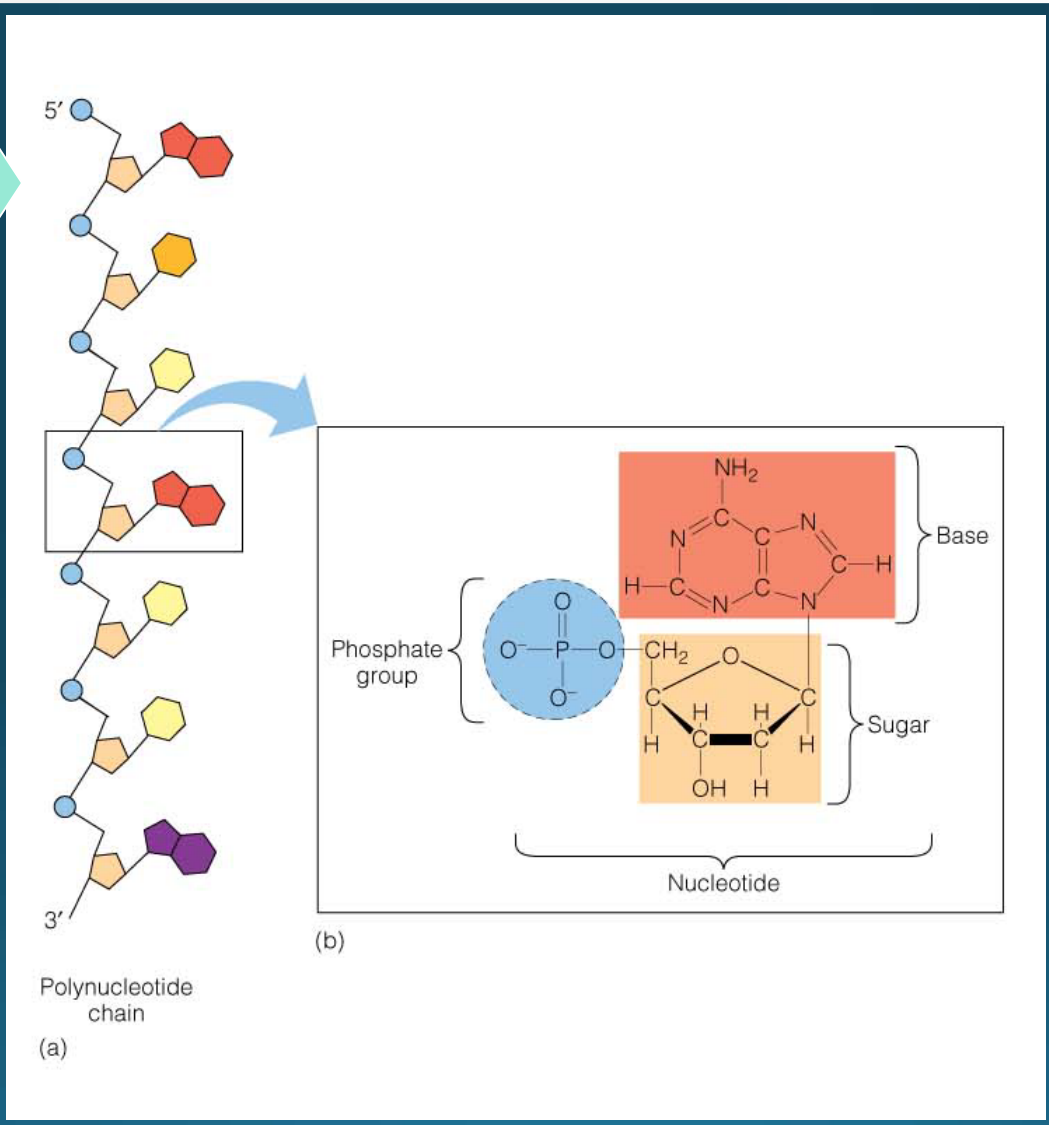
DNA Structure

Polynucleotides Are Directional

Five prime end

Three prime end

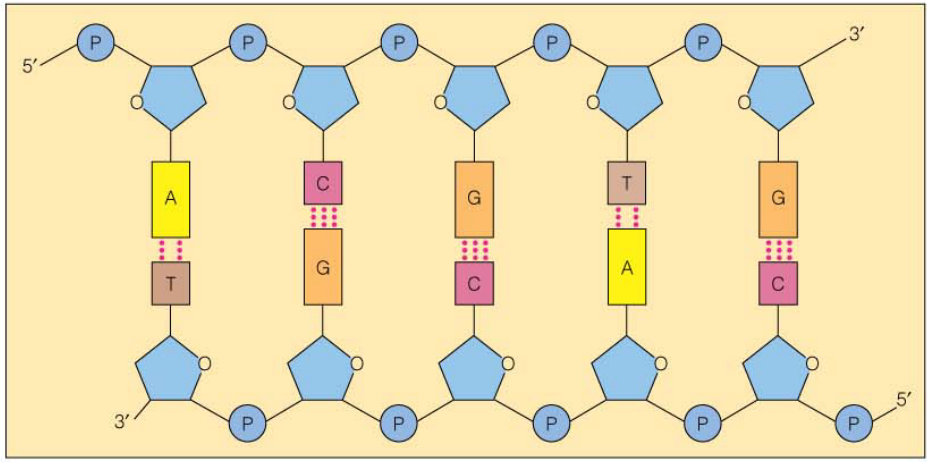


Erwin Chargaff Rule of Base Composition of DNA

