3.4 - Explain how a DNA double helix is formed using complementary base pairing and hydrogen bonds. [3]

- In DNA, Adenine always bonds to Thymine and Guanine always bonds to Cytosine.

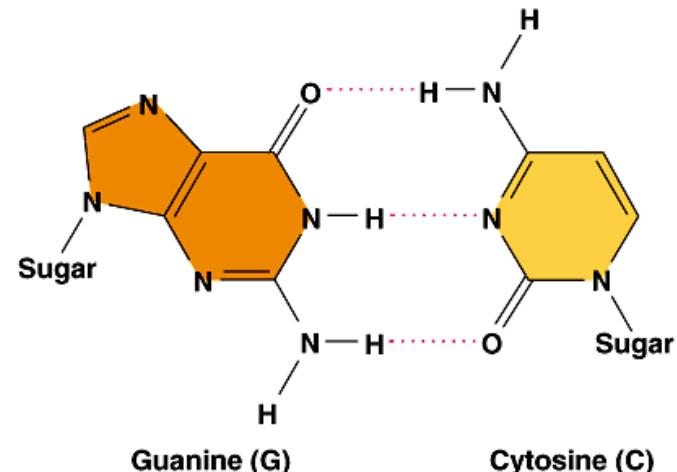
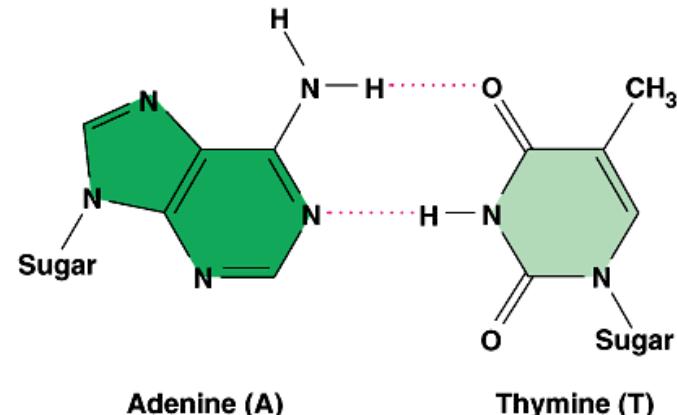
- Why is this?

- What type of bond is formed?

- What is the benefit to this type of bond?

- A purine always bonds to a pyrimidine

- Maintains a constant width in the DNA molecule.



IB Note: An extension of the diagram in 3.3.3 is sufficient to show the complementary base pairs of A-T and G-C, held together by hydrogen bonds and the sugar-phosphate backbones. The number of hydrogen bonds between pairs and details of purine/pyrimidines are not required.

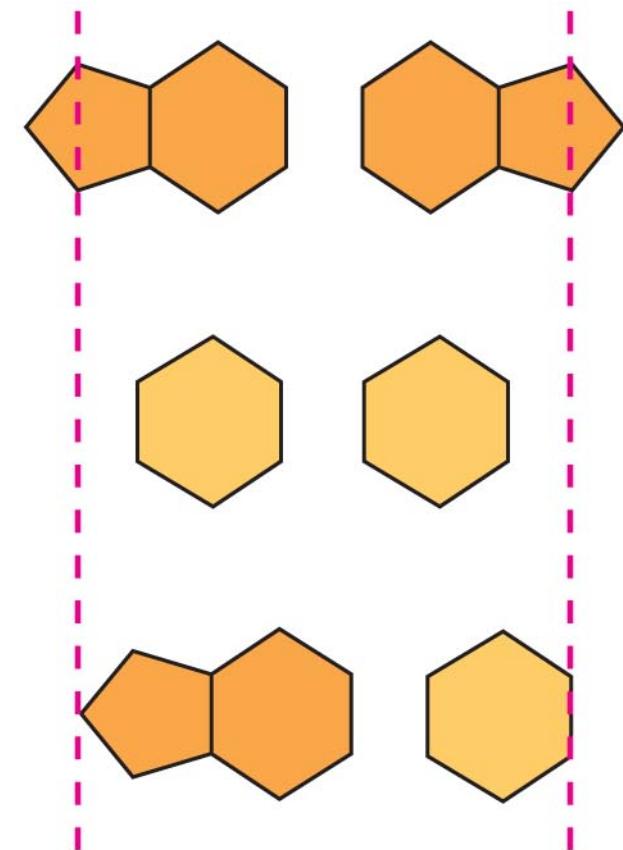
Next

3.3.4 - Explain how a DNA double helix is formed using complementary base pairing and hydrogen bonds. [3]

- How do we know that these bases pair in this manner?

- Rosalind Franklin's X-ray defraction image showed that DNA has a uniform width.

- A purine bonds to a pyrimidine.
- Explains Chargaff's rule.

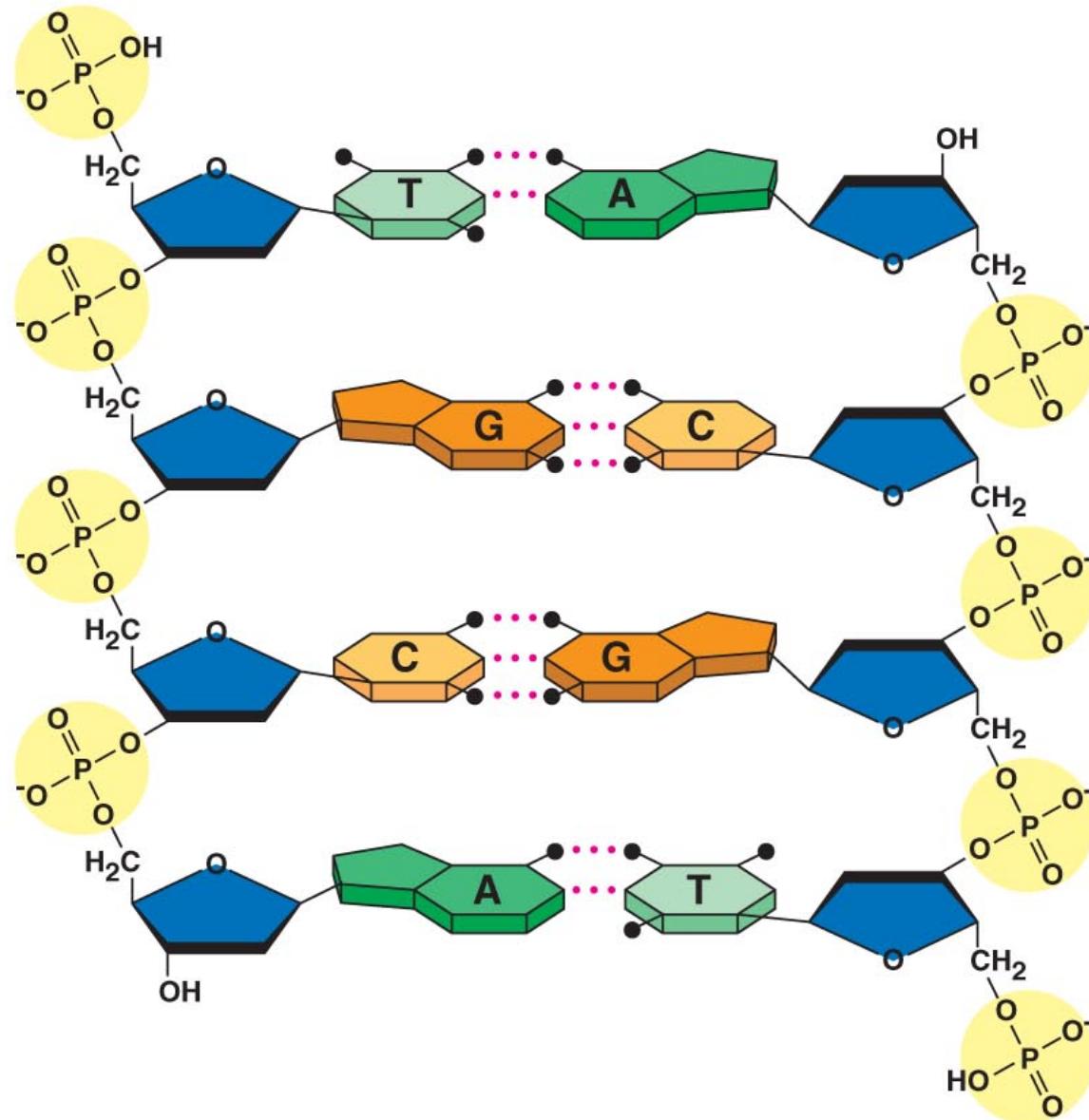


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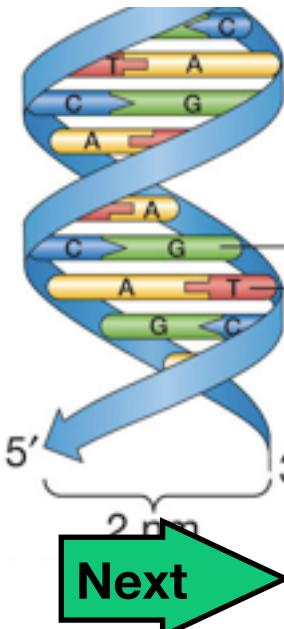
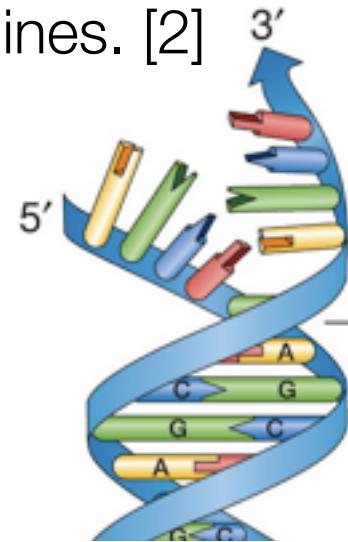
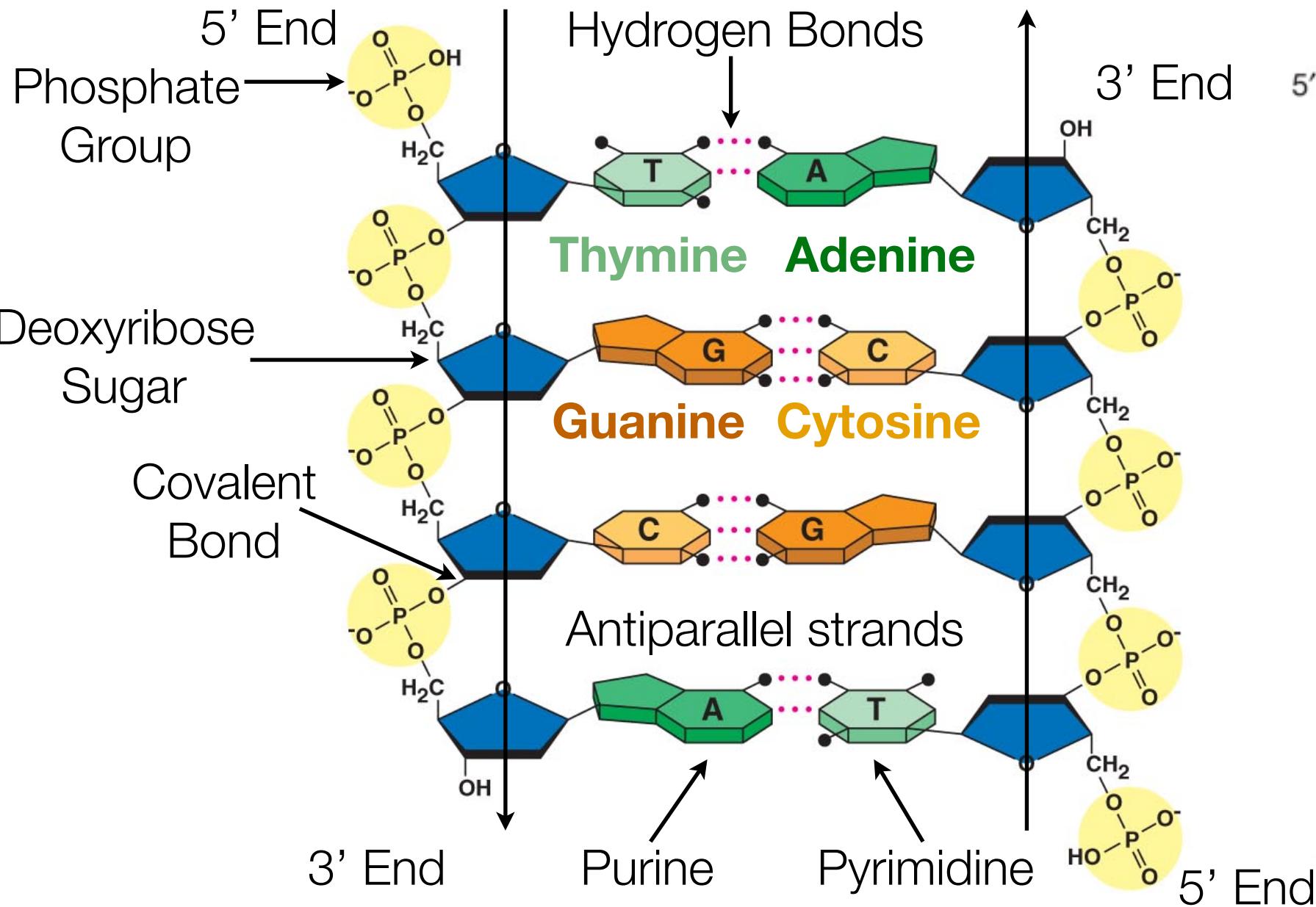


- 3.3.5 - Draw and label a simple diagram of the molecular structure of DNA. [1]
- 7.1.1 - Describe the structure of DNA, including the antiparallel strands, 3'-5' linkages and hydrogen bonding between purines and pyrimidines. [2]



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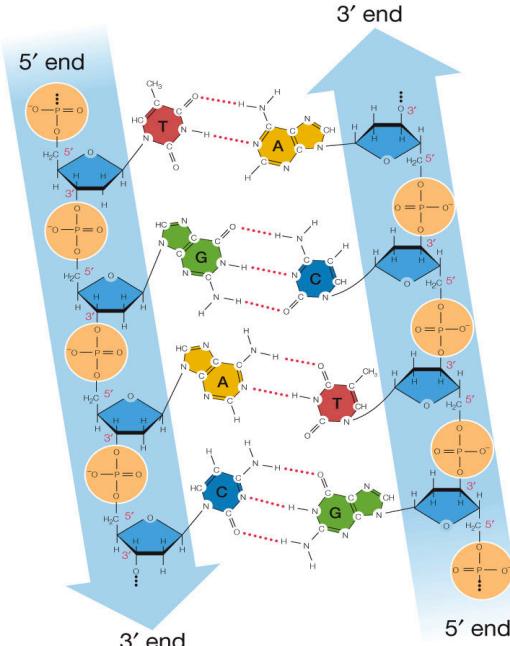
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- Antiparallel Stands of DNA

- Direction of strand is determined by the sugar–phosphate bonds.
- Phosphate groups connect to the 3' C of one sugar, and the 5' C of the next sugar.
- At one end of the chain—a free 5' phosphate group; at the other end a free 3' hydroxyl.



LIFE 8e, Figure 11.9 (Part 2)

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Objectives

4.1.1 - State that eukaryote chromosomes are made of DNA and proteins. [1]

7.1.2 - Outline the structure of nucleosomes. [2]

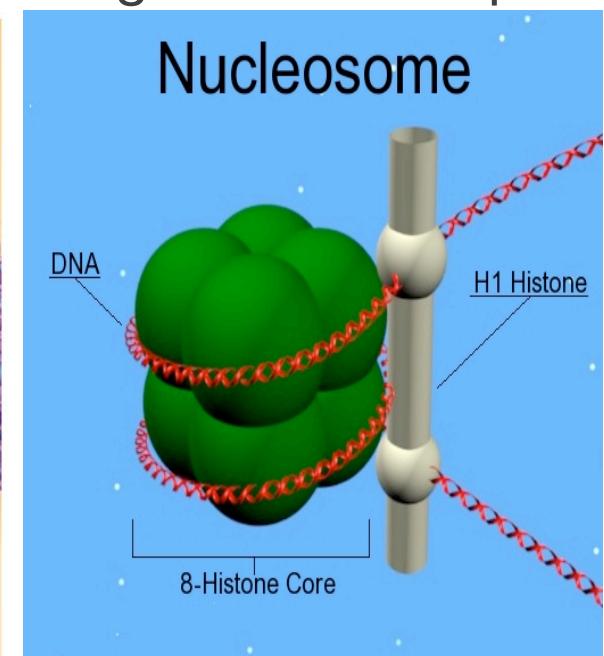
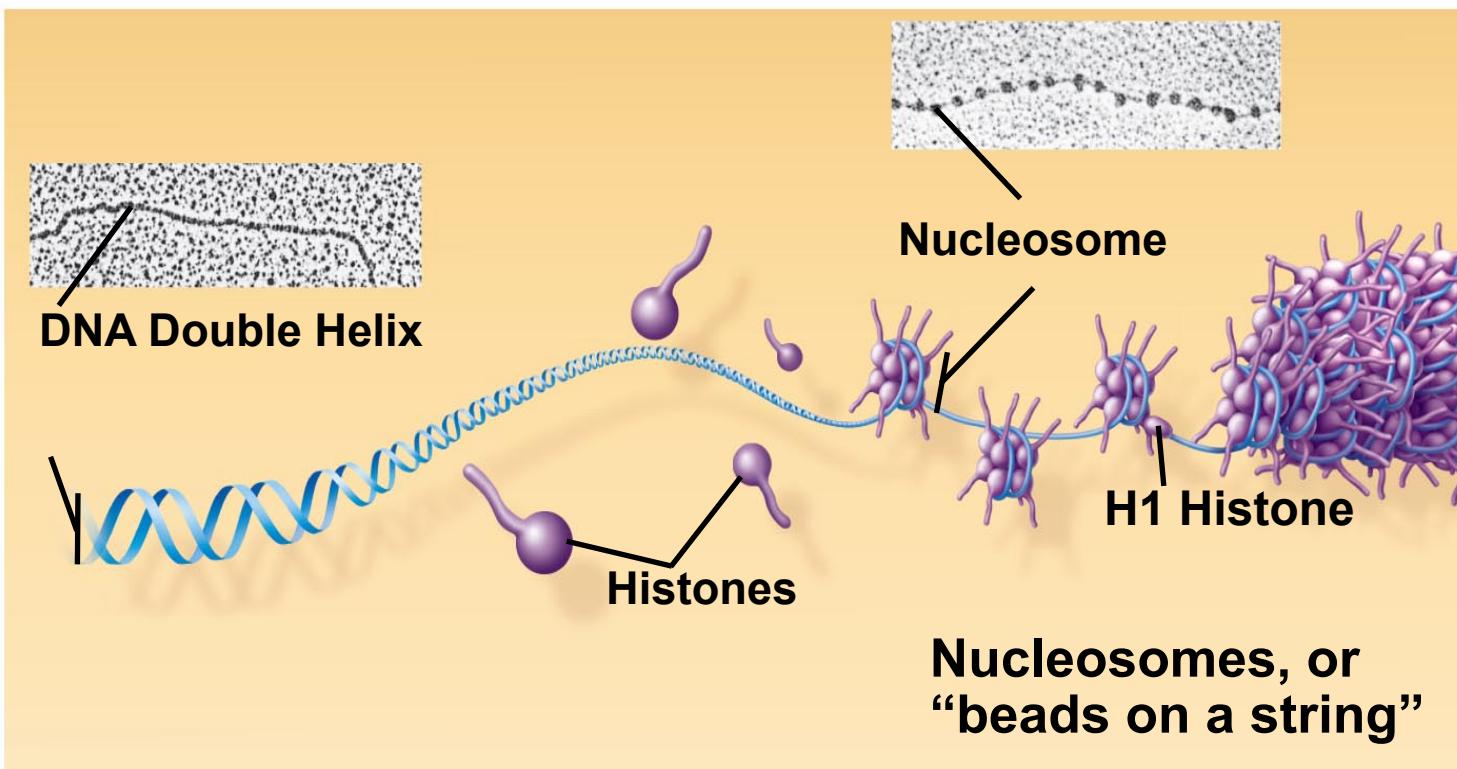
7.1.3 - State that nucleosomes help to supercoil chromosomes and help to regulate transcription. [1]

- Eukaryotic chromosomes are made of DNA and proteins.

- Human DNA in each cell is 3 meters long!

- Nucleosome consists of DNA wrapped around eight histone proteins and held together by another histone protein (H1 Histone).

- Nucleosomes help to supercoil chromosomes and help to regulate transcription.



Objectives

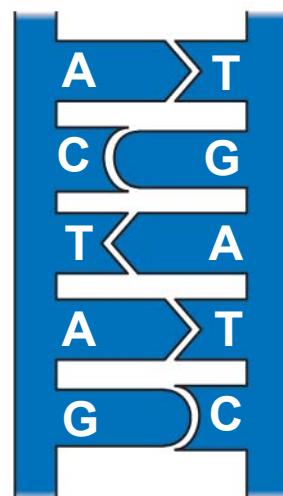
3.4.2 - Explain the significance of complementary base pairing in the conservation of the base sequence of DNA. [3]

3.4.3 - State that DNA replication is semi-conservative. [1]

- DNA replication is semi-conservative

- This type of replication maintains identical base sequences between the two new DNA strands.

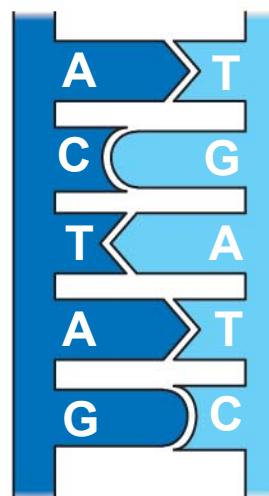
- Outline the qualities of DNA that make semi-conservative replication possible.



(a) Parent molecule



(b) Separation of strands



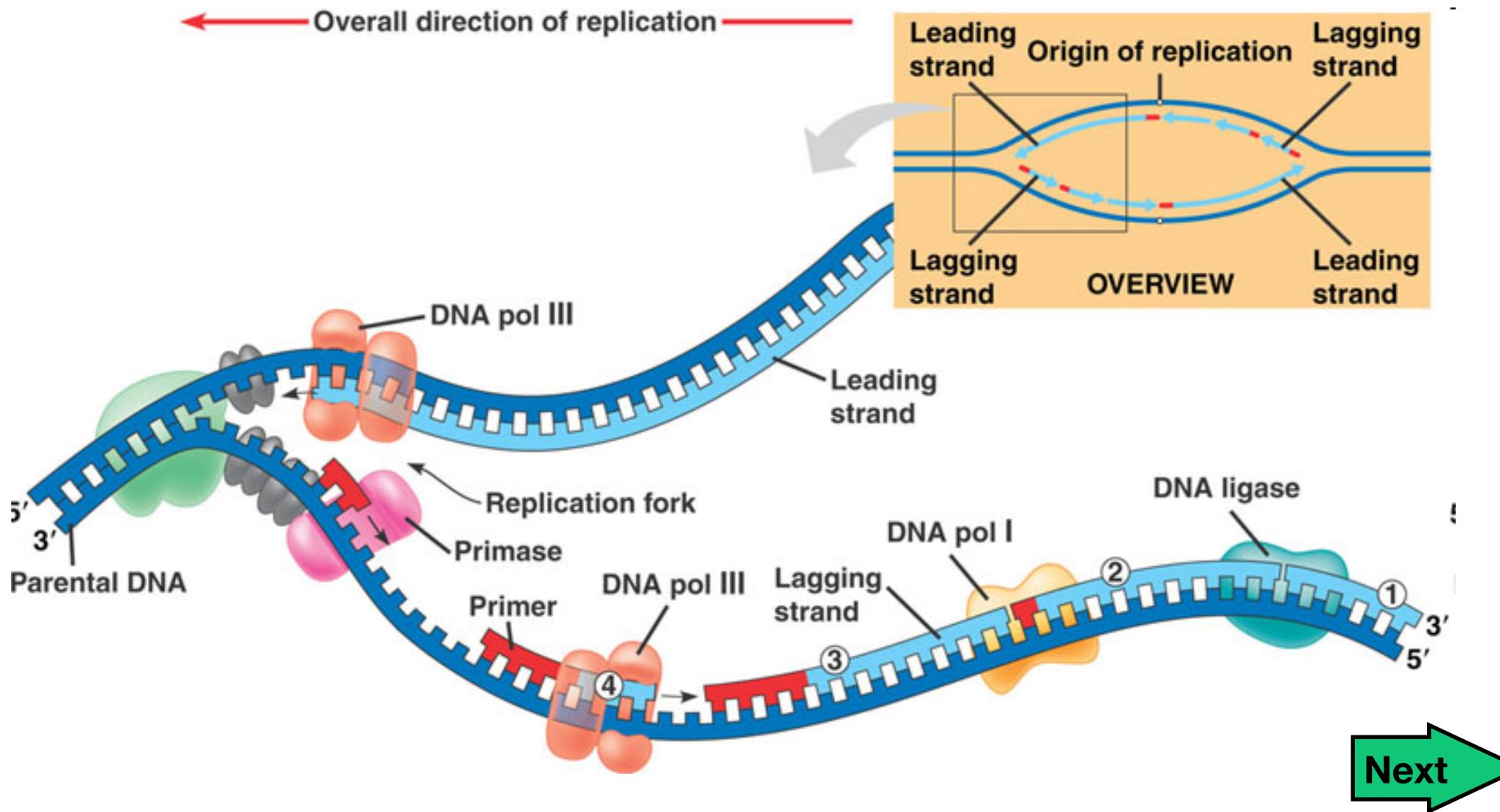
(c) "Daughter" DNA molecules, each consisting of one parental strand and one new strand

Objectives

3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]

7.2.1 - State that DNA replication occurs in a $5' \rightarrow 3'$ direction. [1]

- This whole process of DNA replication looks complicated, but let's break it down step by step...