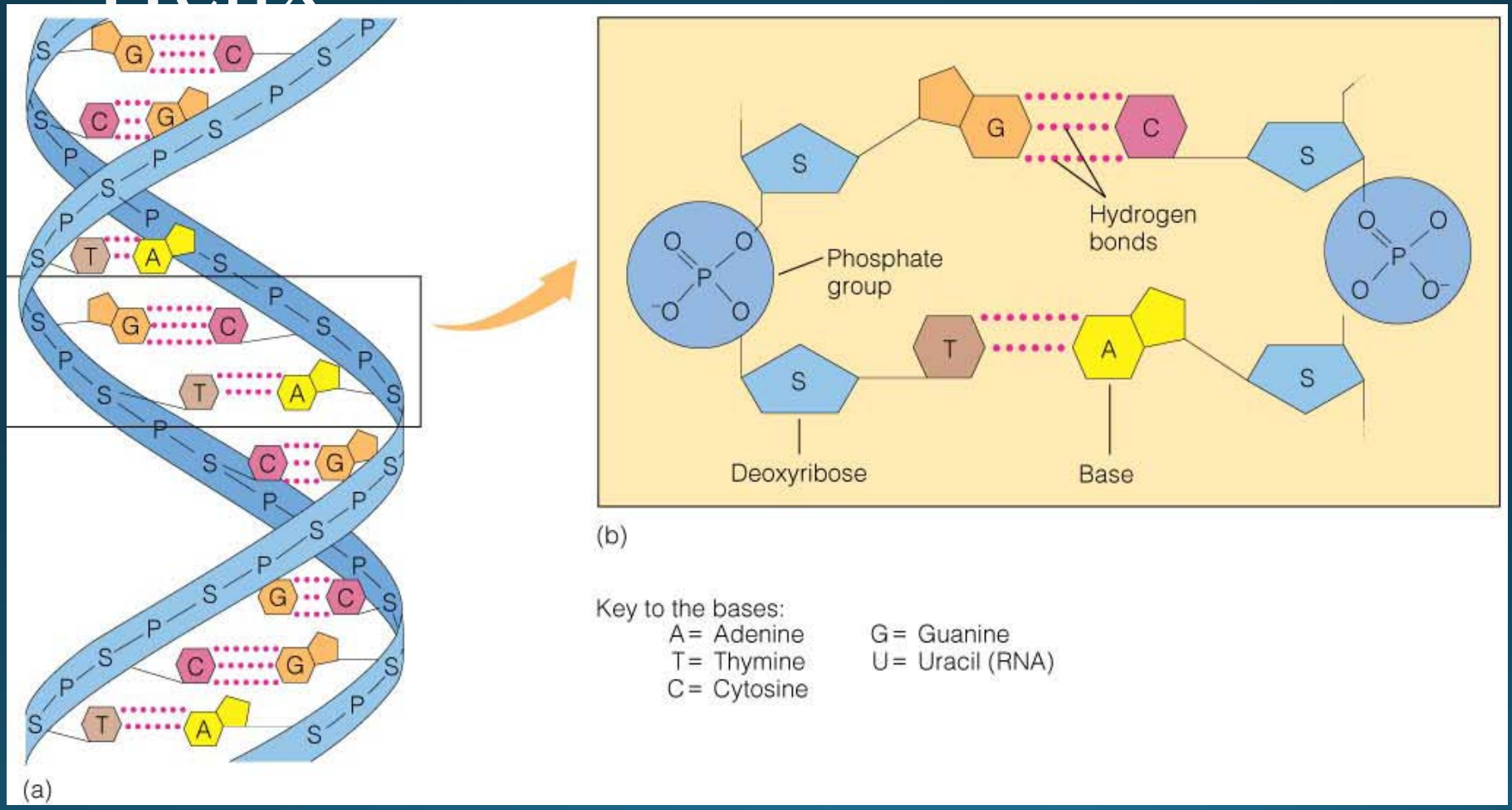
Amount of A = Amount of T

Amount of G = Amount of C

- A forms 2 hydrogen bonds with T
- G forms 3 hydrogen bonds with C



DNA Is a Double-Stranded Helix

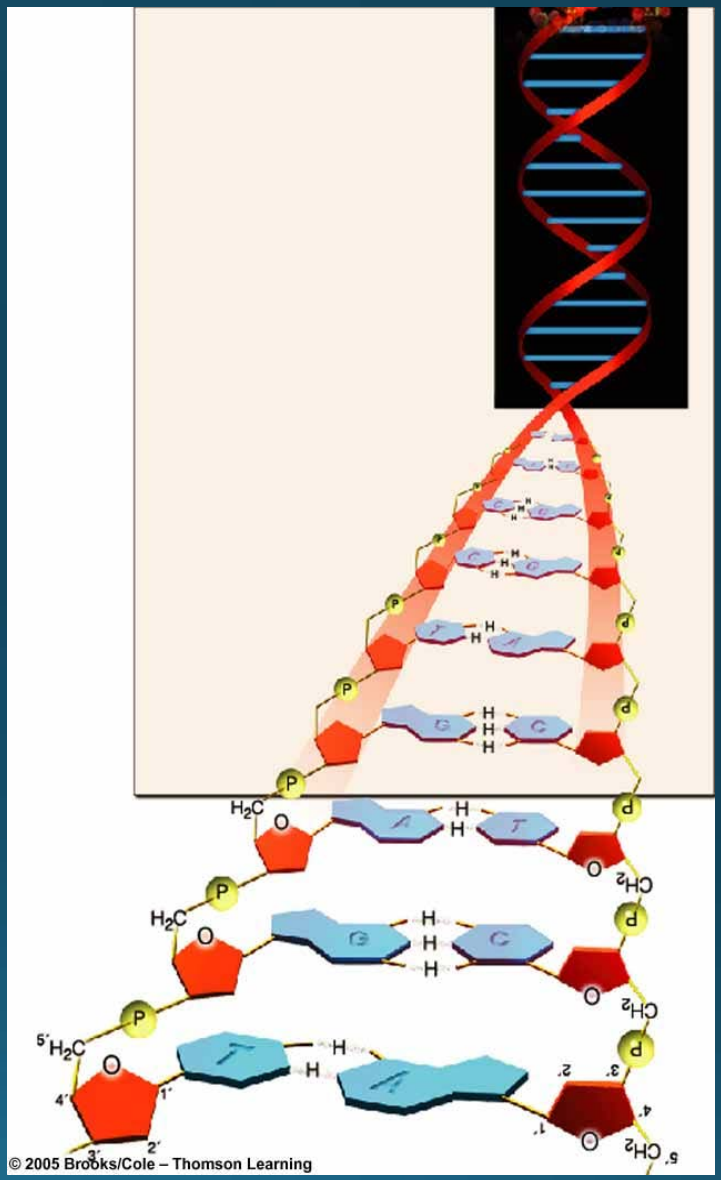


Important Properties of the Model

- Genetic information is stored in the sequence of bases in the DNA
- The model offers a molecular explanation for mutation
- Complementary strands of DNA can be used to explain how DNA copies itself