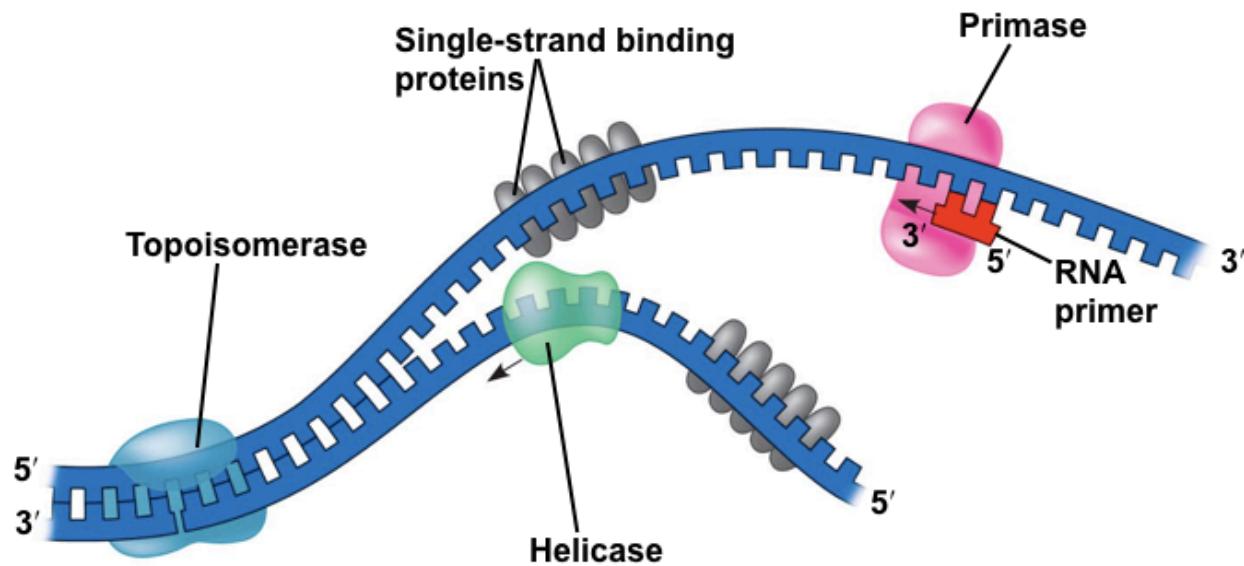


Next

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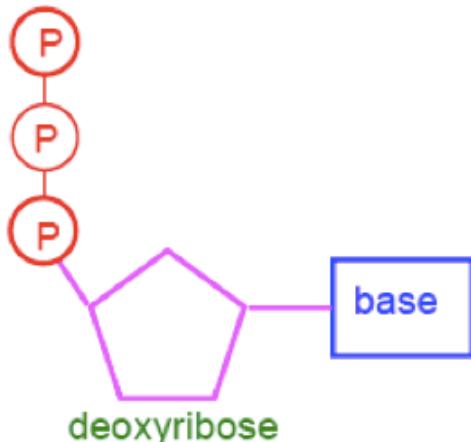
- Chromosomes have specific spots where replication begins. These are called 'origins of replication.'
- At the spots, DNA helicase binds to the DNA and separates the double helix into two single strands by breaking the hydrogen bonds between the nitrogenous bases. This forms a Y-shaped region called a replication fork.
- Single-strand binding proteins keep each single DNA strand separated.



3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]

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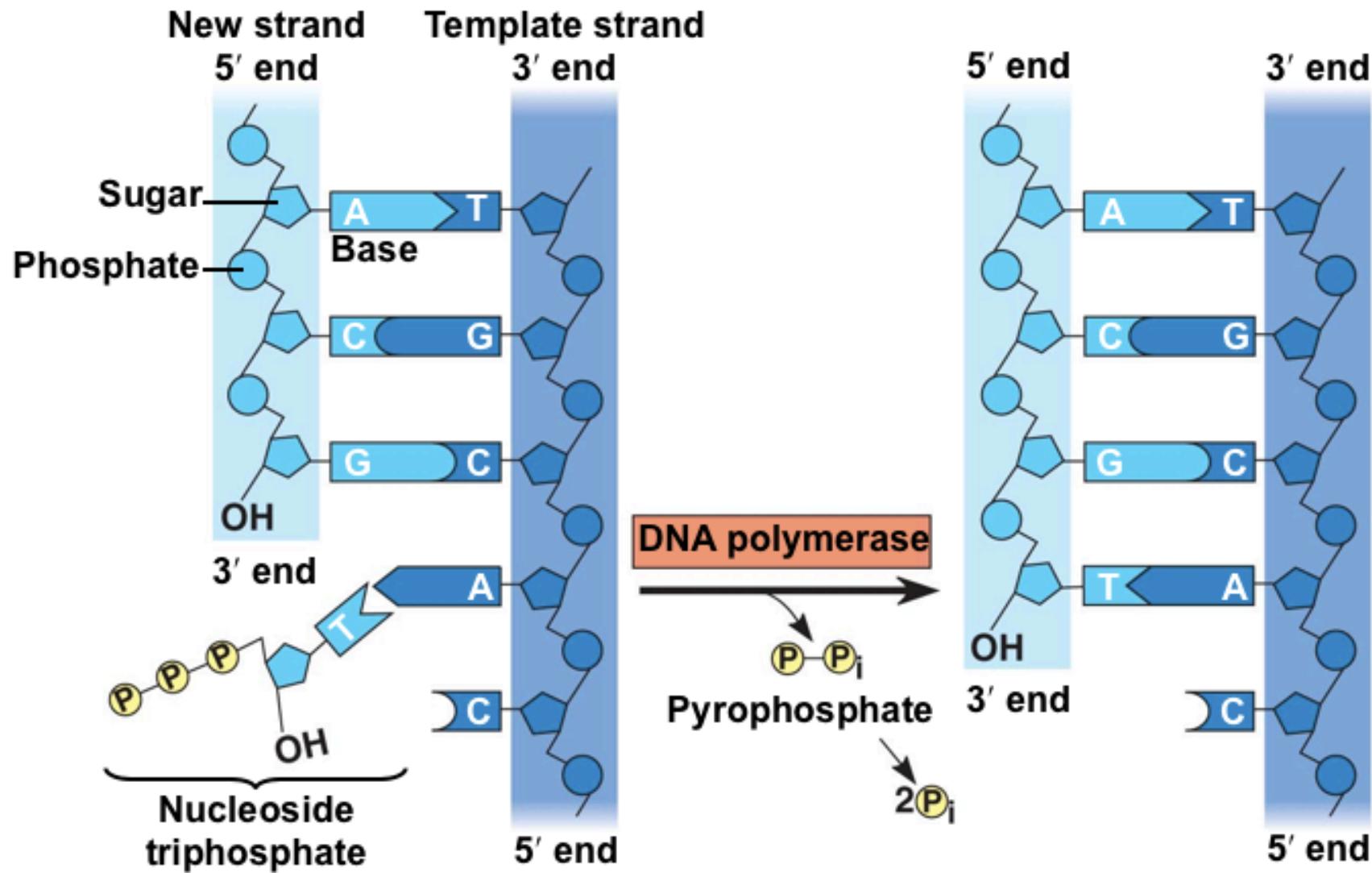
- With the DNA split, RNA primase adds RNA nucleotides to make a primer (5-10 nucleotides long) to initiate the DNA replication.
- DNA polymerase III catalyzes the elongation of new DNA strand.
 - The rate of elongation is about 50 nucleotides per second in human cells
 - DNA polymerase III adds free deoxynucleoside triphosphates.
 - When these are added, two phosphate groups are removed, which provide that energy for the polymerization of the new DNA molecule.



Next

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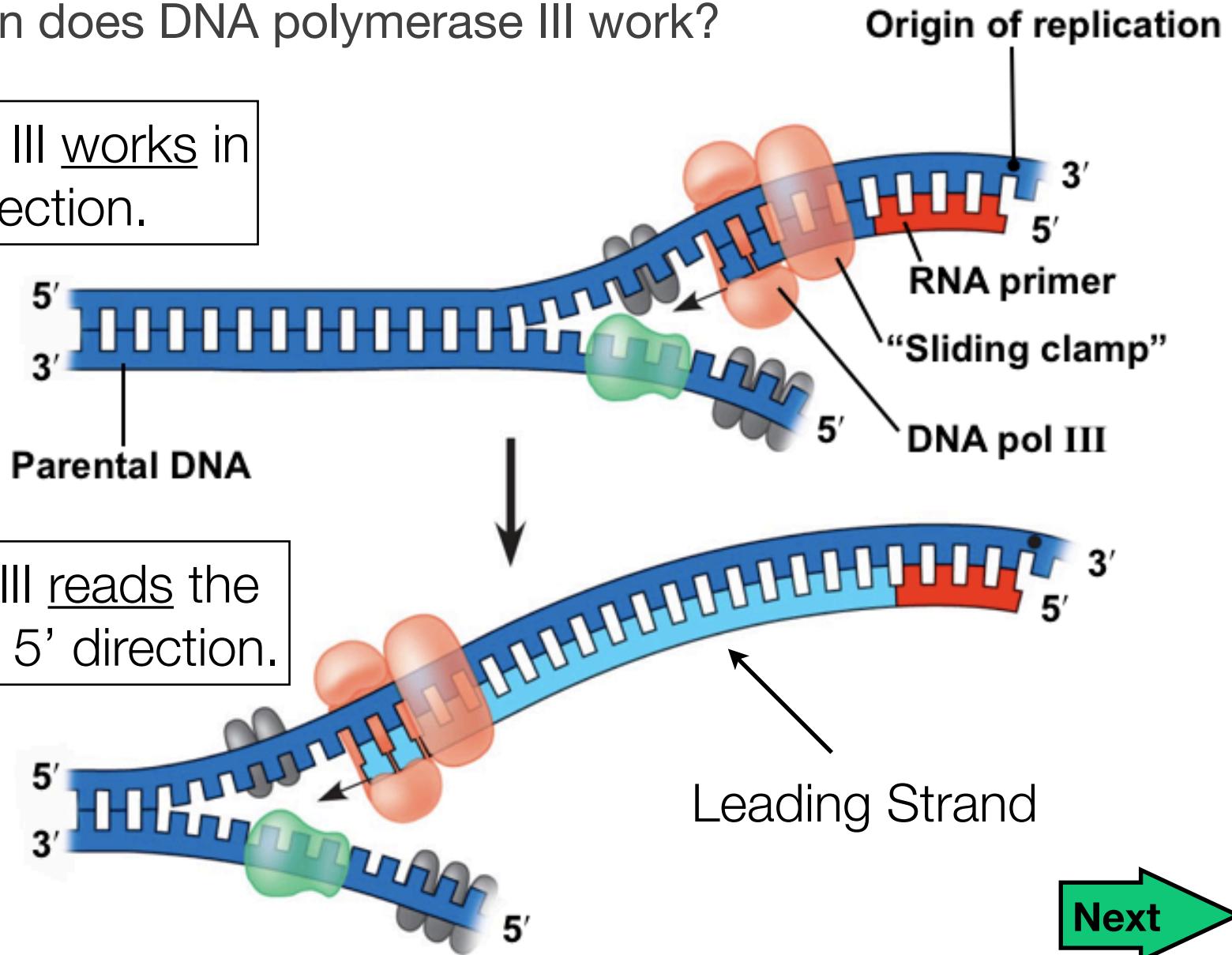
Next

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- In which direction does DNA polymerase III work?

DNA polymerase III works in a $5' \rightarrow 3'$ direction.



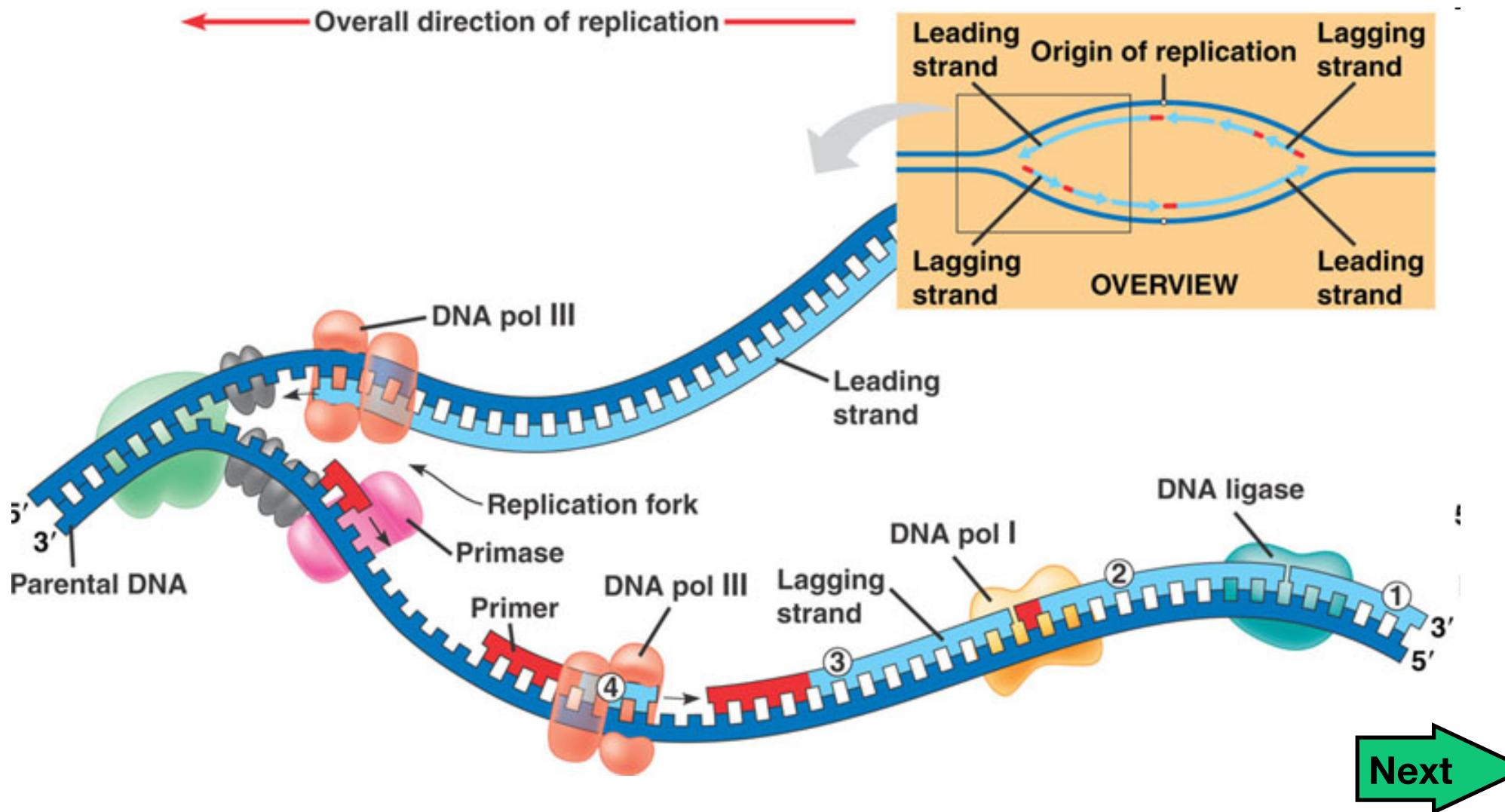
DNA polymerase III reads the template in a $3' \rightarrow 5'$ direction.

Next

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- If DNA polymerase III can only work in one direction, then how is the second DNA strand (lagging strand) synthesized?



Next

3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]

7.2.1 - State that DNA replication occurs in a $5' \rightarrow 3'$ direction. [1]

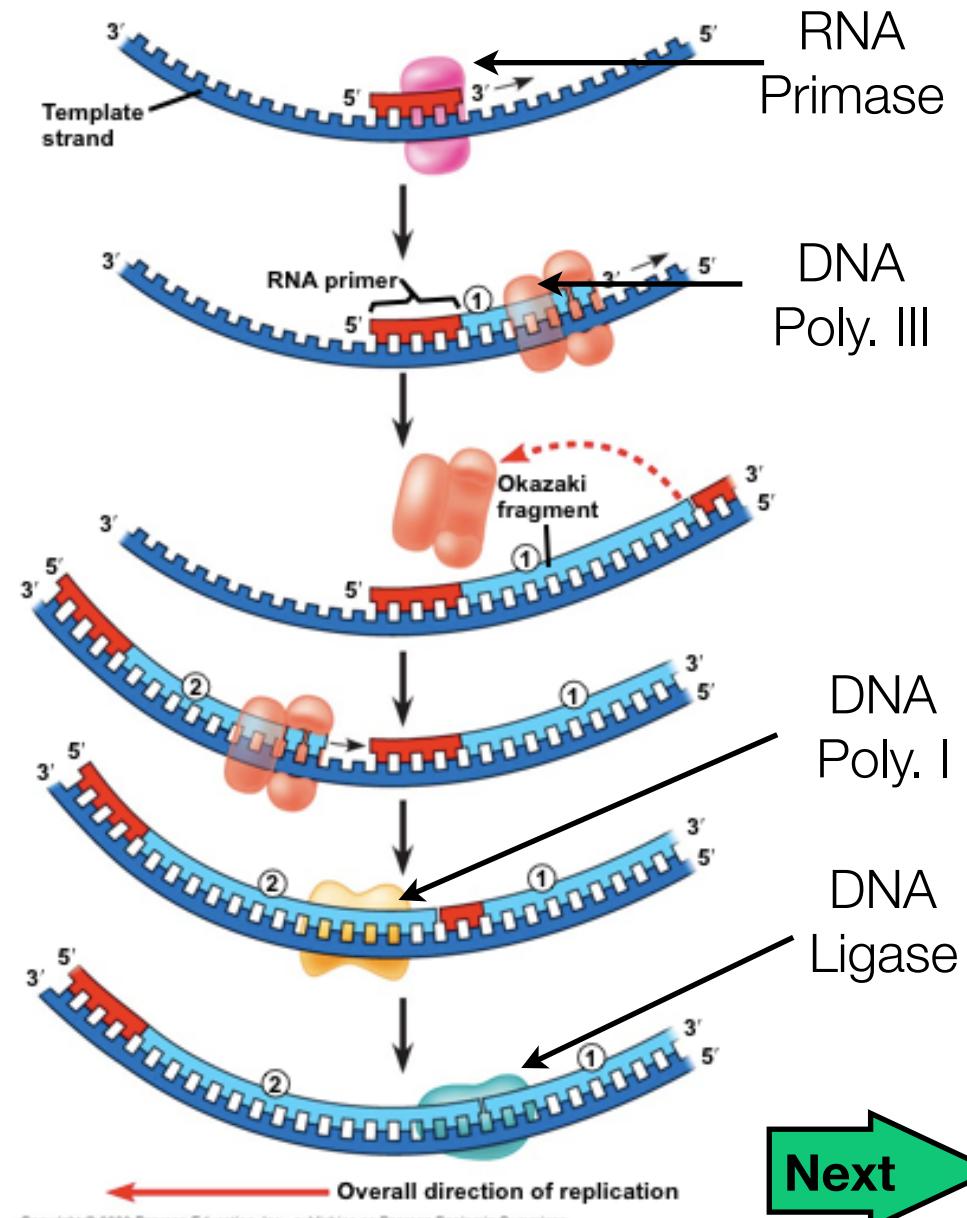
- Since DNA polymerase III can only work in a $5' \rightarrow 3'$ direction, it must work in the opposite direction on the lagging strand.

- This replication creates fragments of DNA called Okazaki fragments.

- DNA polymerase I replaced RNA primers with DNA.

- The fragmented pieces of DNA are connected by DNA ligase.

- Happens in both leading and lagging strand.



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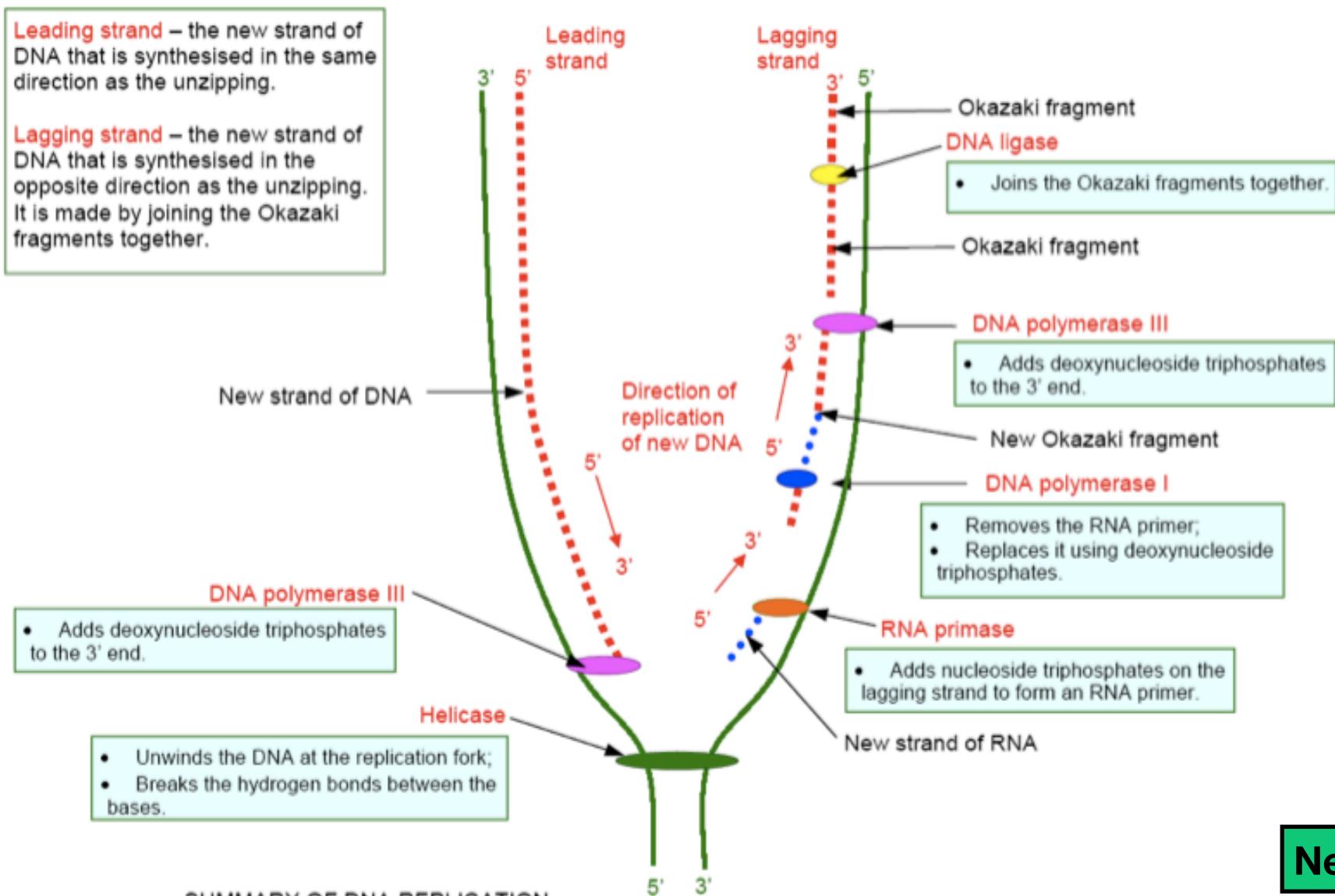
Table 16.1 Bacterial DNA Replication Proteins and Their Functions

Protein	Function
Helicase	Unwinds parental double helix at replication forks
Single-strand binding protein	Binds to and stabilizes single-stranded DNA until it can be used as a template
Topoisomerase	Relieves “overwinding” strain ahead of replication forks by breaking, swiveling, and rejoining DNA strands
Primase	Synthesizes an RNA primer at 5' end of leading strand and of each Okazaki fragment of lagging strand
DNA pol III	Using parental DNA as a template, synthesizes new DNA strand by covalently adding nucleotides to the 3' end of a pre-existing DNA strand or RNA primer
DNA pol I	Removes RNA nucleotides of primer from 5' end and replaces them with DNA nucleotides
DNA ligase	Joins 3' end of DNA that replaces primer to rest of leading strand and joins Okazaki fragments of lagging strand



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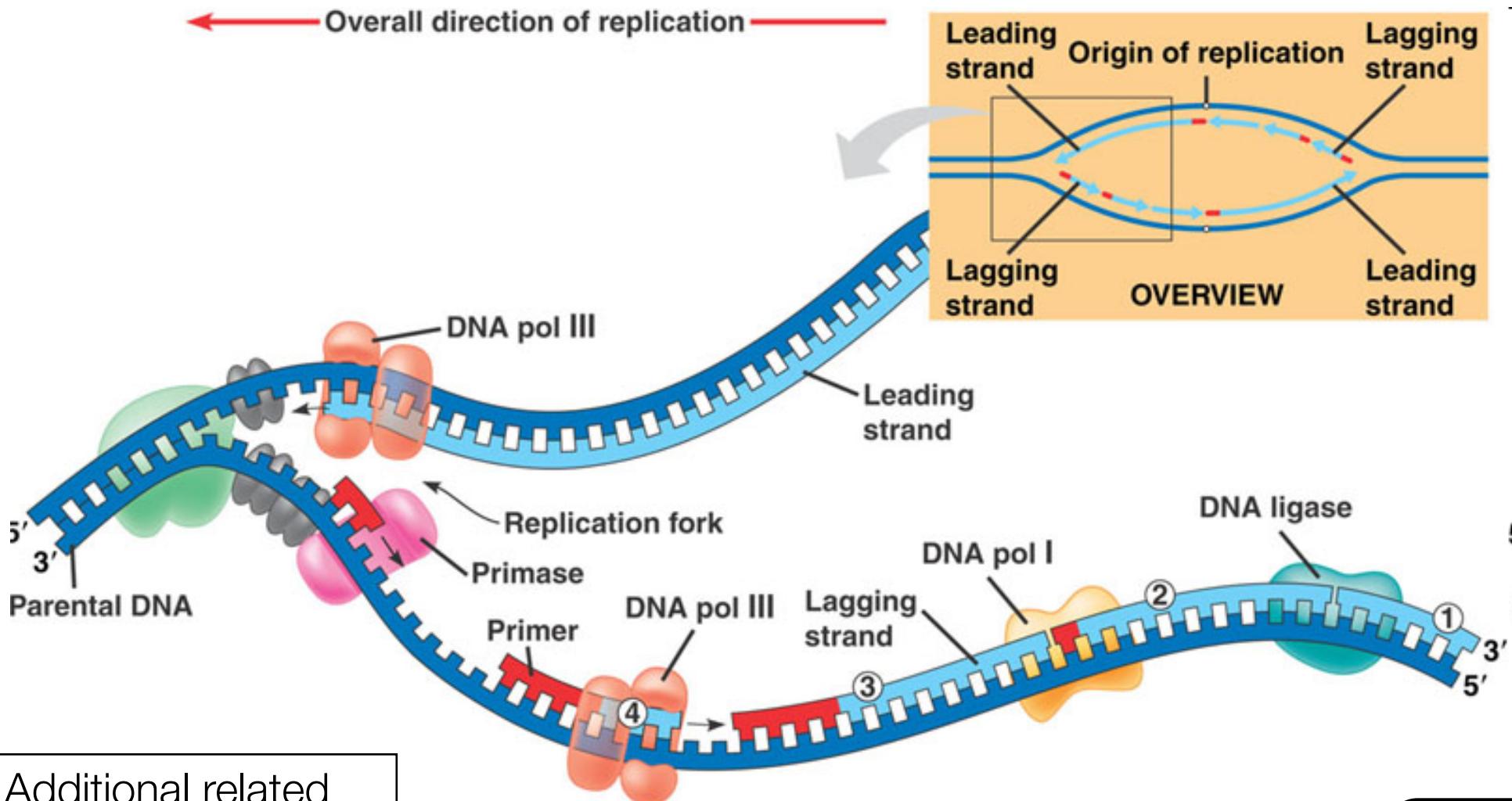


Next

3.4.1 - Explain DNA replication in terms of unwinding the double helix and separation of the strands by helicase, followed by formation of the new complementary strands by DNA polymerase. [3]

7.2.1 - State that DNA replication occurs in a $5' \rightarrow 3'$ direction. [1]

- After replication is complete, two identical strands of DNA are formed.

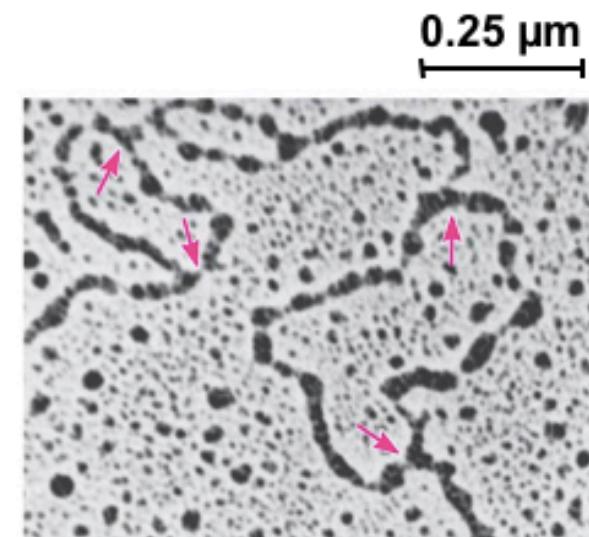
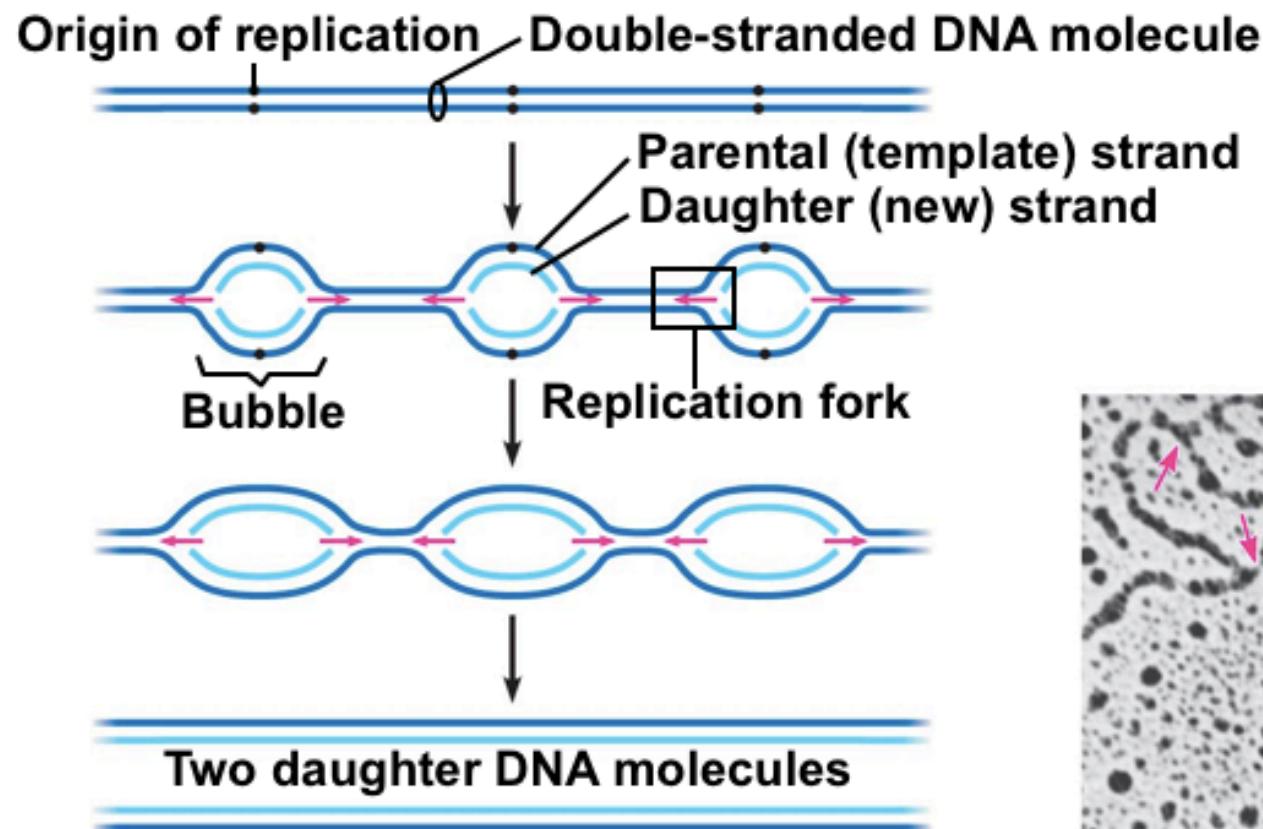


Additional related resources in wiki.

Objectives

7.2.3 - State that DNA replication is initiated at many points in eukaryotic chromosomes. [1]

- DNA replication is initiated at many points in eukaryotic chromosomes.
- These areas are called ‘origins of replication.’



(b) Origins of replication in eukaryotes

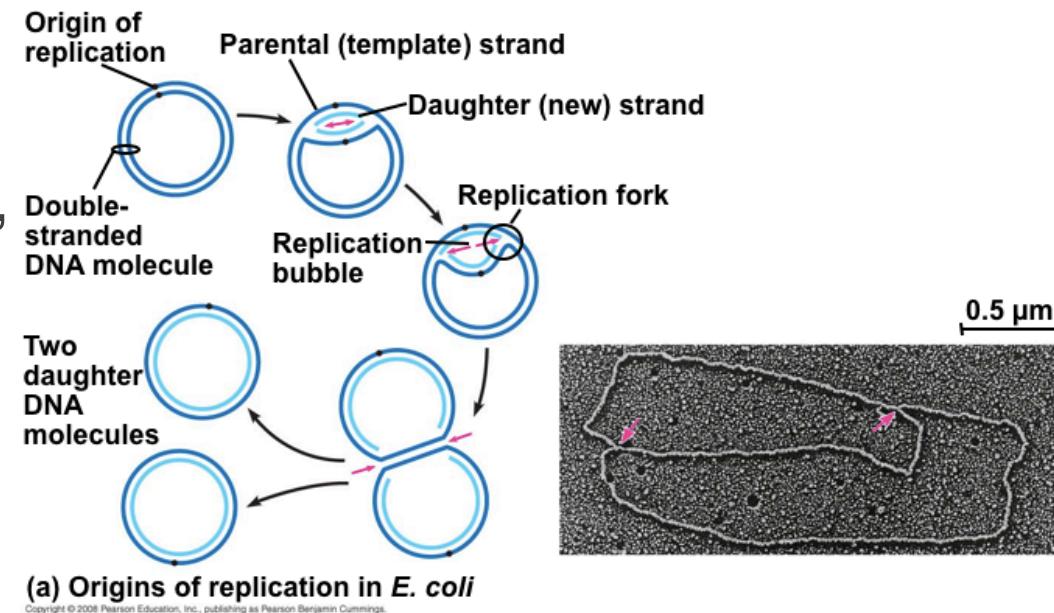
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Objectives

7.2.2 - Explain the process of DNA replication in prokaryotes, including the role of enzymes (helicase, DNA polymerase, RNA primase and DNA ligase), Okazaki fragments and deoxynucleoside triphosphates. [3]

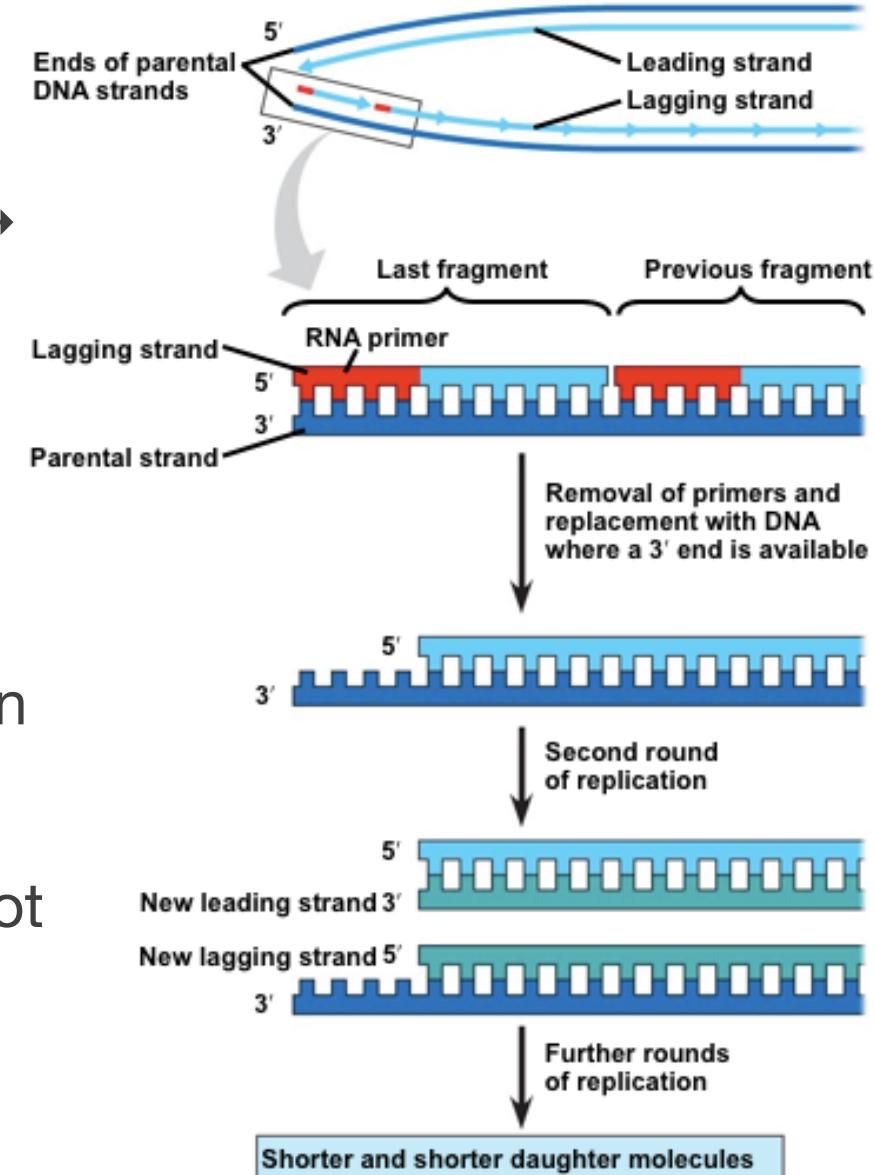
- Prokaryotic DNA replication is very similar to eukaryotes except for a few differences:

- Prokaryotes only have 1 circular strand of DNA
 - Only one ‘origin of replication.’
- DNA polymerase III adds nucleotides faster in prokaryotes than in eukaryotes.
- Prokaryotes lack a nucleus.
 - DNA replication occurs in the cytoplasm.



BONUS - Telomeres

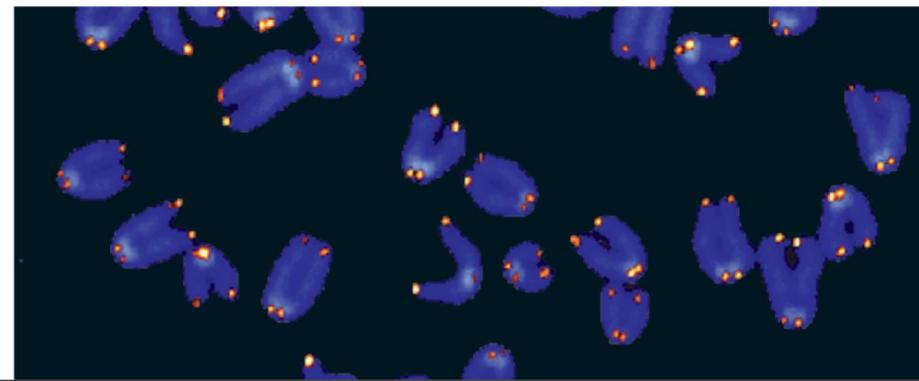
- Eukaryotic DNA is linear, which creates a problem with DNA replication.
- DNA polymerase III can only work in a $5' \rightarrow 3'$ direction. The $5'$ ends of each daughter DNA strand cannot be replicated.
 - DNA polymerase III needs to attach to a $3'$ end in order to add new nucleotides
 - This is why RNA primase is required in DNA replication.
- Since the ends of each chromosome cannot be replicated, each new daughter DNA strand is shorter than the parental strand.



Next

BONUS - Telomeres

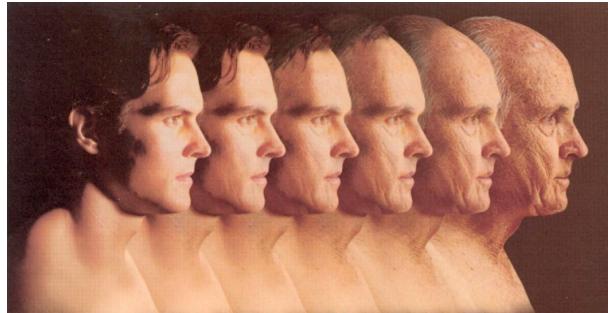
- Eukaryotic chromosomal DNA molecules have at their ends nucleotide sequences called telomeres.
 - Telomeres contain repetitive, noncoding nucleotide sequences.
 - Human chromosome telomeres (TTAGGG) are repeated about 2500 times.
- Telomeres do not prevent the shortening of DNA molecules, but they do postpone the erosion of genes near the ends of DNA molecules.
 - Chromosomes can lose 50–200 base pairs with each replication. After 20–30 divisions, the cell dies.



Next 

BONUS - Telomeres

- Why has evolution not fixed this problem? Maybe this is the solution to a problem...
 - The shortening of telomeres might protect cells from cancerous growth by limiting the number of cell divisions.
 - Some cells—bone marrow stem cells, gamete-producing cells—have telomerase, an enzyme that catalyzes the addition of telomeres.
 - 90% of human cancer cells have telomerase; normal cells do not.
 - Some anticancer drugs target telomerase.
 - It has also been proposed that the shortening of telomeres is connected to aging.



Additional related resource in wiki.

Objectives

3.5.1 - Compare the structure of RNA and DNA. [3]

- Shape:

DNA - Double-Stranded

RNA - Single-stranded

- Sugar:

DNA - Deoxyribose

Ribose - Ribose

- Bases:

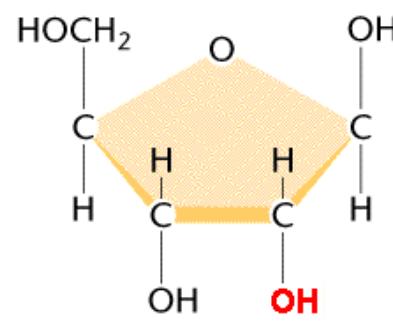
DNA - Thymine

RNA - Uracil

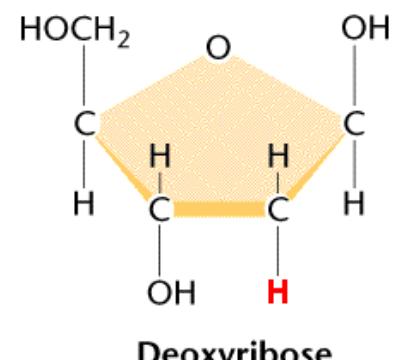
- Location

DNA - Nucleus

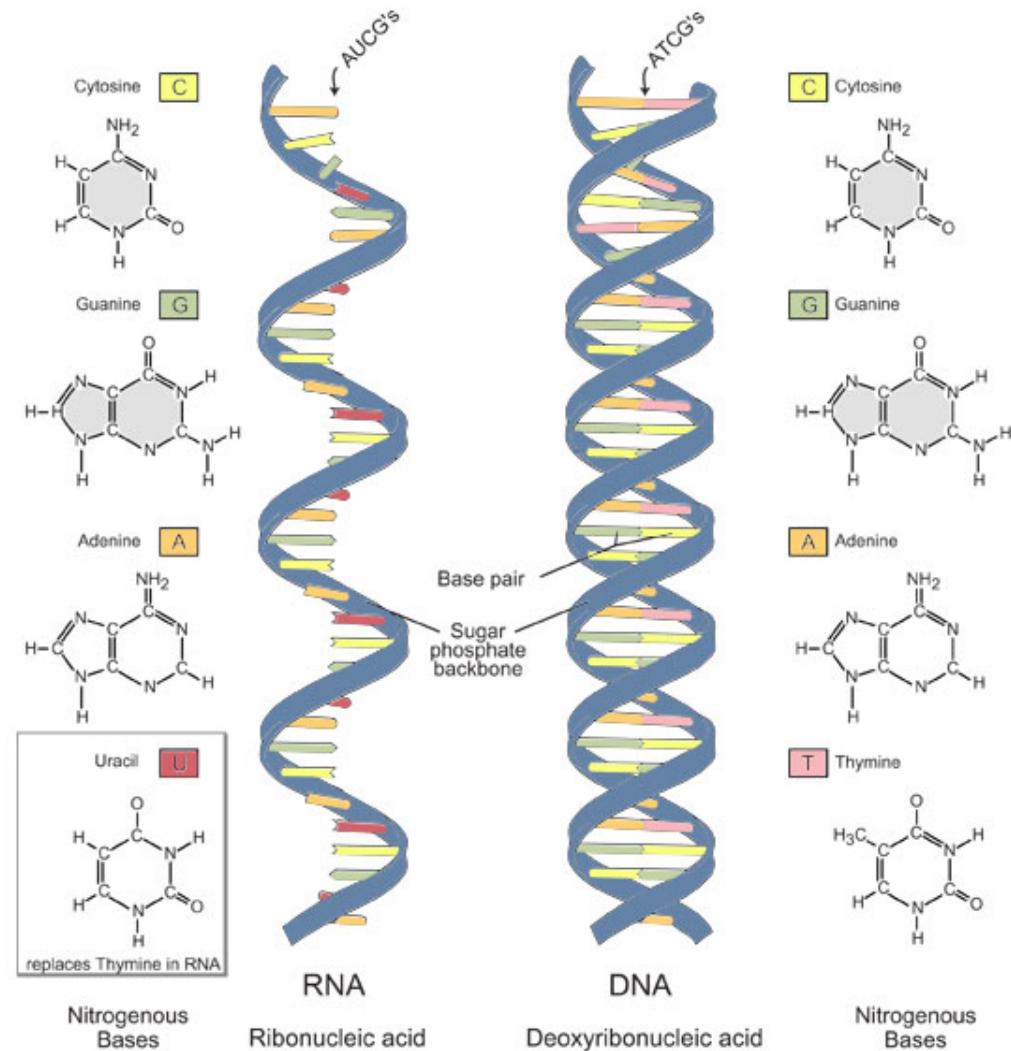
RNA - Leaves the nucleus



Ribose



Deoxyribose



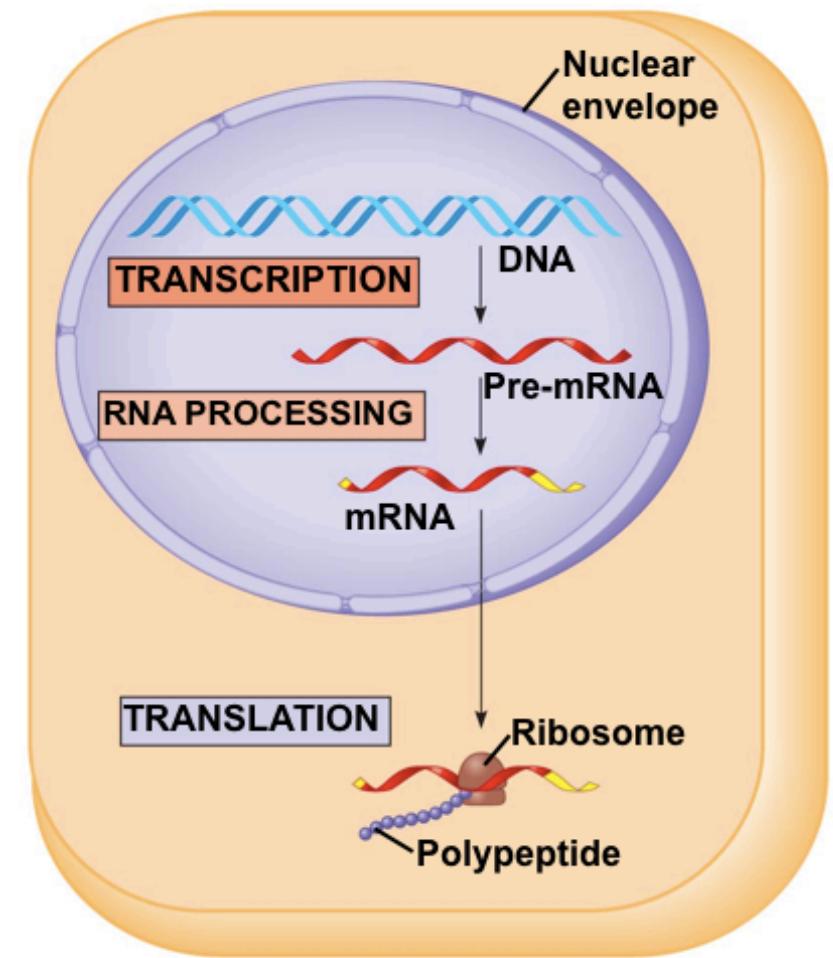
IB Note: Limit this to the names of sugars, bases and the number of strands.

Image adapted from: National Human Genome Research Institute. Talking Glossary of Genetic Terms. Available at: www.genome.gov/Pages/Hyperion/DIR/VIP/Glossary/Illustration/rna.shtml.

Objectives

3.5.2 - Outline DNA transcription in terms of the formation of an RNA strand complementary to the DNA strand by RNA polymerase. [2]

- RNA is the intermediate between genes and the proteins for which they code
- **Transcription** is the synthesis of RNA under the direction of DNA
 - Transcription produces **messenger RNA (mRNA)**
- **Translation** is the synthesis of a polypeptide, which occurs under the direction of mRNA
 - **Ribosomes** are the sites of translation



(b) Eukaryotic cell

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Additional related resource in wiki.



Next

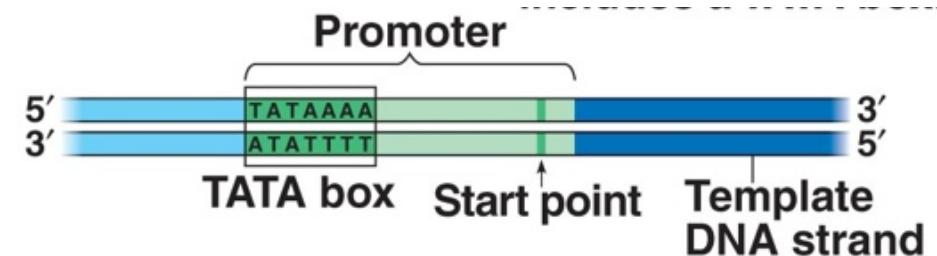
3.5.2 - Outline DNA transcription in terms of the formation of an RNA strand complementary to the DNA strand by RNA polymerase. [2]

7.3.2 - Distinguish between the sense and antisense strands of DNA. [2]

- Promoter region

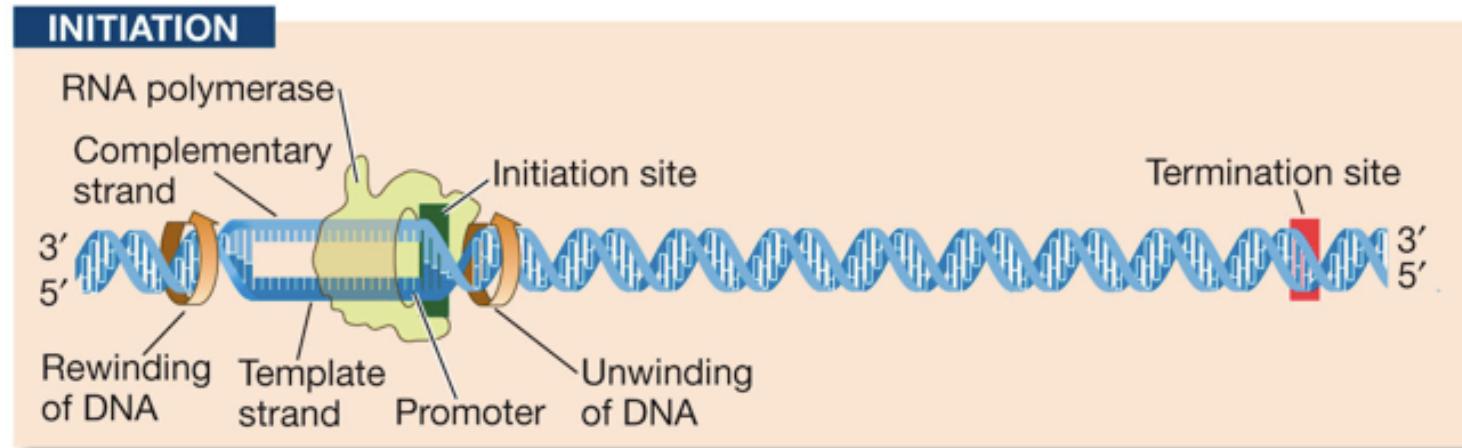
Start point – Contains the TATA box – Promoter DNA sequence

- ONLY 1 of the 2 DNA strands is used:



- Template strand (anti-sense)

- The non-template (sense) strand is identical to RNA created (except Ts are replaced with Us)



IB Note: The sense strand (coding strand) has the same base sequence as mRNA with uracil instead of thymine. The antisense (template) strand is transcribed.

Next

3.5.2 - Outline DNA transcription in terms of the formation of an RNA strand complementary to the DNA strand by RNA polymerase. [2]

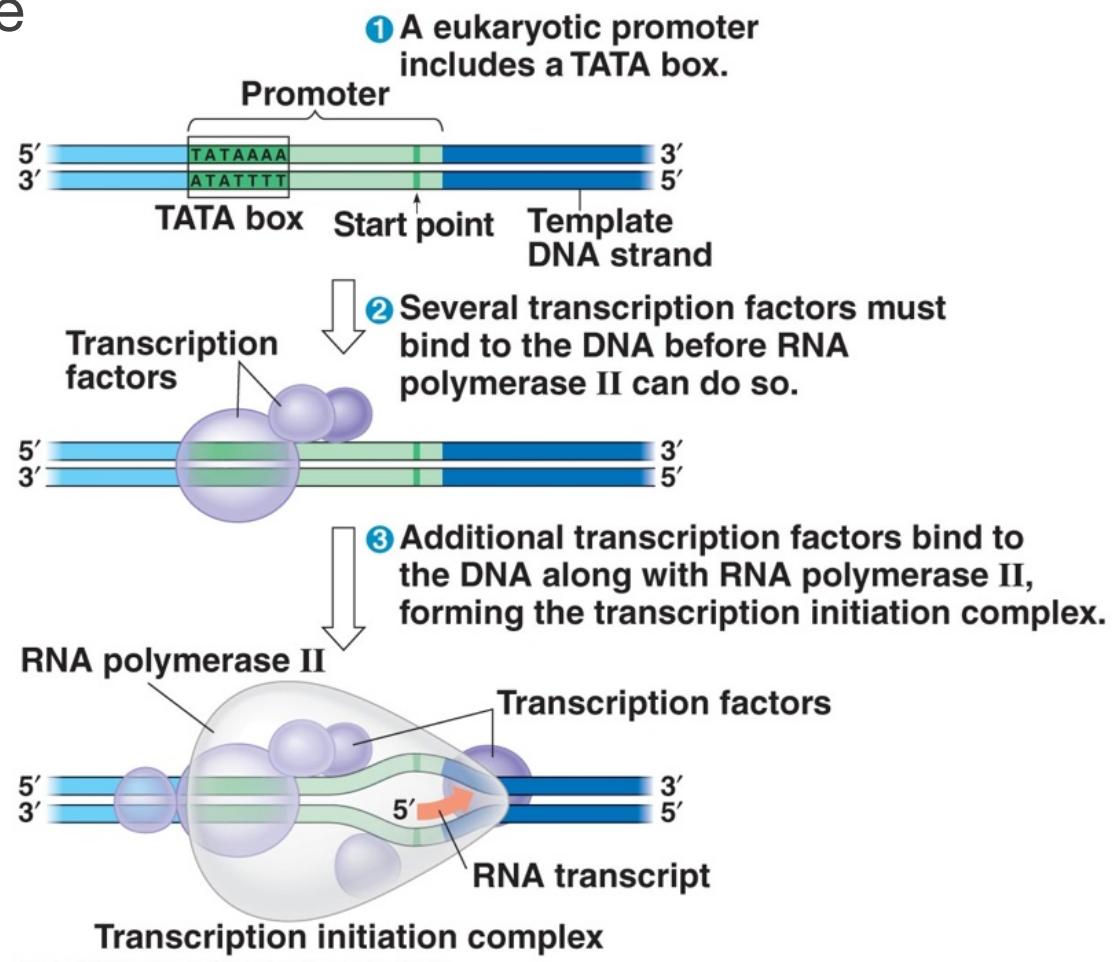
7.3.1 - State that transcription is carried out in a $5' \rightarrow 3'$ direction. [1]

- RNA polymerase: attaches to the promoter region, unwinds DNA and adds free RNA nucleotides in $5' \rightarrow 3'$ direction (7.3.1)

- Terminator – DNA sequence signals the release of RNA

- Again, energy comes from nucleoside triphosphates being added

- A gene can be transcribed simultaneously by several RNA polymerases

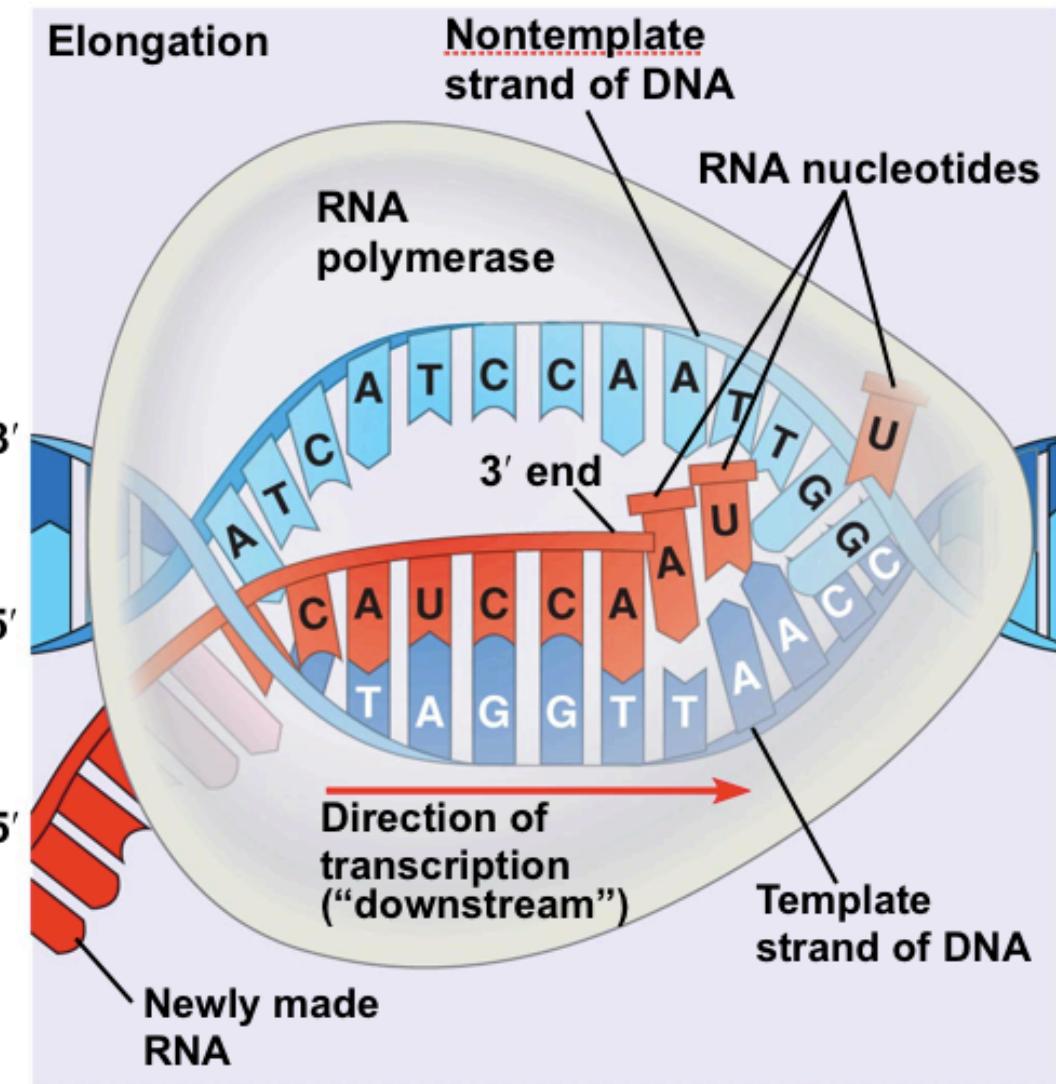


IB Note: The 5' end of the free RNA nucleotide is added to the 3' end of the RNA molecule that is already synthesized.

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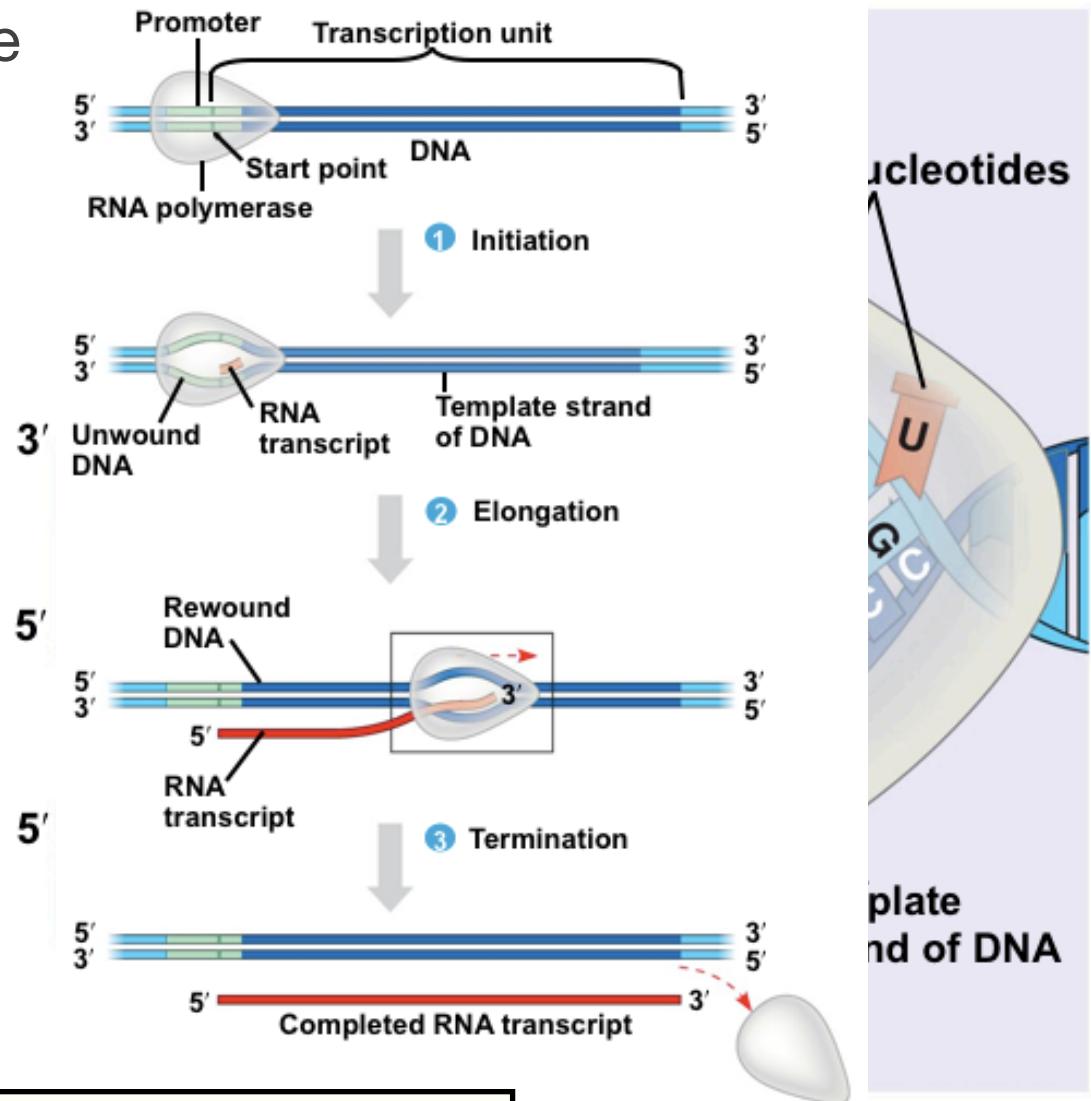


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Objectives

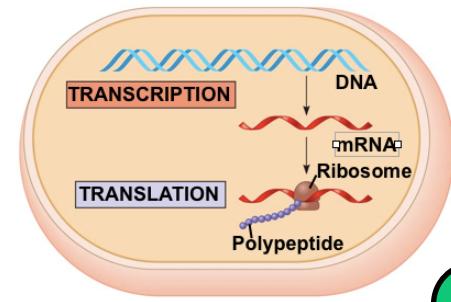
7.3.3 - Explain the process of transcription in prokaryotes, including the role of the promoter region, RNA polymerase, nucleoside triphosphates and the terminator. [3]

- Eukaryotes:

- RNA transcripts are modified through RNA processing to yield finished mRNA
- At least three types of RNA polymerase
 - RNA polymerase II makes mRNA, other polymerase make other types of RNA.
- Use transcription factors to help initiate transcription.
- Polyadenylation signal terminates transcription.
 - Proteins downstream cut RNA and release it from DNA.

- Prokaryotes:

- mRNA produced by transcription is immediately translated without more processing
- Only one type of RNA polymerase
- No transcription factors
- Has a specific DNA terminator sequence



(a) Bacterial cell
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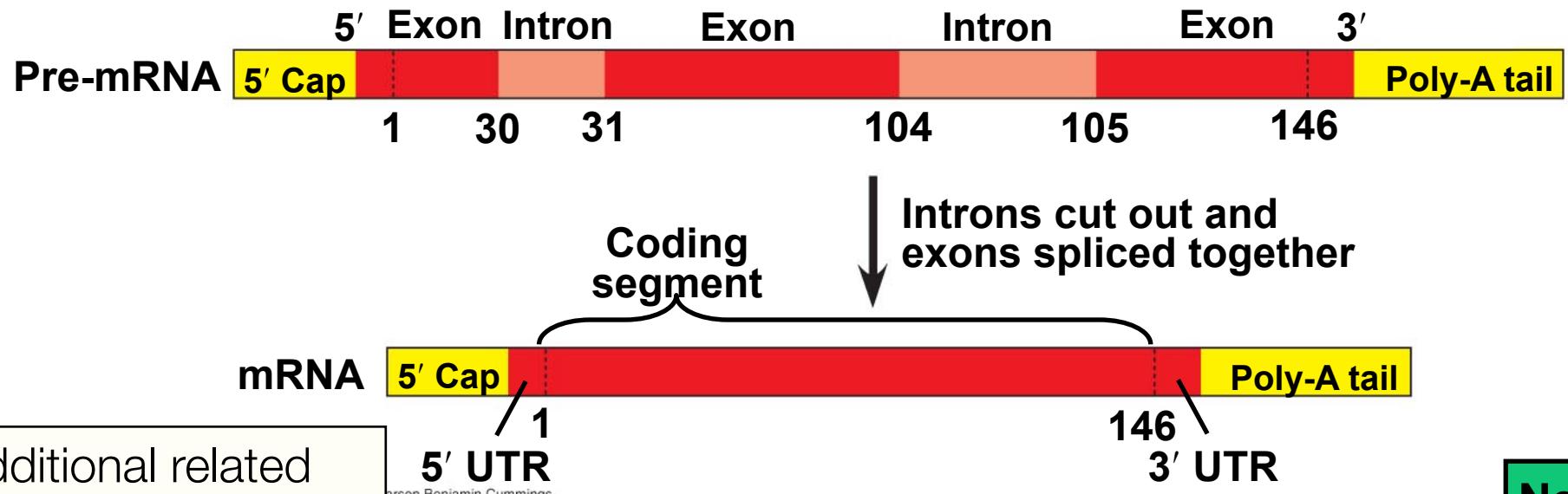
Objectives

7.1.5 - State that eukaryotic genes can contain exons and introns. [1]

7.3.4 - State that eukaryotic RNA needs the removal of introns to form mature mRNA. [1]

- Further Processing

- 5' cap added – guanosine triphosphate
- Poly-A tail – helps it get out of nucleus
 - Both protect RNA from degradation, help it exit the nucleus AND attach to a ribosome for translation



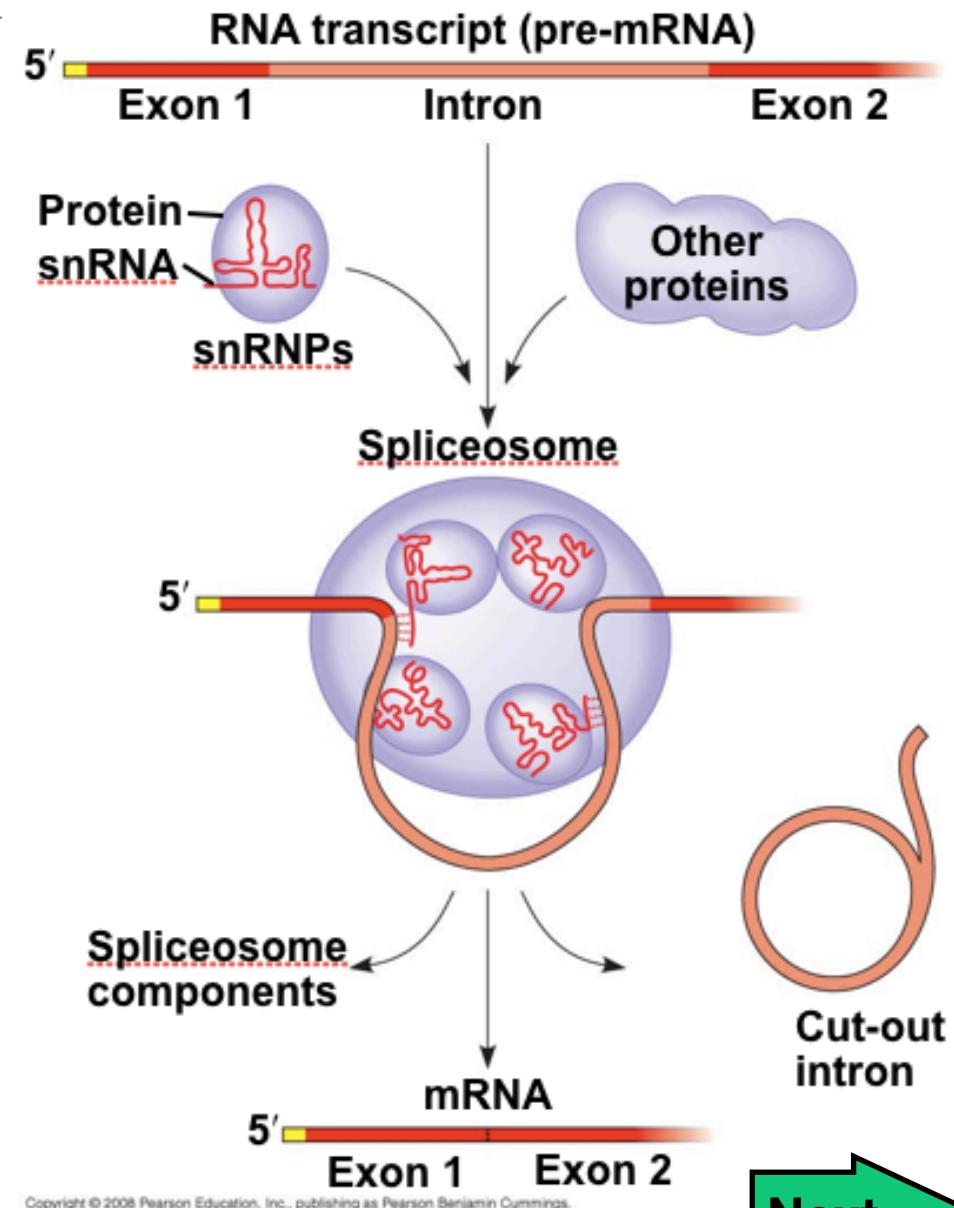
Additional related resource in wiki.