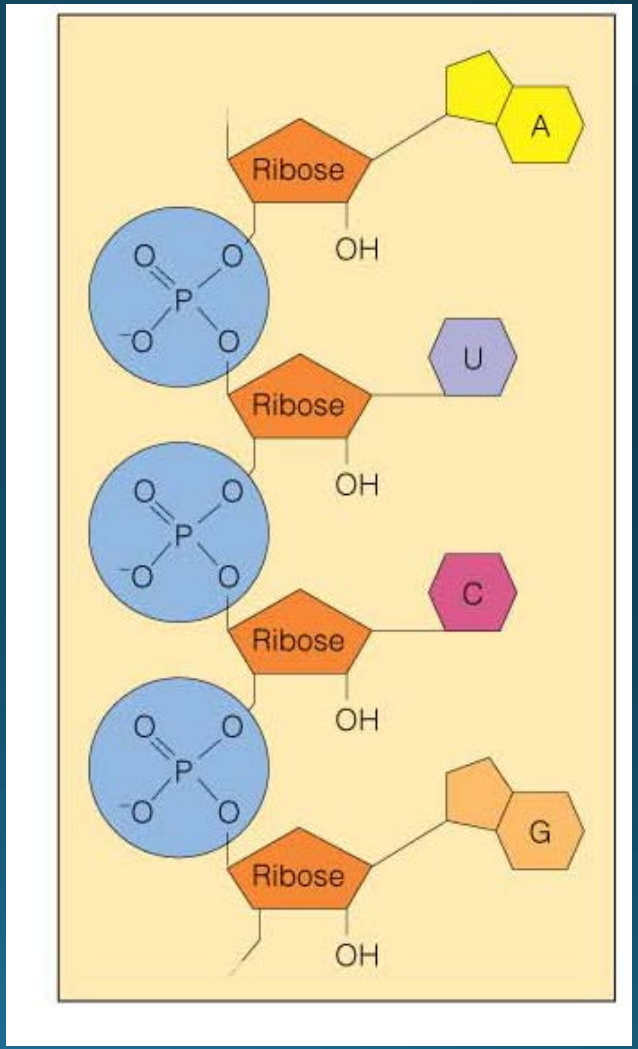
Molecular Model of DNA

Fig. 8.9



RNA Is Single Stranded

- Transfers genetic information from the nucleus to the cytoplasm
- Participates in protein synthesis
- It is a component of ribosomes
- Contains ribose sugar and A, U, G, and C