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Next

- 7.1.5 - State that eukaryotic genes can contain exons and introns. [1]
7.3.4 - State that eukaryotic RNA needs the removal of introns to form mature mRNA. [1]

- The RNA made contains non-coding regions not directly used in making the polypeptide – INTRONS
- Small Nuclear Ribonucleoproteins (snRNPs) assemble to form spliceosomes that recognize these sequences and help splice the RNA at the ends of an intron
 - LEAVES EXONS (coding regions) in tact



Additional related resource in wiki.

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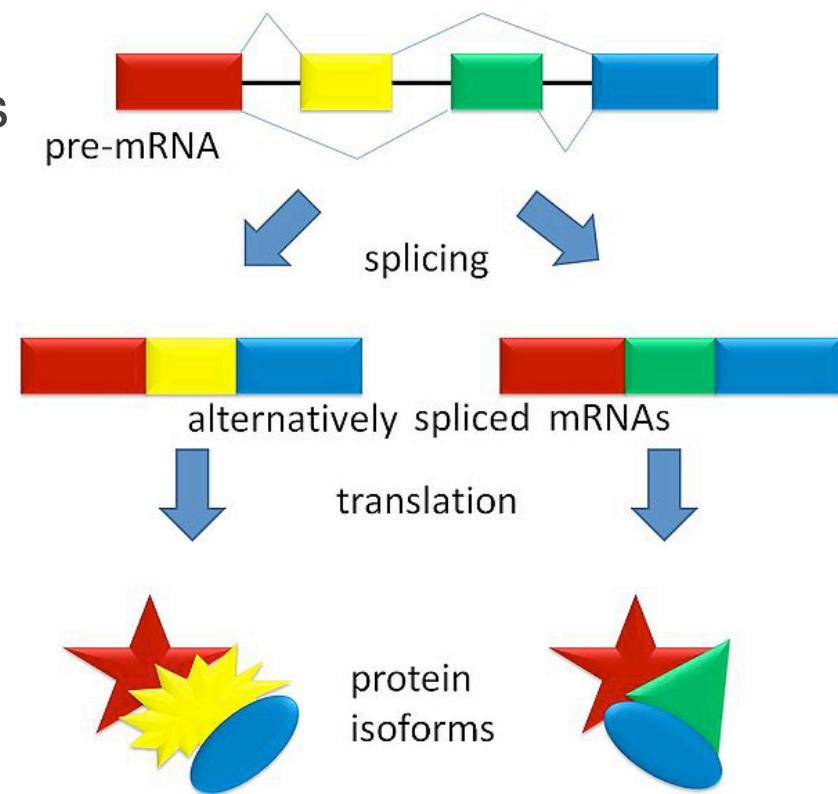
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7.3.4 - State that eukaryotic RNA needs the removal of introns to form mature mRNA. [1]

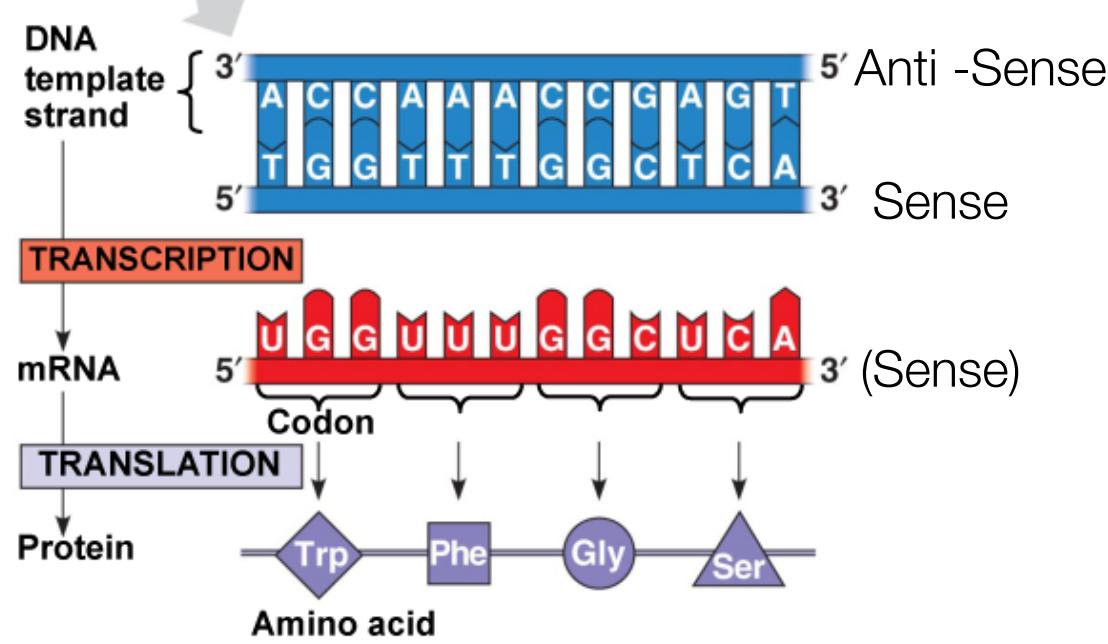
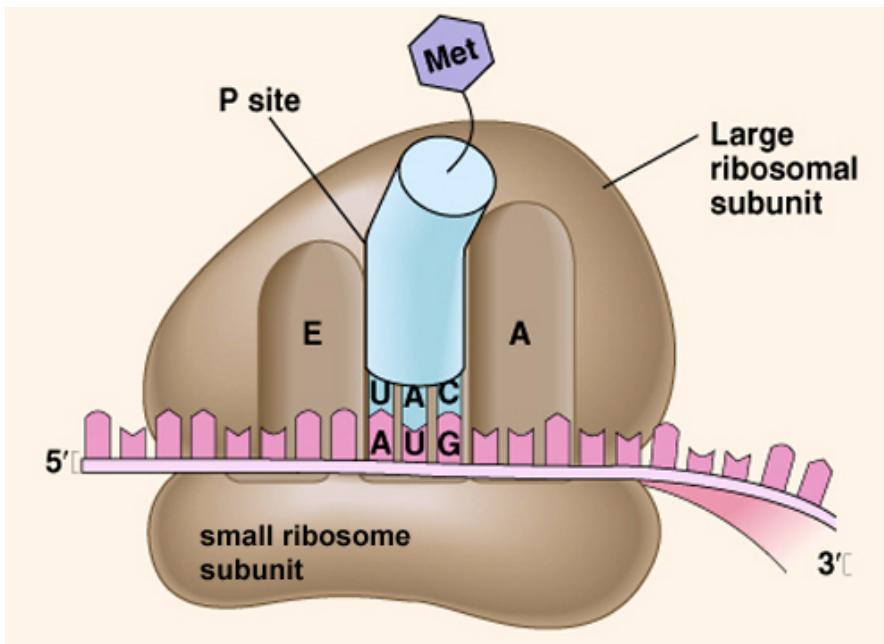
3.5.5 - Discuss the relationship between one gene and one polypeptide. [3]

- Originally it was thought that each gene only coded for one single protein.
- Today there have been many exceptions that have been discovered.
- Some genes can encode more than one kind of polypeptide, depending on which segments are treated as exons during RNA splicing
 - Such variations are called alternative RNA splicing
- Because of alternative splicing, the number of different proteins an organism can produce is much greater than its number of genes
- Regulates gene expression with splicing activators and splicing suppressors



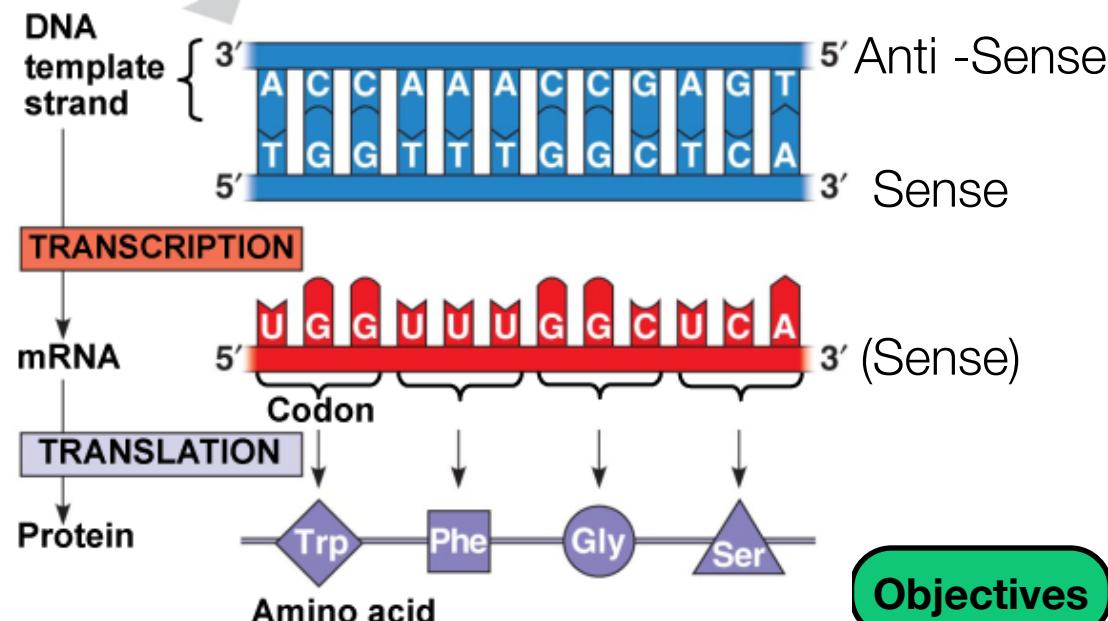
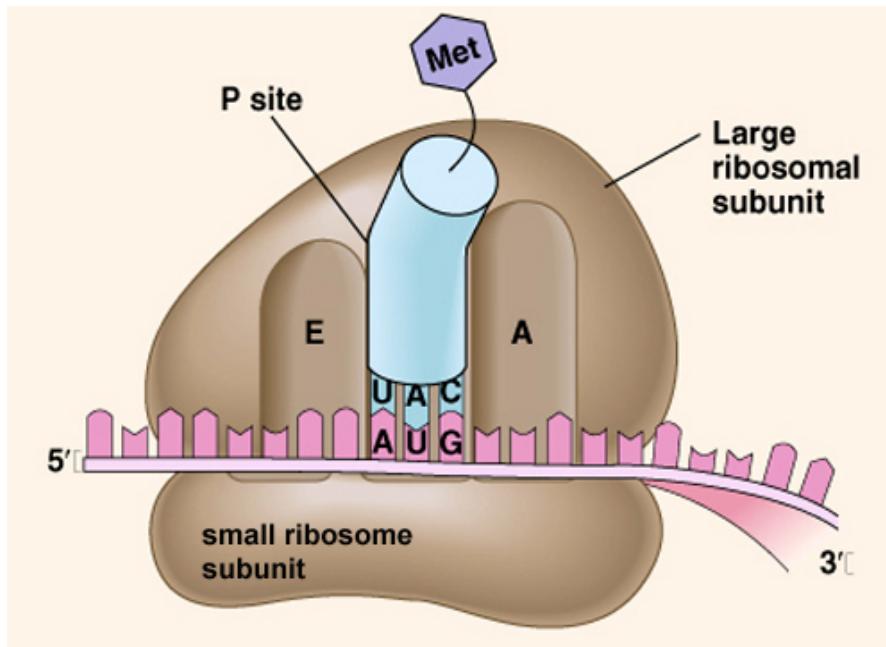
3.5.3 - Describe the genetic code in terms of codons composed of triplets of bases. [2]

- Now that your cell has a mature mRNA, what happens next?
 - The mRNA is translated into a series of amino acids with the help of ribosomes and tRNA molecules
 - The mRNA carries information and is translated in 3-letter sequences called codons (1 codon = 1 amino acid)
 - The tRNA carries the amino acid (as well as anticodon to match codon)



3.5.3 - Describe the genetic code in terms of codons composed of triplets of bases. [2]

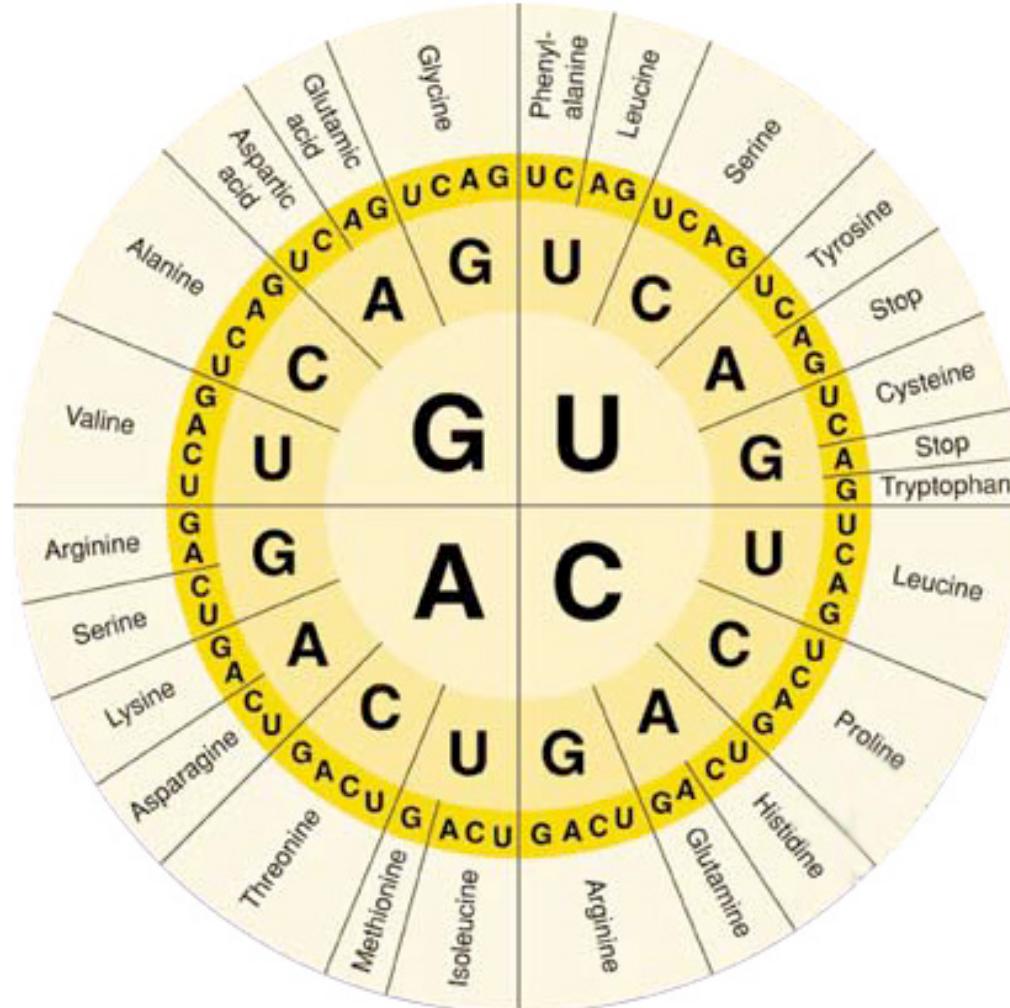
- Now that your cell has a mature mRNA, what happens next?
 - The mRNA is translated into a series of amino acids with the help of ribosomes and tRNA molecules
- The mRNA sequence is read in groups of three bases called codons. Using 4 nucleotides (ATCG) to make 3-letter sequences, how many possible codons are there?
 - The genetic code is read from the 5' end of the mRNA strand (on)



3.5.4 - Explain the process of translation, leading to polypeptide formation. [3]

7.4.6 - Explain the process of translation, including ribosomes, polysomes, start codons and stop codons. [3]

- There are 64 possible codons, but only 20 amino acids
- WE use the image below to translate mRNA into a polypeptide
- How do our cells do it?



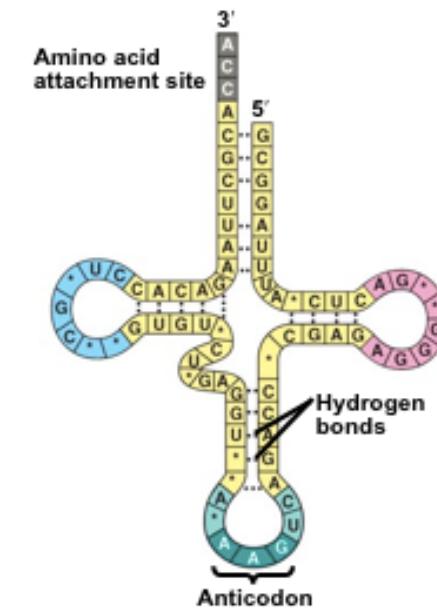
Next 

7.4.1 - Explain that each tRNA molecule is recognized by a tRNA-activating enzyme that binds a specific amino acid to the tRNA, using ATP for energy. [3]

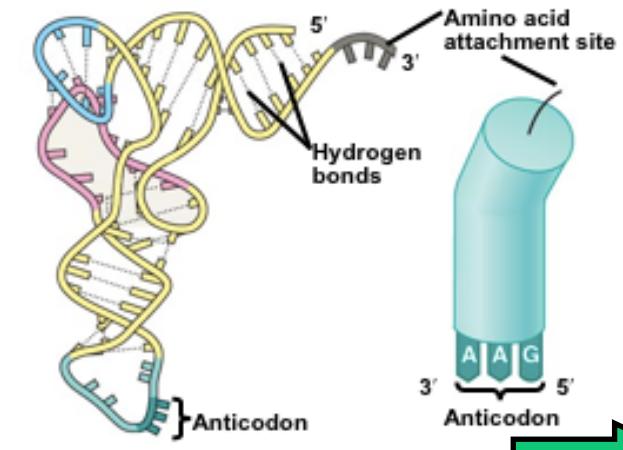
- Our cells use transfer RNA molecules (tRNA) to help with the process of translation

- Molecules of tRNA are not identical:

- Each carries a specific amino acid on one end
- Each has an anticodon on the other end; the anticodon base-pairs with a complementary codon on mRNA
- A tRNA molecule consists of a single RNA strand that is only about 80 nucleotides long
- Because of hydrogen bonds, tRNA actually twists and folds into a three-dimensional molecule



(a) Two-dimensional structure



(b) Three-dimensional structure

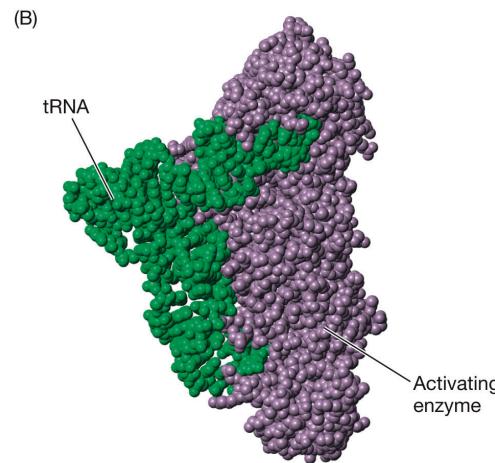
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Next

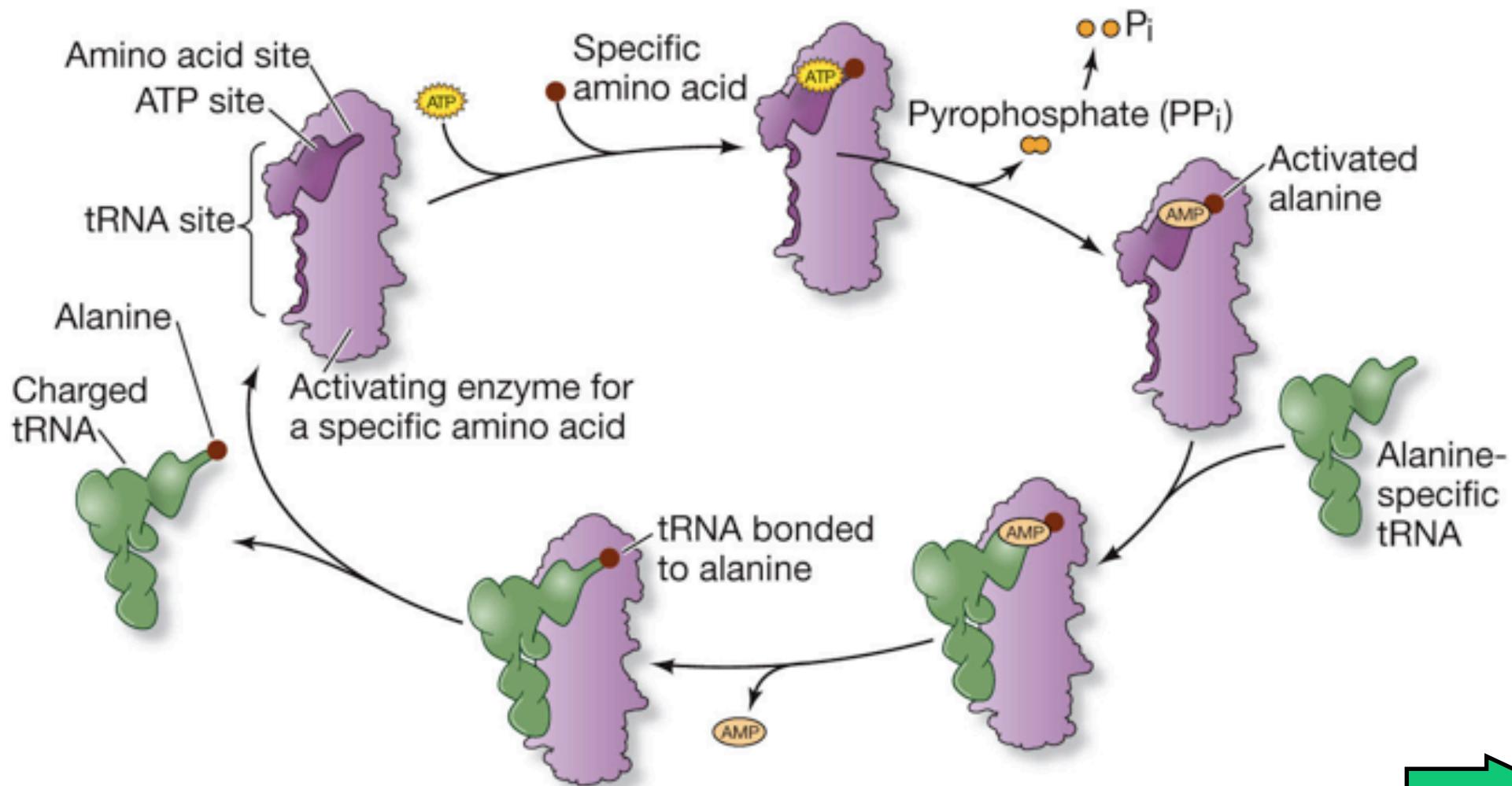
7.4.1 - Explain that each tRNA molecule is recognized by a tRNA-activating enzyme that binds a specific amino acid to the tRNA, using ATP for energy. [3]

- tRNA is transcribed from specific genes in the DNA
- Only RNA is transcribed, so how does it get the amino acid?
- Aminoacyl-tRNA synthetases are used to properly match specific tRNAs to the appropriate amino acids
- Each enzyme is specific for one amino acid and its corresponding tRNA.
- Amino acid is attached to the CAA 3' end of tRNA by an energy-rich bond (ester bond) —this will provide energy for synthesis of the peptide bond to join amino acids.



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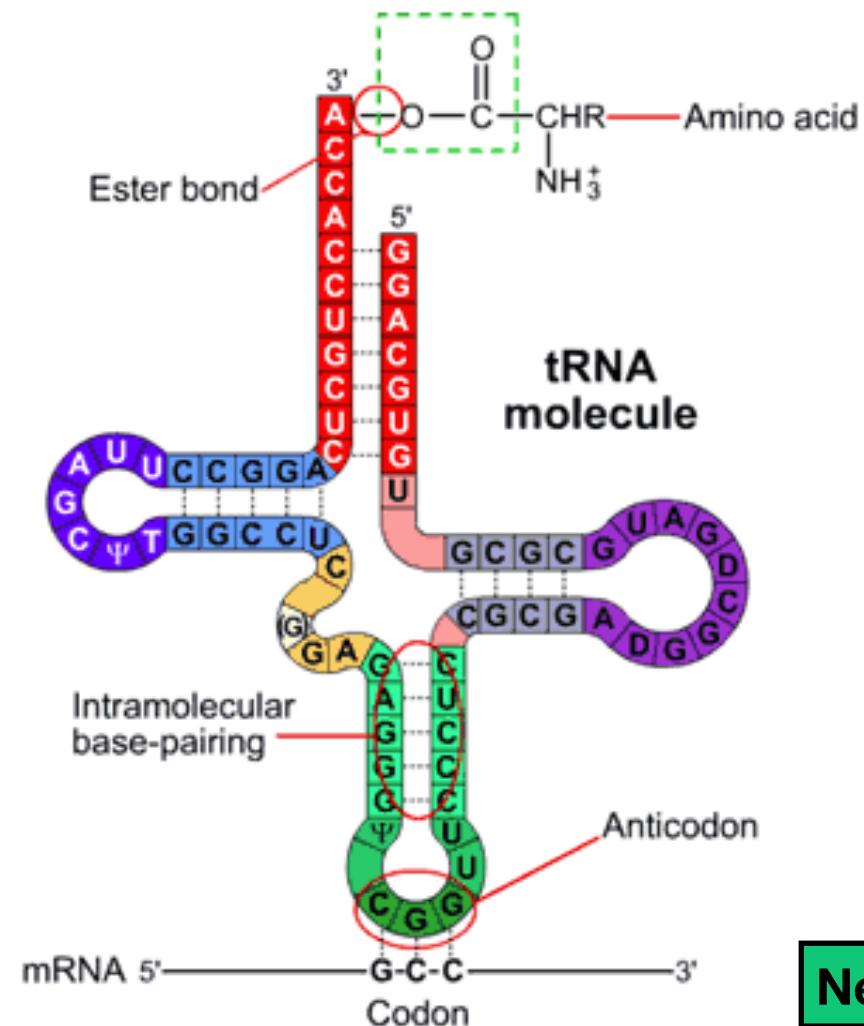
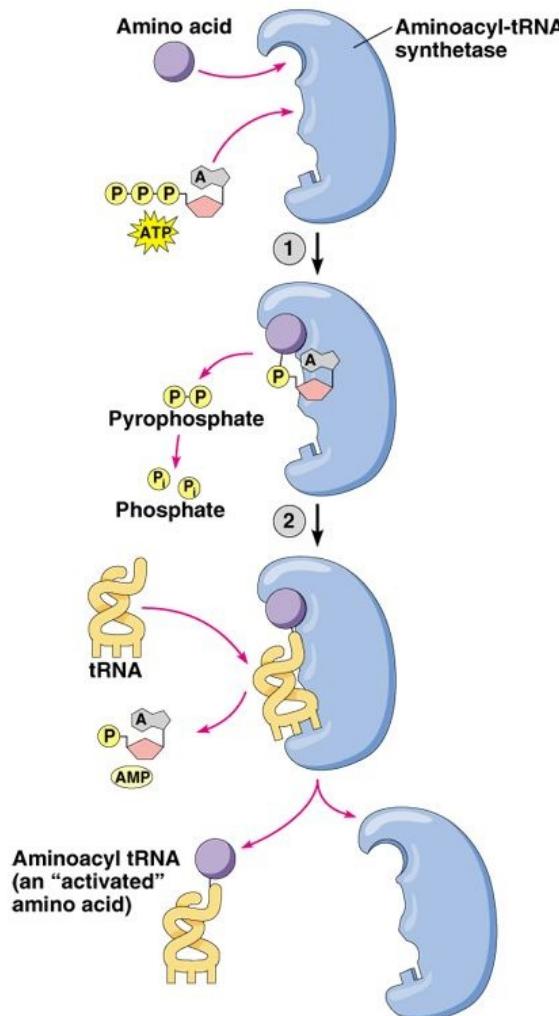
(A)



Next

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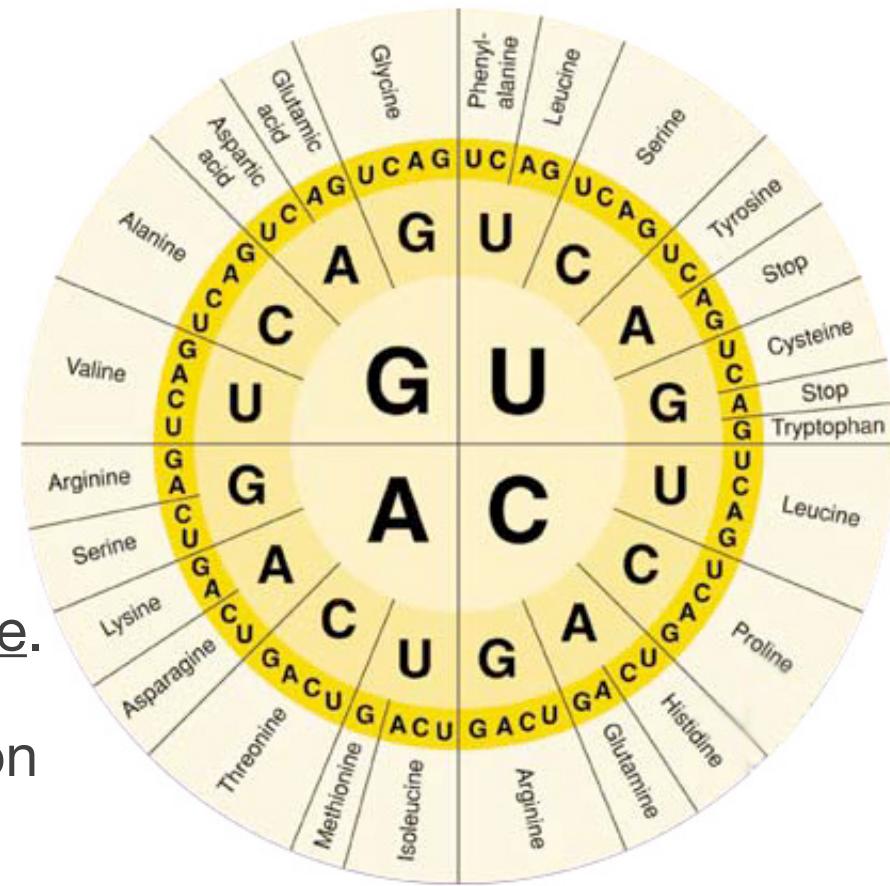
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Next

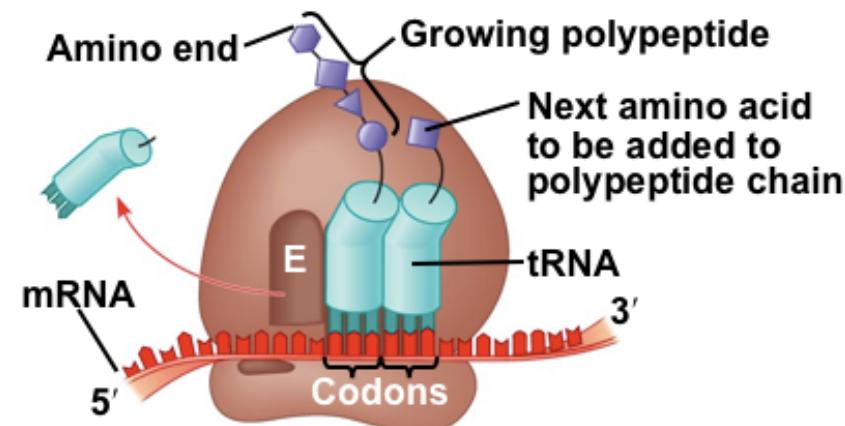
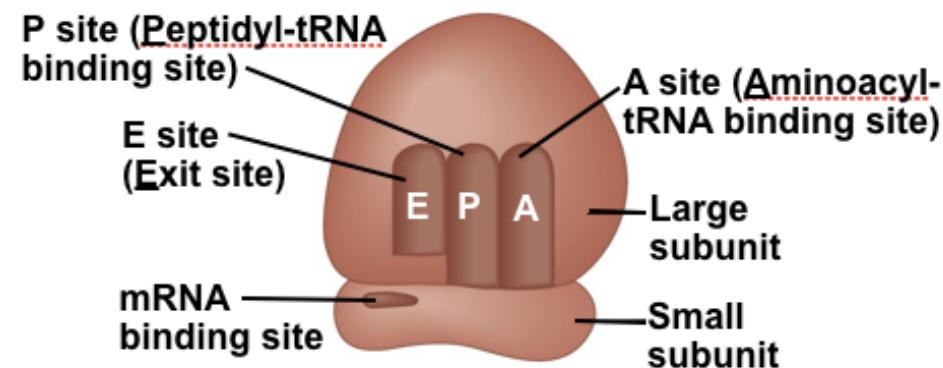
7.4.1 - Explain that each tRNA molecule is recognized by a tRNA-activating enzyme that binds a specific amino acid to the tRNA, using ATP for energy. [3]

- In order to correctly translate an mRNA sequence, the proper tRNA with the complementary anticodon is brought in by the ribosome.
- There are 64 codons, but only about 45 tRNAs.
 - So what about the missing anticodons?
 - Flexible base pairing, also known as wobble.
 - The same tRNA with a specific anticodon can be paired with multiple codons.
 - Ex: The tRNA with the anticodon UCU can be paired with the codons AGA or AGG.



7.4.2 - Outline the structure of ribosomes, including protein and RNA composition, large and small subunits, three tRNA binding sites and mRNA binding sites. [2]

- Ribosomes facilitate specific coupling of tRNA anticodons with mRNA codons in protein synthesis
- The two ribosomal subunits (large and small) are made of proteins and ribosomal RNA (rRNA)
 - Subunits combine at the beginning of translation
 - Ribosomes have 3 tRNA binding sites (A, P, E)
 - A = Aminoacyl tRNA binding site
 - P = Peptidyl site
 - E = Exit site



7.4.2 - Outline the structure of ribosomes, including protein and RNA composition, large and small subunits, three tRNA binding sites and mRNA binding sites [2]



(Aminoacyl-binding site)

peptidyl

peptide

amino acid added to peptide chain

- Ribosomes are composed of rRNA and proteins
- The two subunits are made of rRNA (large and small) and proteins
- Subunits join to form a complete ribosome
- Ribosomes have three tRNA binding sites
- A = amino acid
- P = peptidyl transferase center
- E = exit site

7.4.4 - State that translation occurs in a 5' → 3' direction. [1]

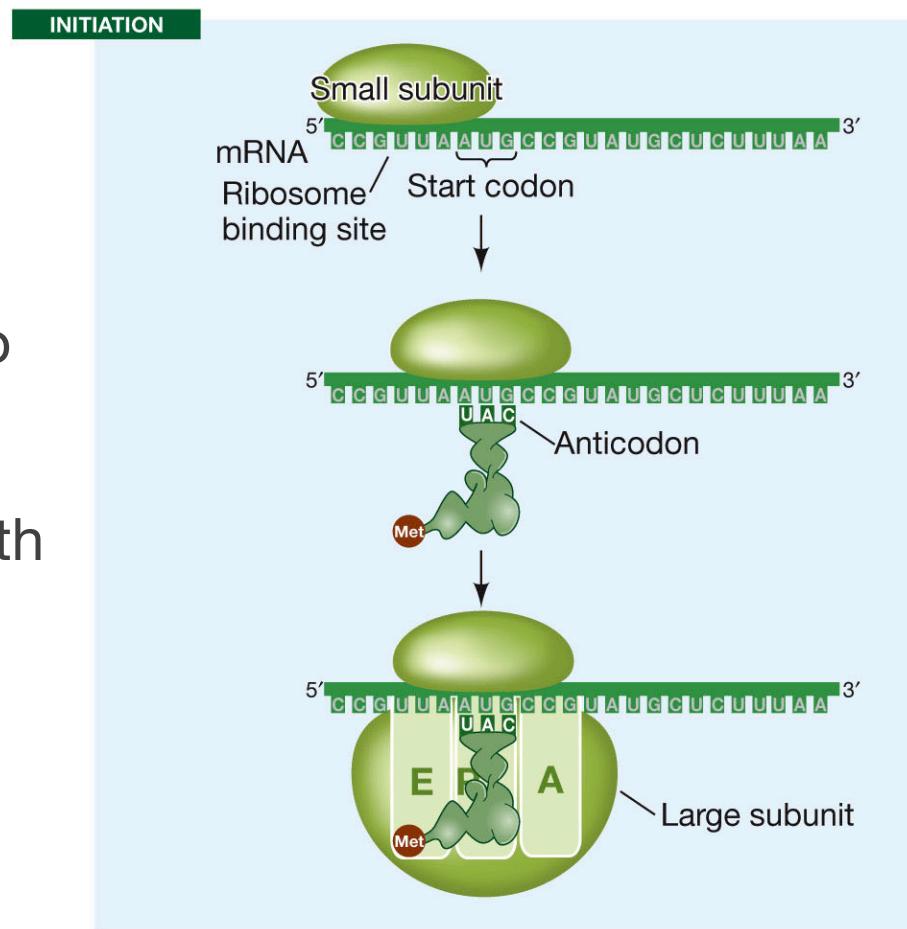
7.4.3 - State that translation consists of initiation, elongation, translocation and termination. [1]

- During translation, the ribosome moves along the mRNA towards the 3' end. The start codon is nearer to the 5' end.

- The initiation stage of translation brings together mRNA, a tRNA with the first amino acid, and the two ribosomal subunits

- First, a small ribosomal subunit binds with mRNA and a special initiator tRNA
- Then the small subunit moves along the mRNA until it reaches the start codon (AUG)

- Proteins called initiation factors bring in the large subunit that completes the translation initiation complex



LIFE 8e, Figure 12.11 (Part 2)

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Next

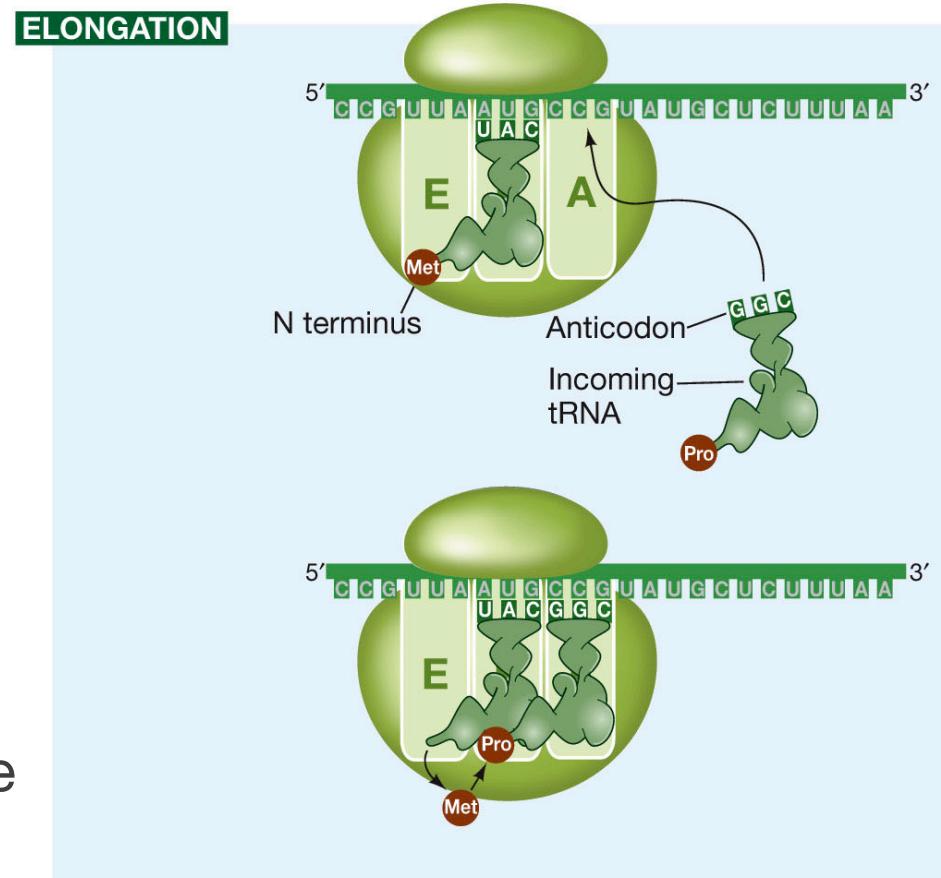
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- During the elongation stage, amino acids are added one by one to the preceding amino acid

- Each addition involves proteins called elongation factors and occurs in three steps: codon recognition, peptide bond formation, and translocation

- Large RNA subunit breaks the bond between the amino acid and tRNA at the P site and forms a new peptide bond between that amino acid and the amino acid on the tRNA in the A site.



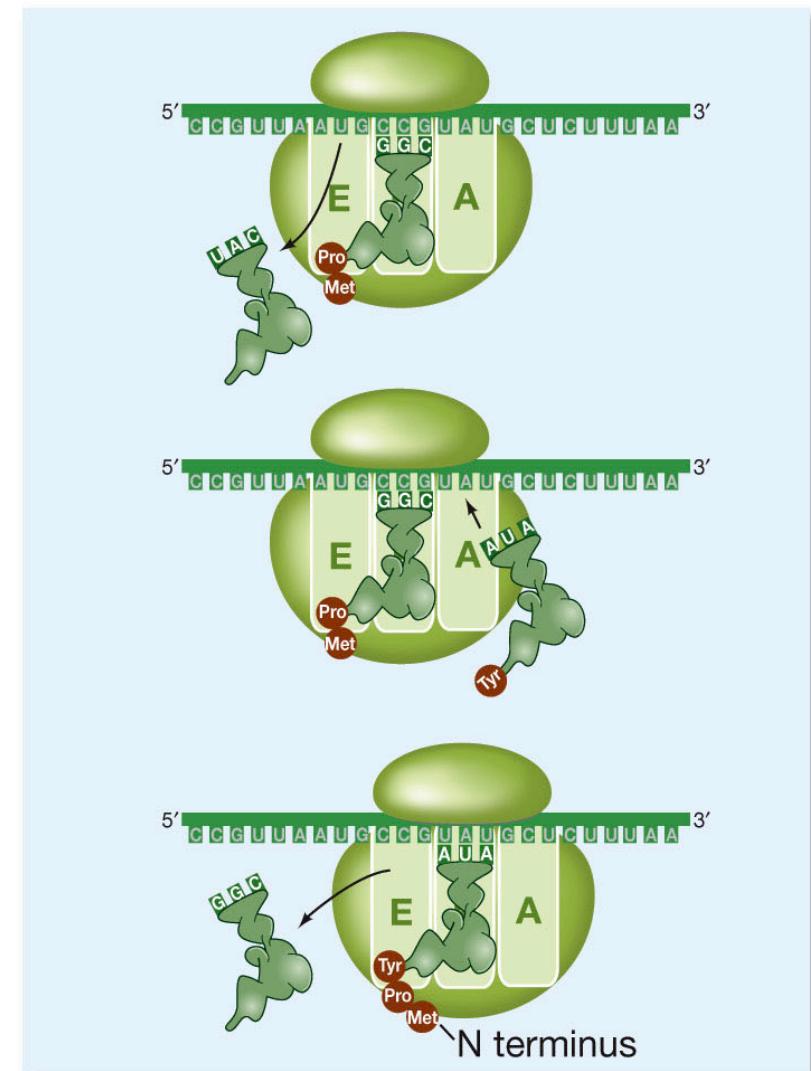
LIFE 8e, Figure 12.12 (Part 1)

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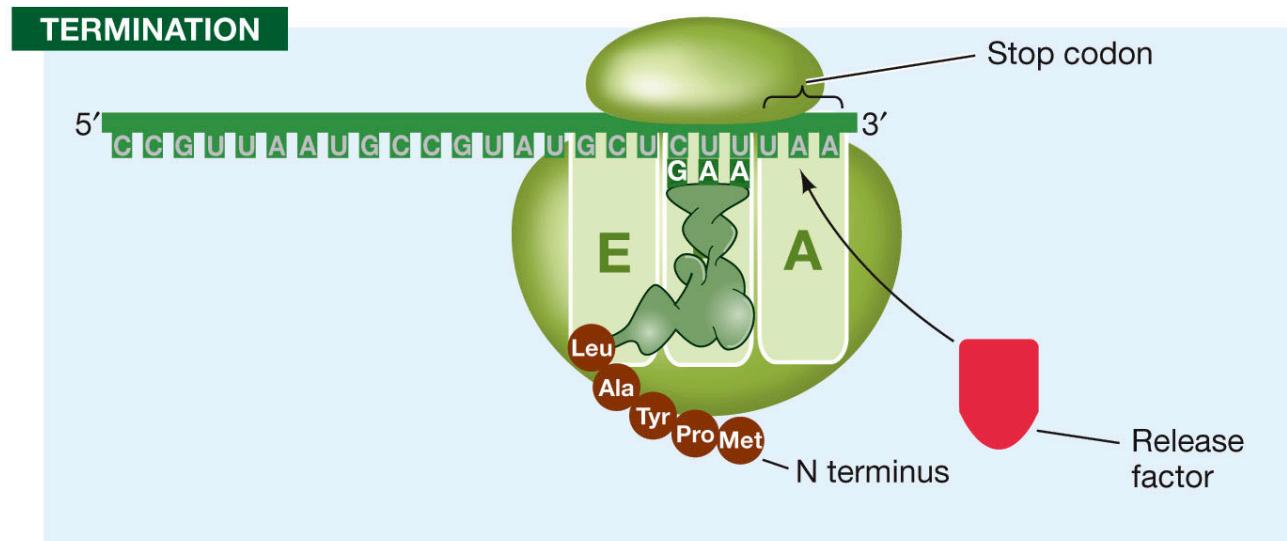