DNA to Chromosomes

DNA stores the genetic information

Mitochondrial chromosome

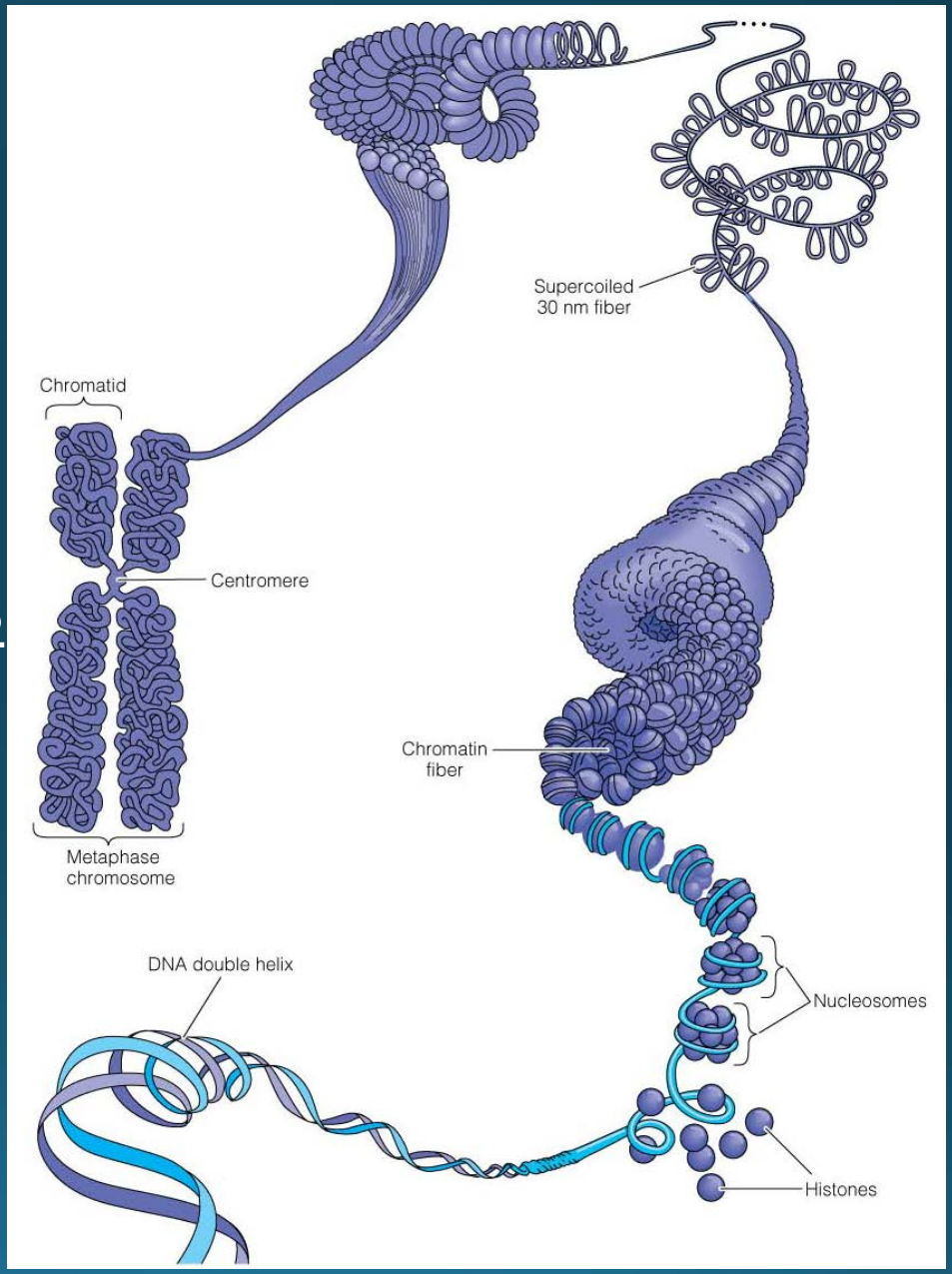
- It is a circular DNA molecule
- It is not compacted
- Similar to prokaryotic chromosomes
- Reflects evolutionary history of mitochondria