LIFE 8e, Figure 12.12 (Part 2)

7.4.4 - State that translation occurs in a 5' → 3' direction. [1]

7.4.3 - State that translation consists of initiation, elongation, translocation and termination. [1]

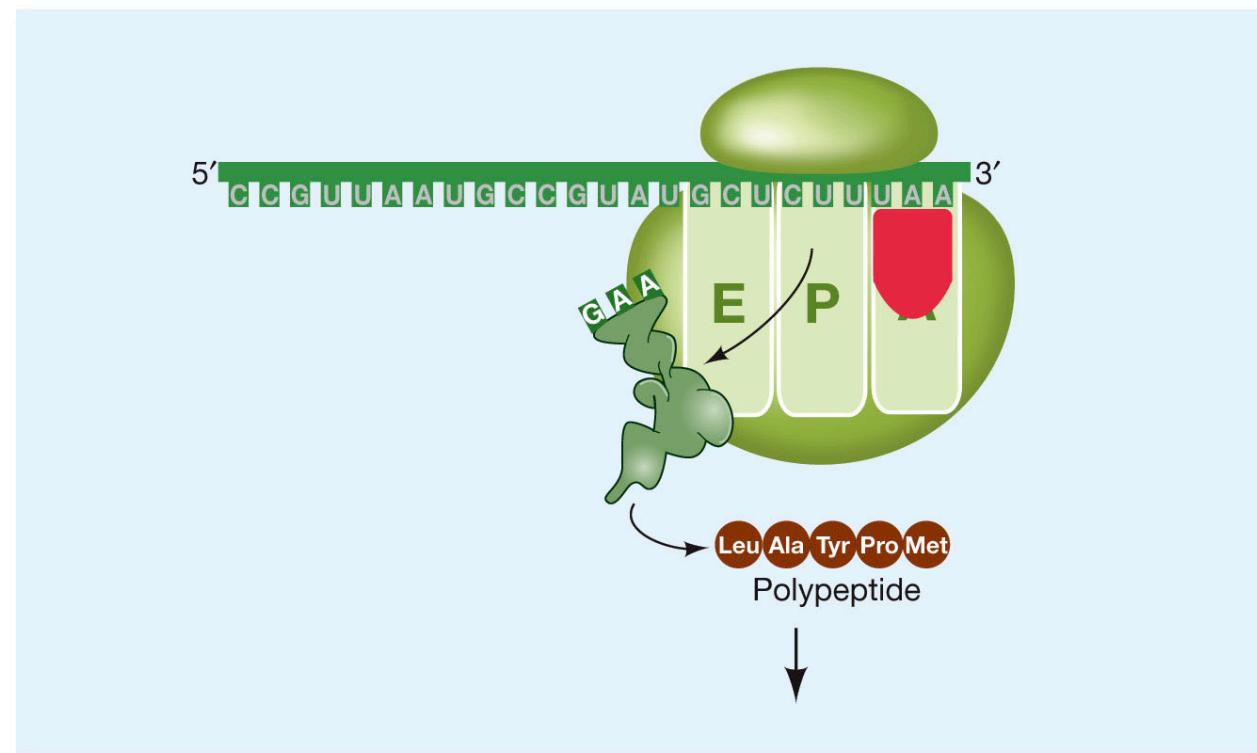
- Termination: translation ends when a stop codon enters the A site.
- Stop codon binds a protein release factor—allows hydrolysis of bond between polypeptide chain and tRNA on the P site.
- Polypeptide chain is released and the ribosomal subunits detach from the mRNA



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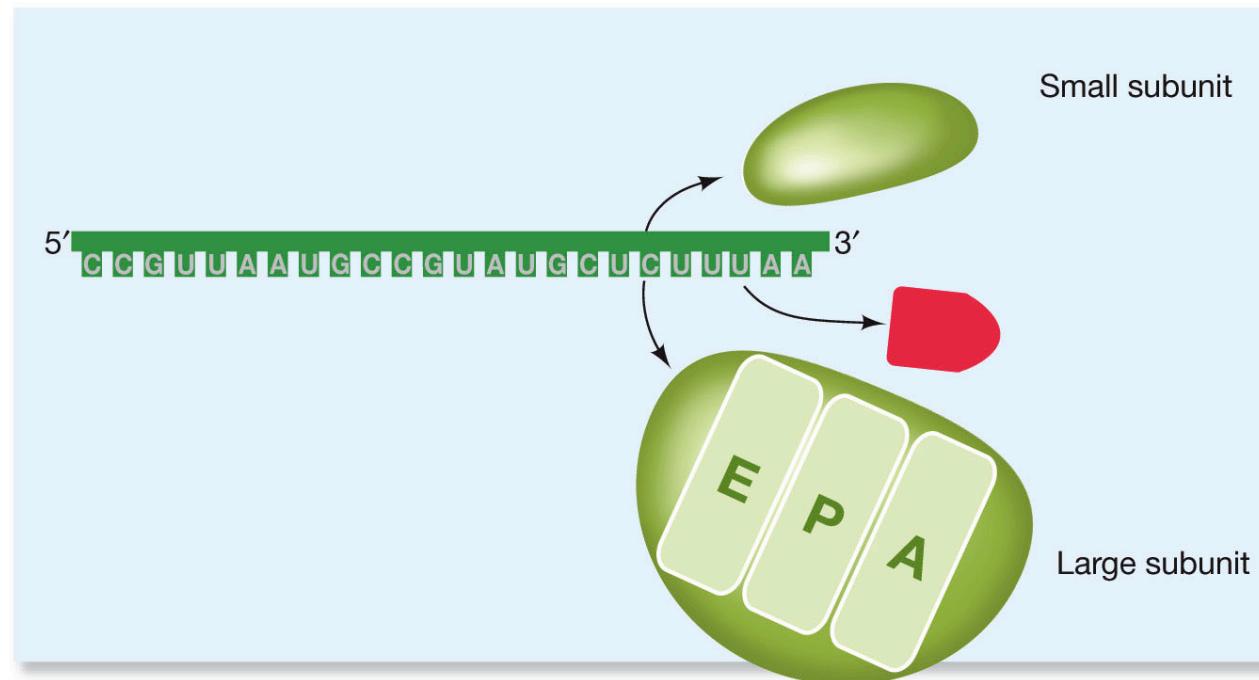
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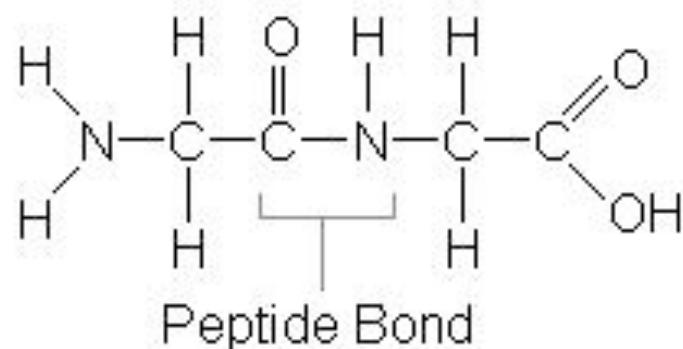
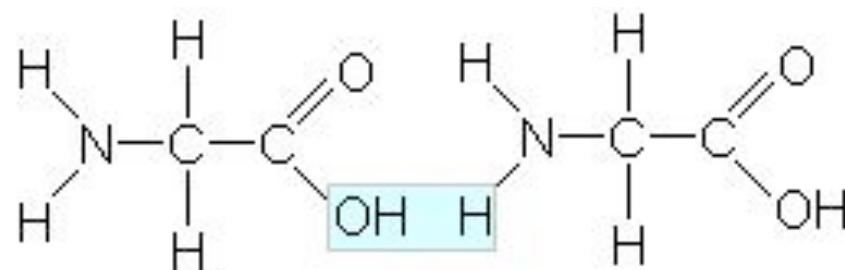
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7.4.5 - Draw and label a diagram showing the structure of a peptide bond between two amino acids. [1]

- Amino group of one amino acid attaches to the carboxyl group of another amino acid
- Peptide bond formed between the amino acids.
 - Dehydration reaction



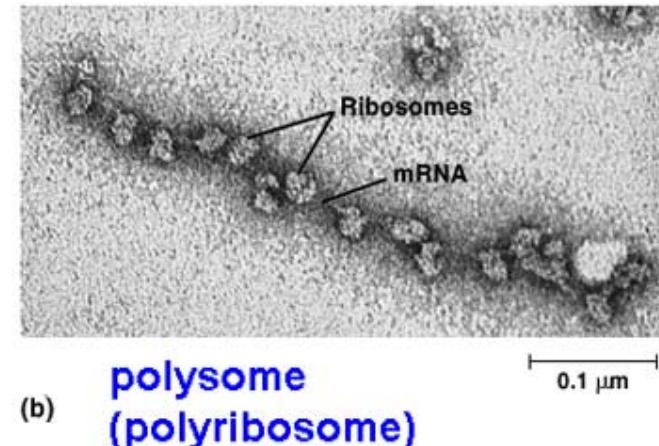
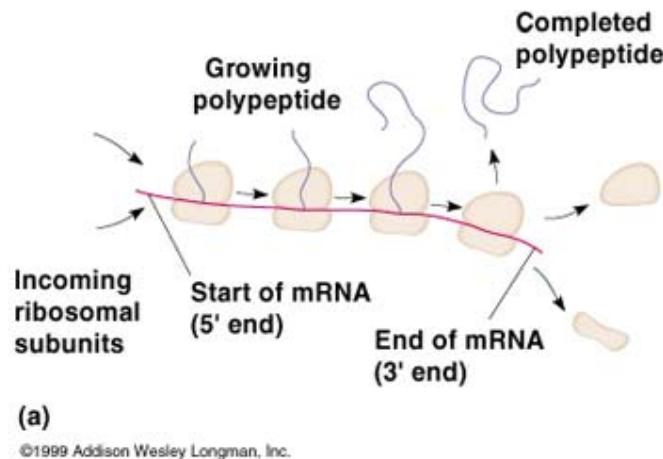
A molecule of water is removed from two glycine amino acids to form a peptide bond.

7.4.6 - Explain the process of translation, including ribosomes, polysomes, start codons and stop codons. [3]

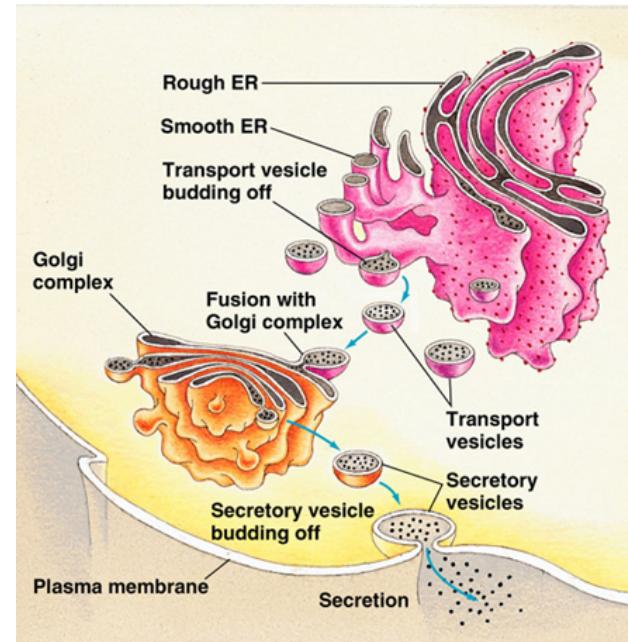
7.4.7 - State that free ribosomes synthesize proteins for use primarily within the cell, and that bound ribosomes synthesize proteins primarily for secretion or for lysosomes. [1]

- Many ribosomes can translate the same strand of mRNA at the same time

- Polysome

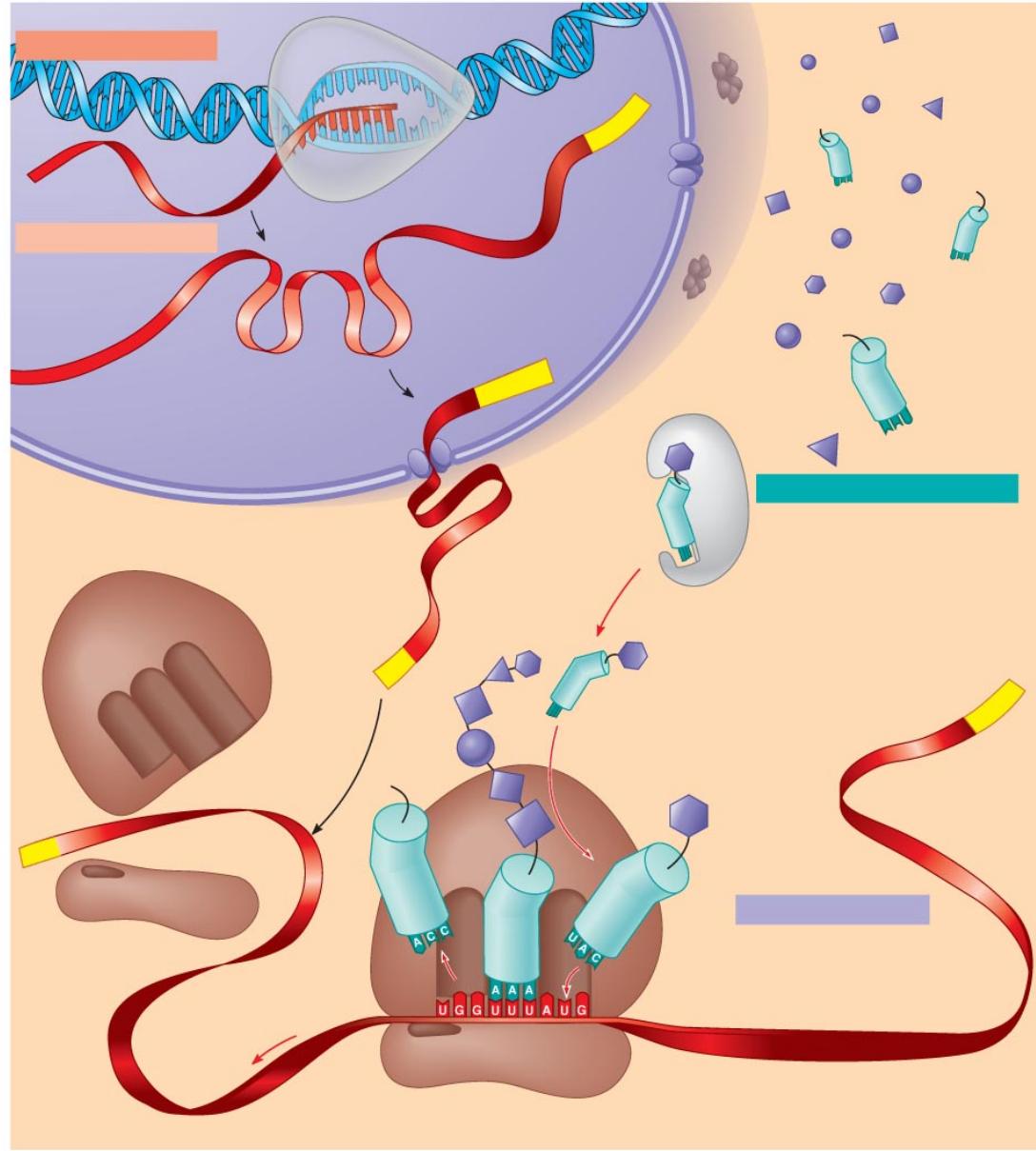


- Free ribosomes synthesize proteins for use primarily within the cell
- Bound ribosomes synthesize proteins primarily for secretion or for lysosomes



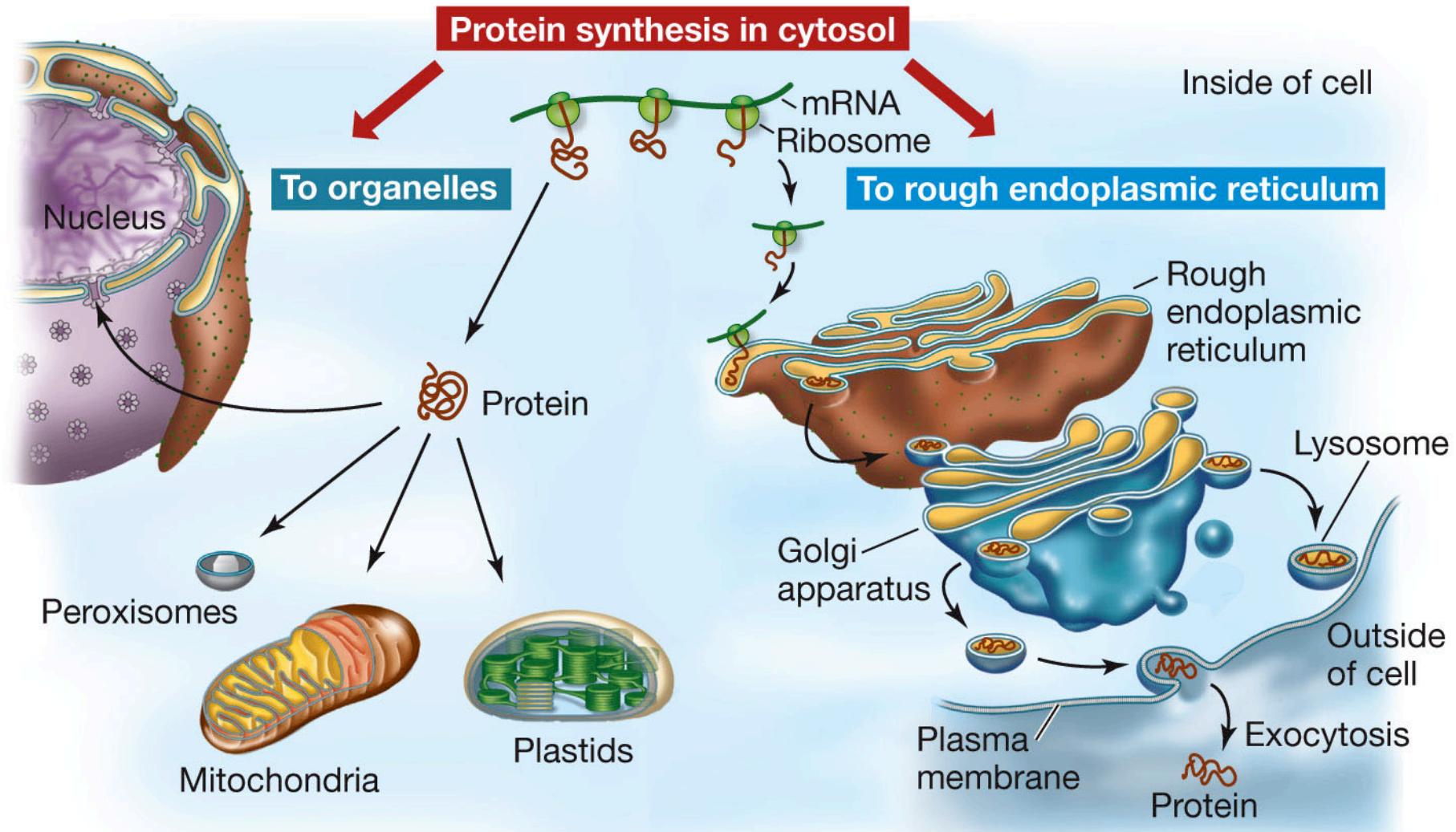
3.5.4 - Explain the process of translation, leading to polypeptide formation. [3]

7.4.6 - Explain the process of translation, including ribosomes, polysomes, start codons and stop codons. [3]



3.5.4 - Explain the process of translation, leading to polypeptide formation. [3]

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Bonus - RNAi

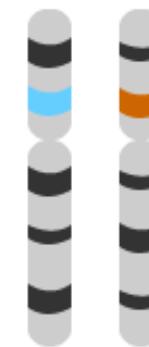


Objectives

4.1.2 - Define gene, allele and genome. [1]

- Gene

A heritable factor that controls a specific characteristic. (The differences between structural genes, regulator genes and genes coding for tRNA and rRNA are not expected at SL).

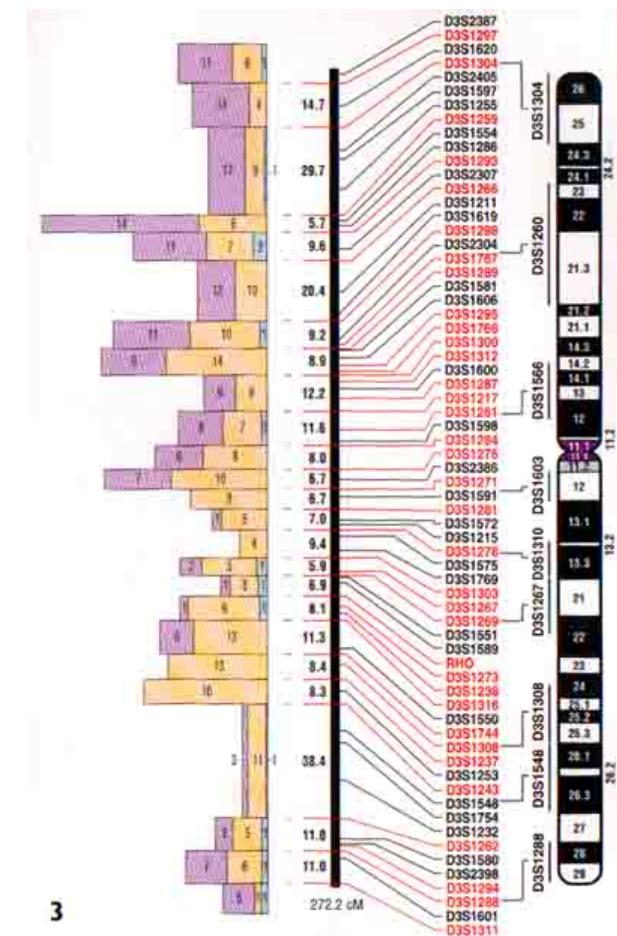


- Allele

One specific form of a gene, differing from other alleles by one or a few bases only and occupying the same gene locus as other alleles of the gene.

- Genome

The whole of the genetic information of an organism.

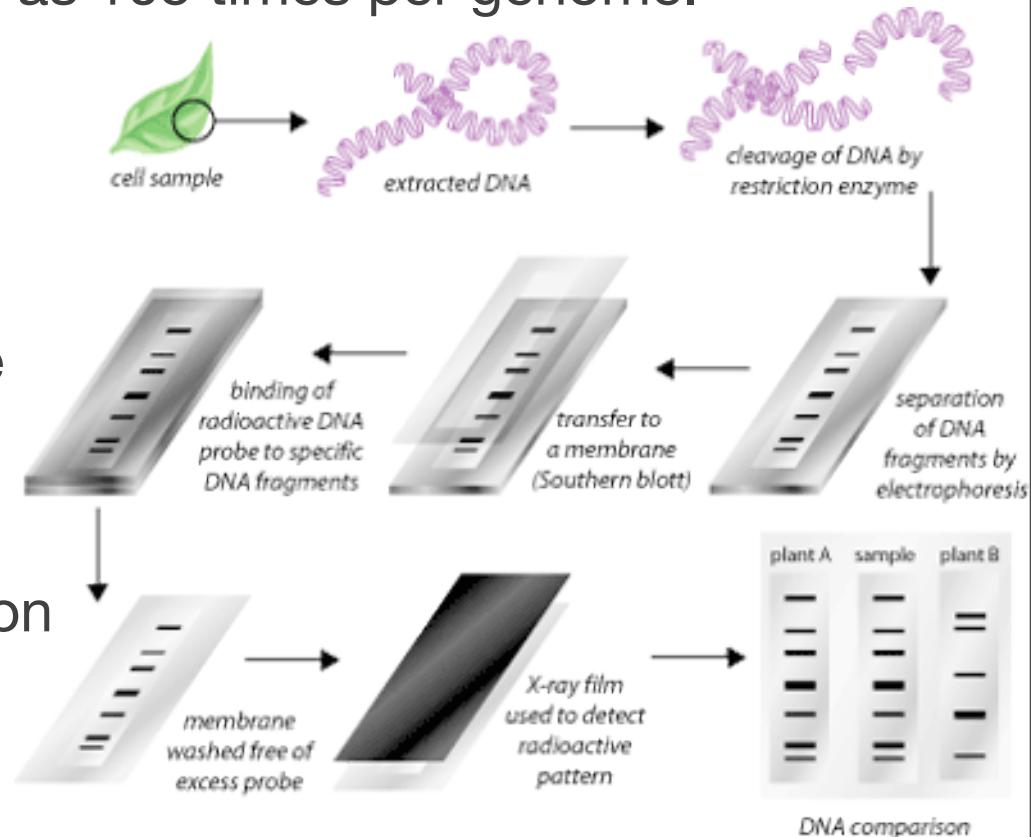


7.1.4 - Distinguish between unique or single-copy genes and highly repetitive sequences in nuclear DNA. [2]

- Highly repetitive sequences (satellite DNA) constitutes 5–45% of the genome. The sequences are typically between 5 and 300 base pairs per repeat, and may be duplicated as many as 105 times per genome.

- Junk DNA

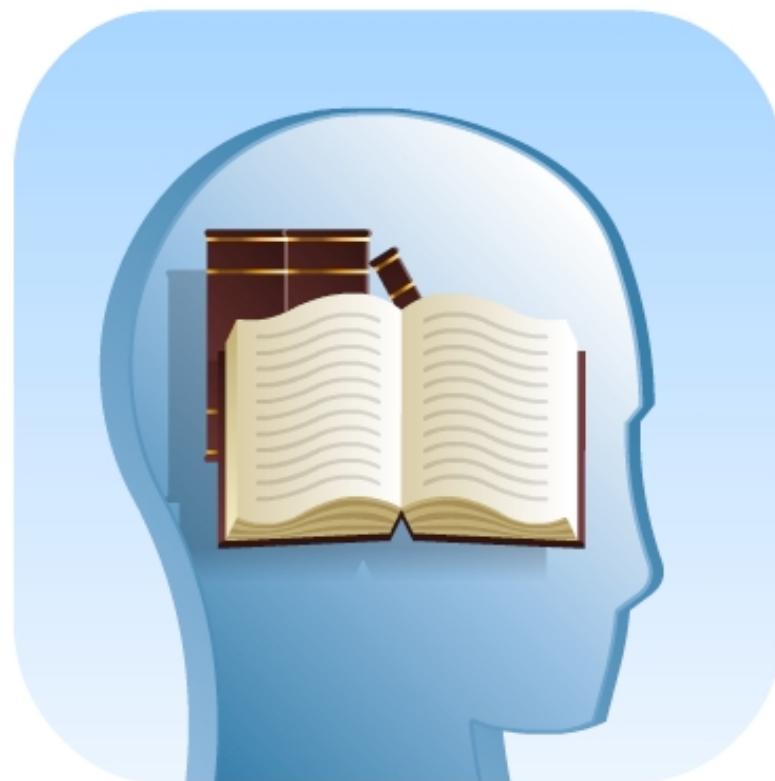
- Telomeres and Centromeres
- Very high % of Adenine and Thymine
- Not transcribed to RNA
- Shows variation from person to person
- Used in DNA fingerprinting



7.1.4 - Distinguish between unique or single-copy genes and highly repetitive sequences in nuclear DNA. [2]

- **TOK**

Highly repetitive sequences were once classified as “junk DNA”, showing a degree of confidence that it had no role. This addresses the question: To what extent do the labels and categories used in the pursuit of knowledge affect the knowledge we obtain?



4.1.3 - Define gene mutation. [1]

- Mutation

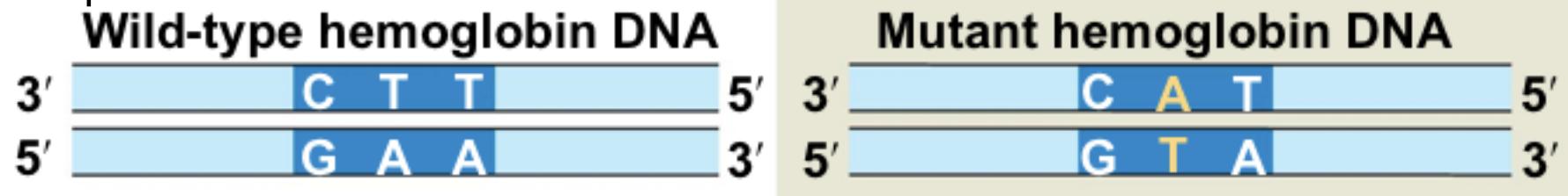
Mutations are changes in the genetic material of a cell or virus

- Gene Mutation

Point mutations are chemical changes in just one base pair of a gene

- The substitution of a single nucleotide in a DNA template strand can lead to the production of an abnormal protein
- The change of a single nucleotide in a DNA template strand can lead to the production of an abnormal protein

Example: Sickle Cell Anemia



Codon is changed, therefore, what else is changed?

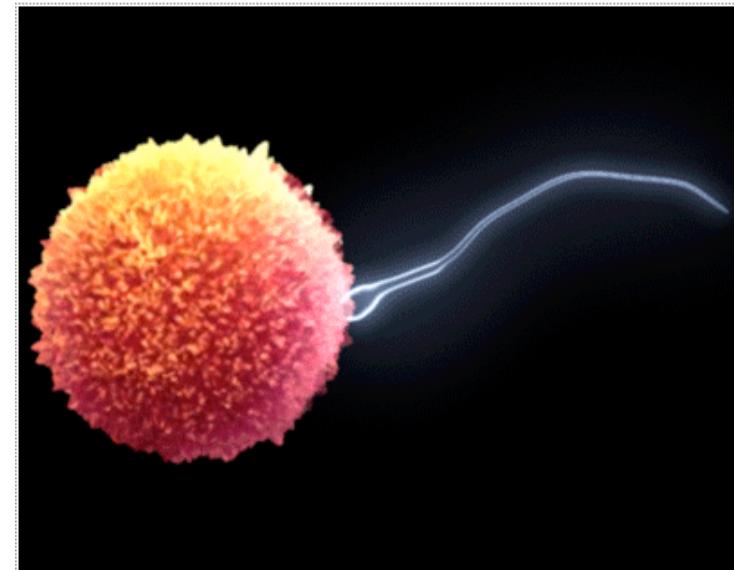
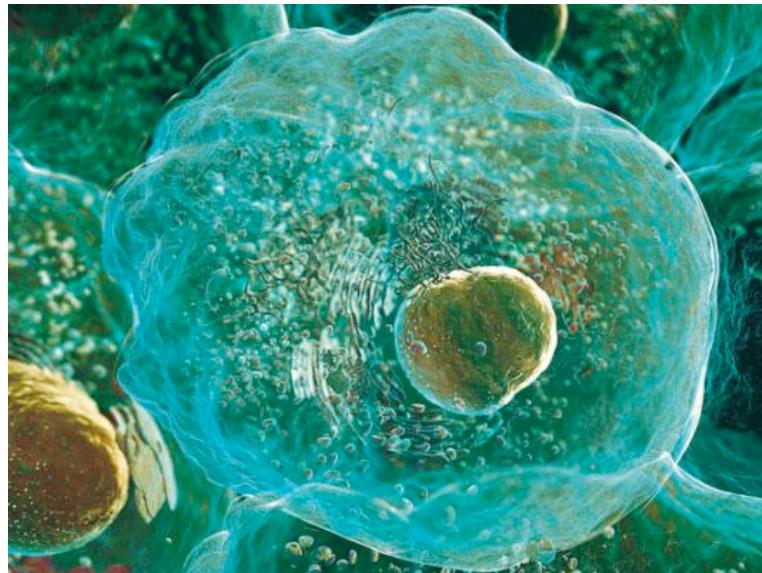
4.1.3 - Define gene mutation. [1]

- Somatic mutations

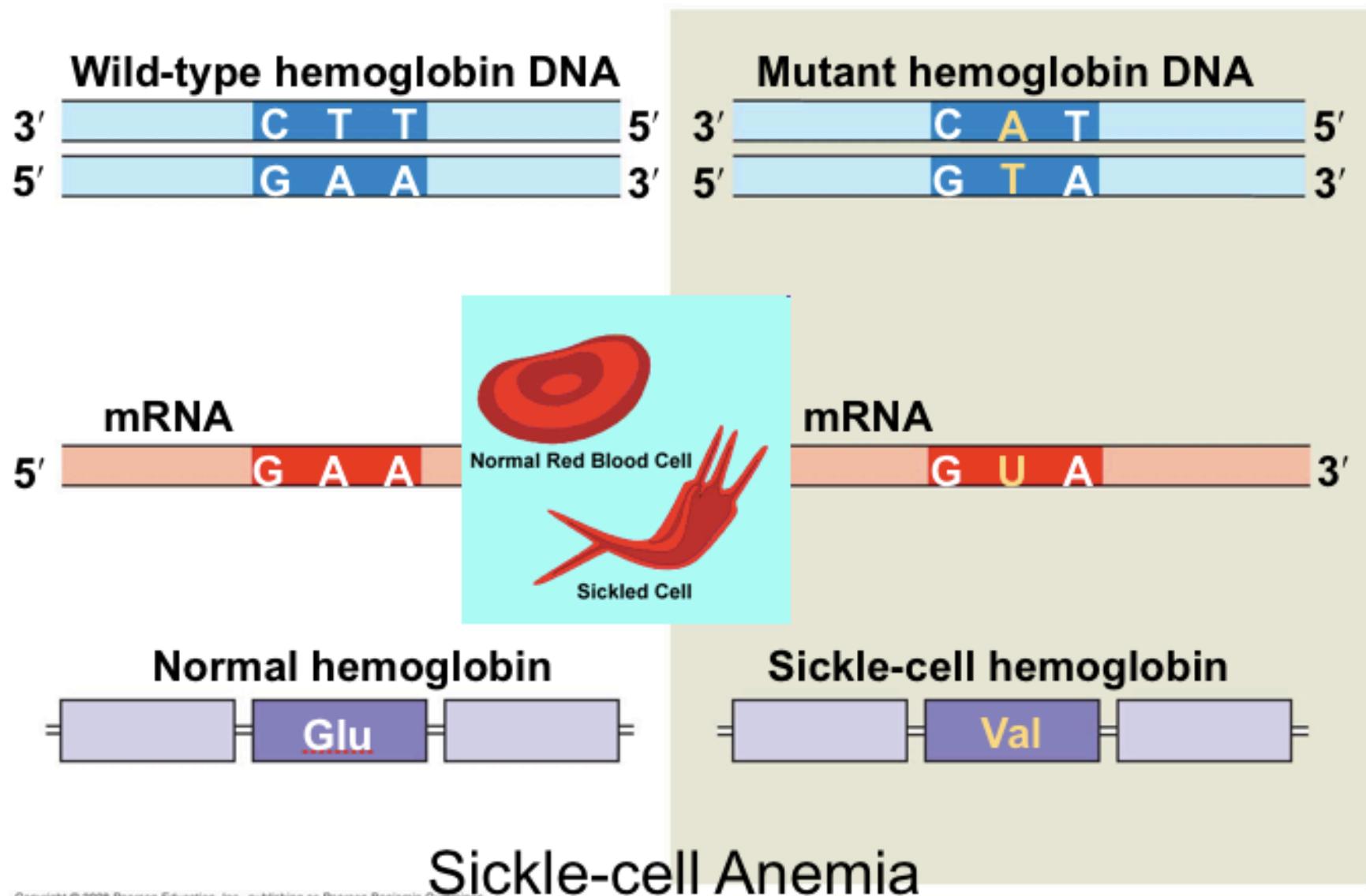
Occur in somatic (body) cells. Mutation is passed to daughter cells, but not to sexually produced offspring.

- Germ line mutations

Occur in cells that produce gametes. Can be passed to next generation.

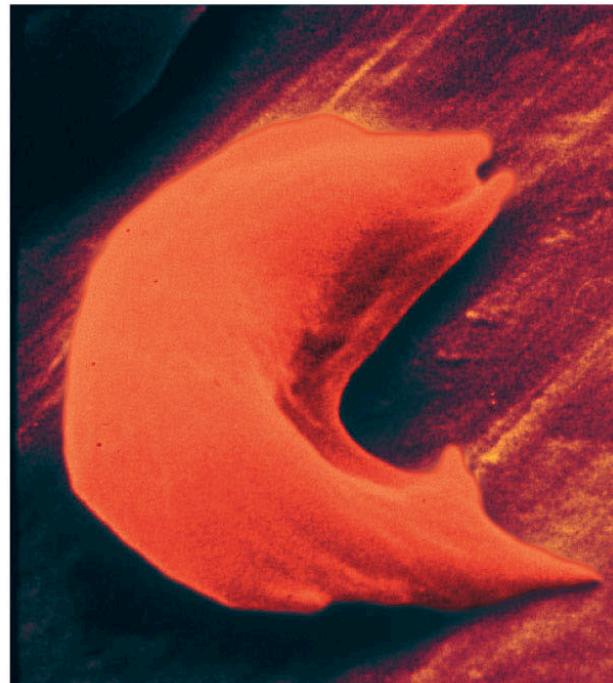


4.1.4 - Explain the consequence of a base substitution mutation in relation to the processes of transcription and translation, using the example of sickle-cell anemia. [3]

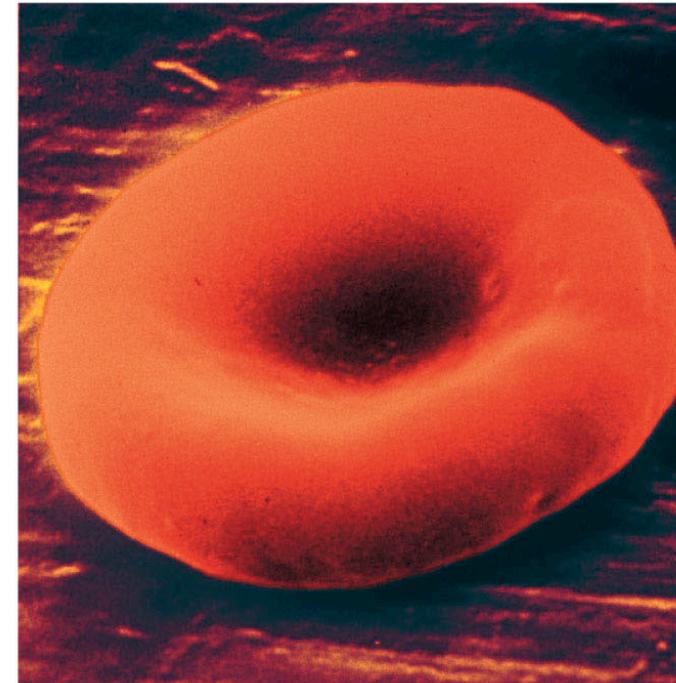


4.1.4 - Explain the consequence of a base substitution mutation in relation to the processes of transcription and translation, using the example of sickle-cell anemia. [3]

- Sickle allele for human β -globin is a missense mutation.
- Sickle allele differs from normal by only one base—the polypeptide differs by only one amino acid.
- A single point mutation can have an extremely large effect on an organism

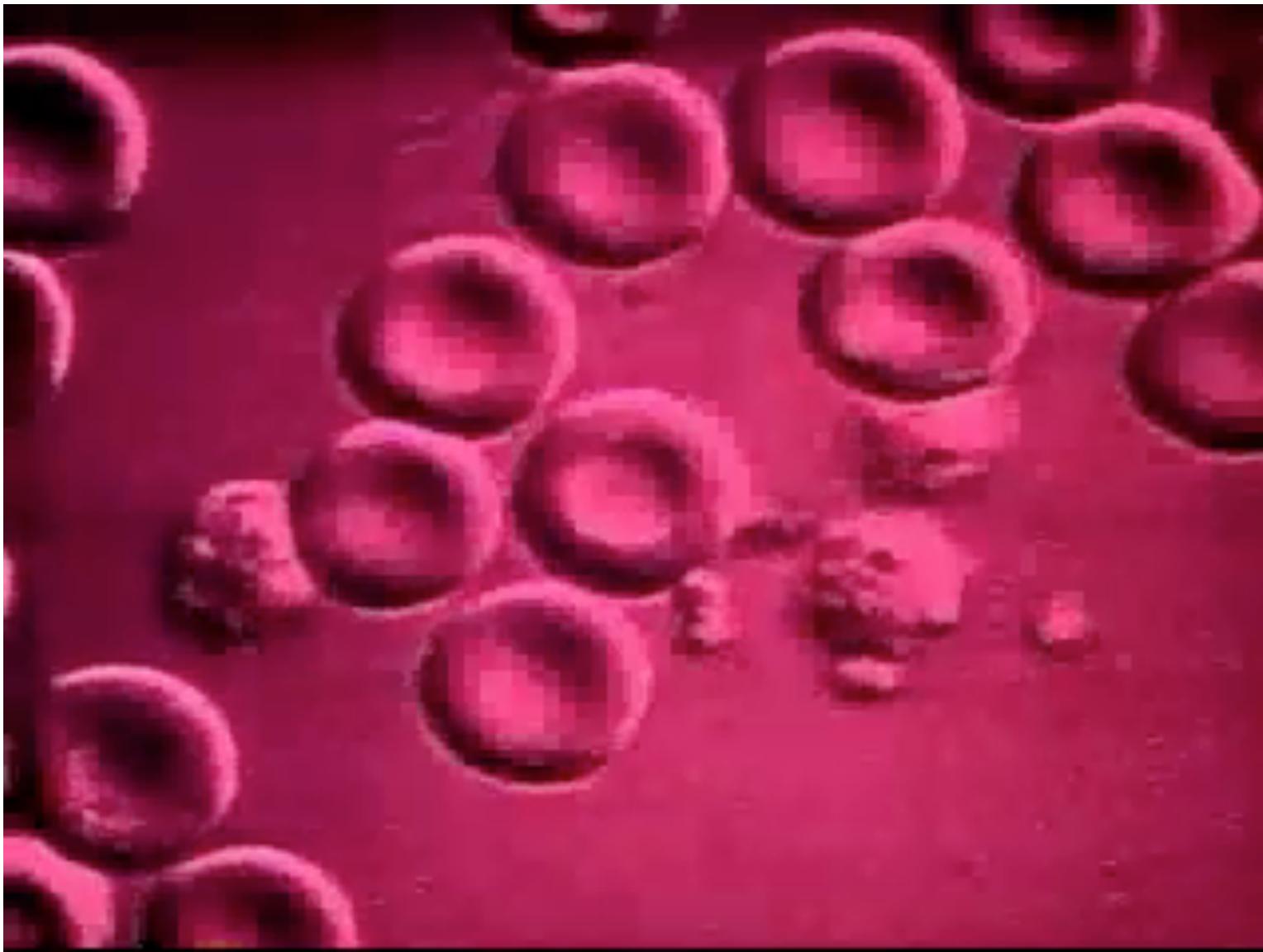


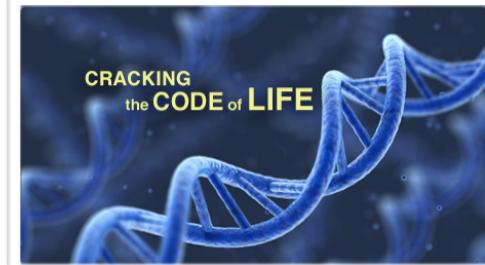
Sickle-cell phenotype



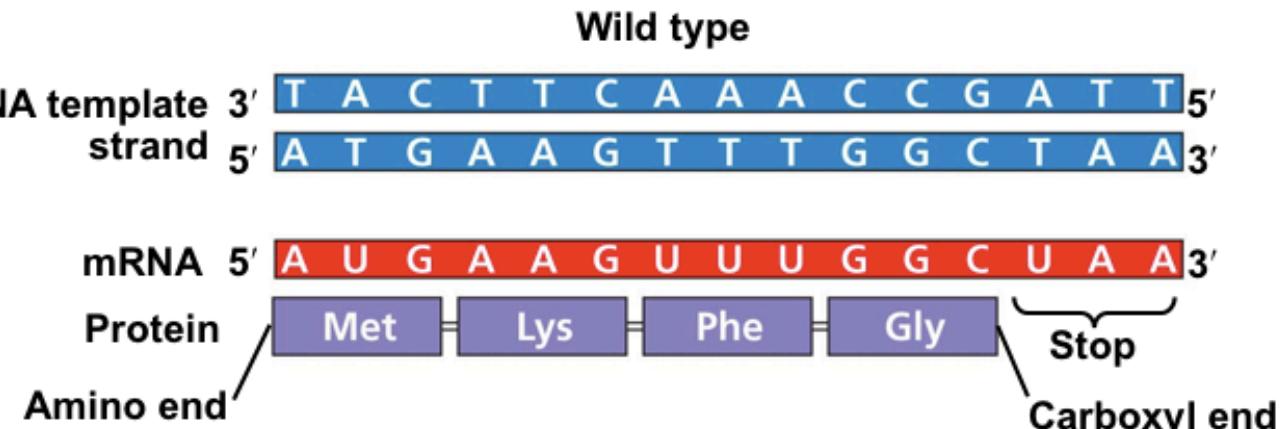
Normal phenotype

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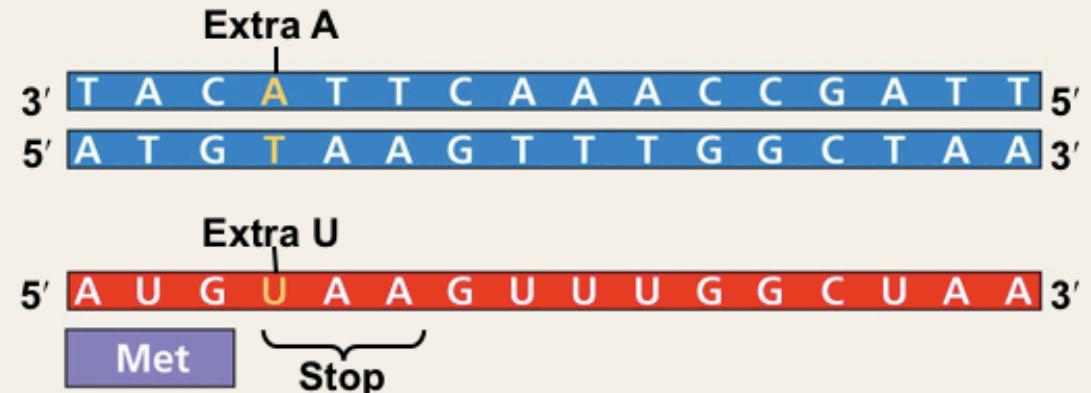


Bonus - One Wrong Letter



- Frameshift mutation

Insertions and deletions are additions or losses of nucleotide pairs in a gene. Insertion or deletion of nucleotides may alter the reading frame, producing a frameshift mutation.



Frameshift causing immediate nonsense (1 base-pair insertion)

- Tay Sachs is an example of an insertion mutation.