Nuclear chromosomes

- Have a complex structure

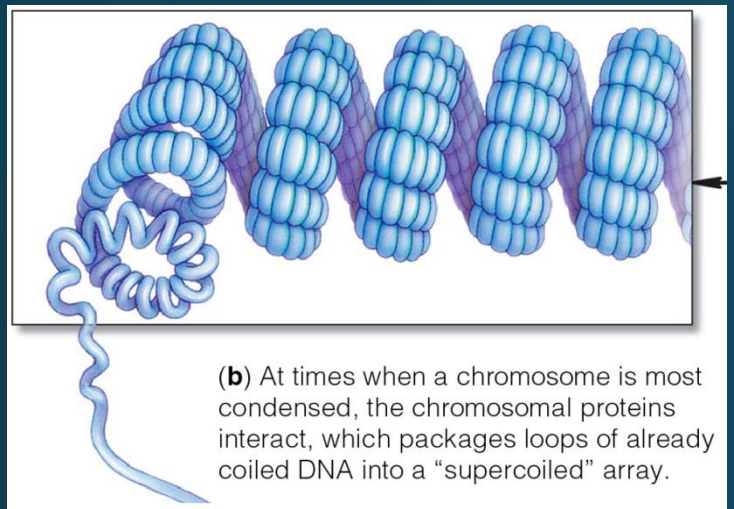
Nuclear Chromosomes

- DNA is packed into chromosomes by several levels of coiling and compaction

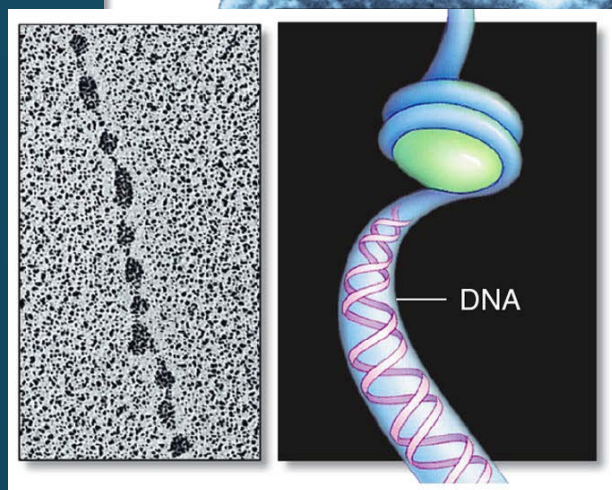


Nuclear Chromosomes

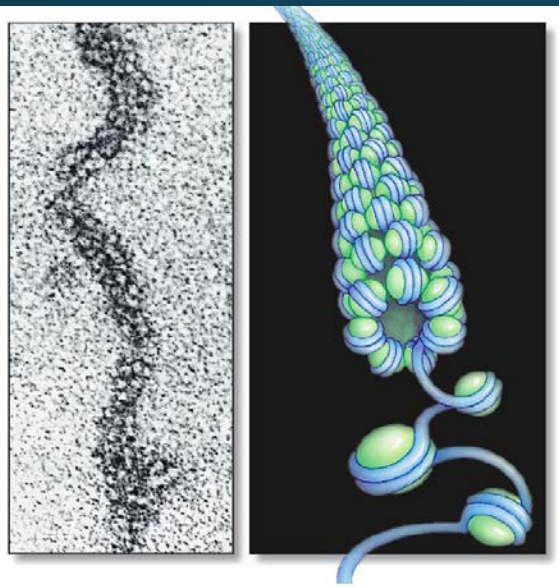
- **Chromatin**
  - makes up chromosomes
  - it is a complex of DNA and protein
- **Histones**
  - DNA-binding proteins
  - They assist in compacting and folding DNA into a chromosome
  - Shorten the DNA length by a factor of 6 or 7
- **Nucleosomes**
  - bead-like structures composed of histones wrapped with DNA



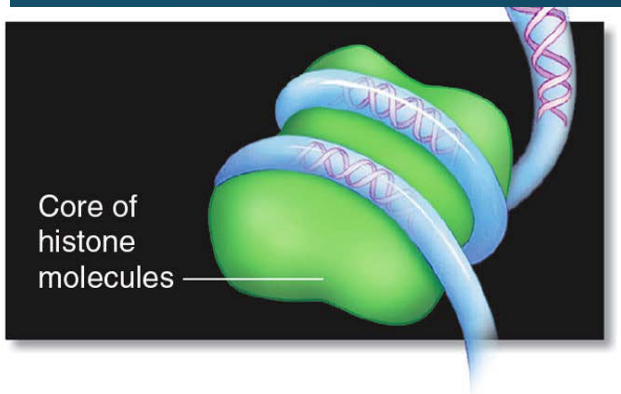
(**b**) At times when a chromosome is most condensed, the chromosomal proteins interact, which packages loops of already coiled DNA into a "supercoiled" array.



(**d**) Immerse a chromosome in saltwater and it loosens up to a beads-on-a-string organization. The "string" is one DNA molecule. Each "bead" is a nucleosome.



(**c**) At a deeper level of structural organization, the chromosomal proteins and DNA are organized as a cylindrical fiber.

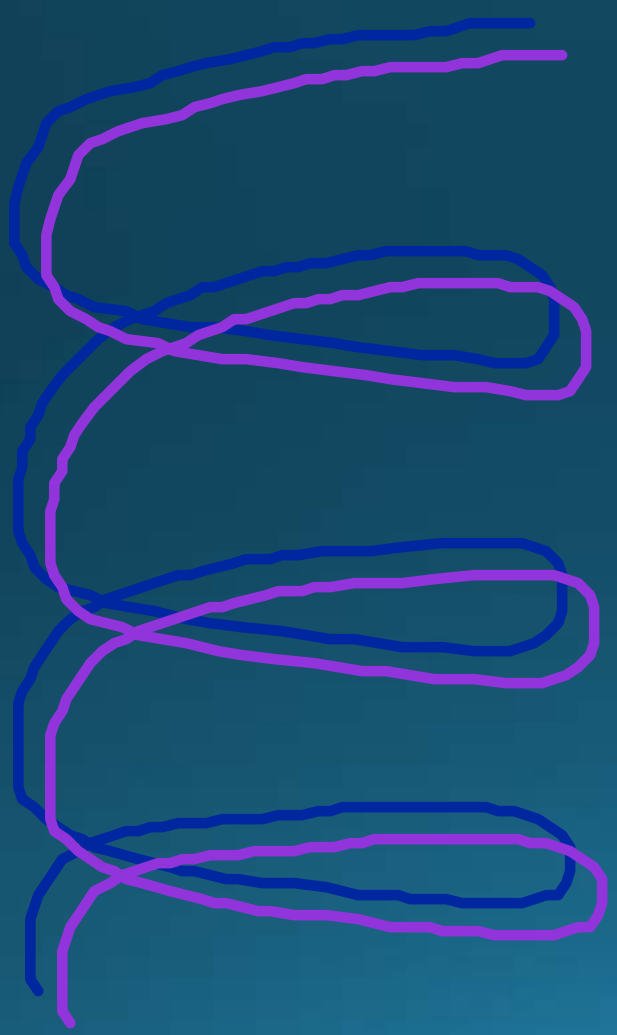


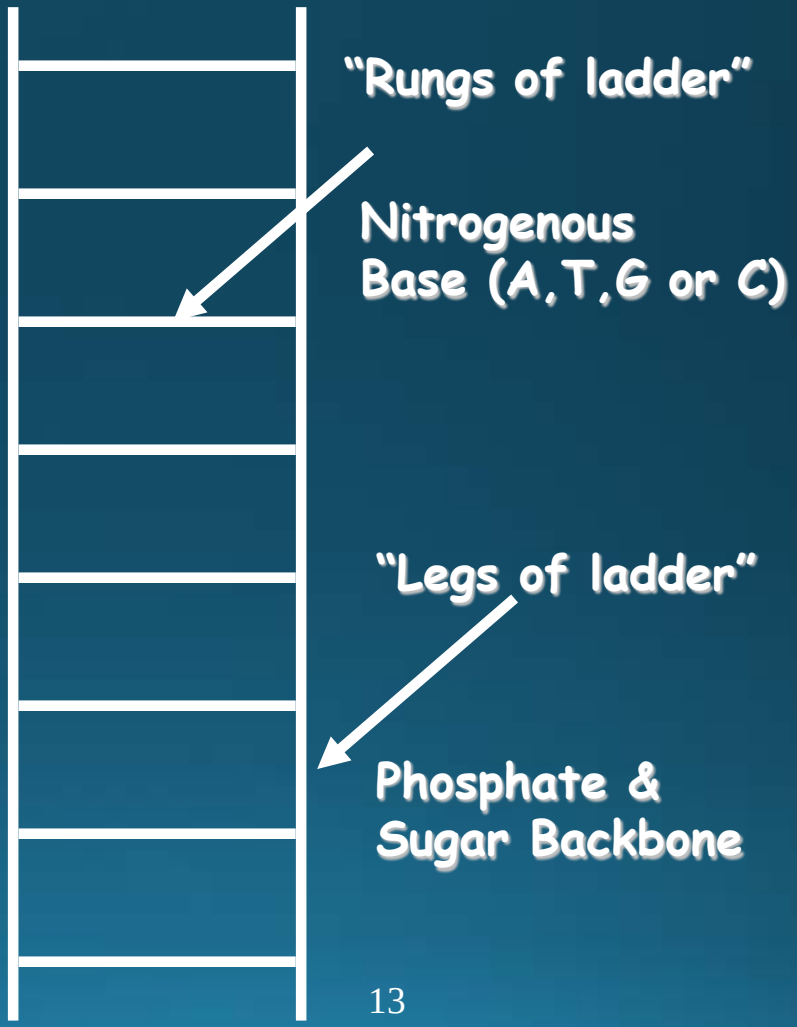
(**e**) A nucleosome consists of part of a DNA molecule looped twice around a core of histones.

DNA

- Two strands coiled called a double helix
- Sides made of a pentose sugar Deoxyribose bonded to phosphate (PO_4) groups by **phosphodiester bonds**
- Center made of nitrogen bases bonded together by weak hydrogen bonds

DNA Double Helix





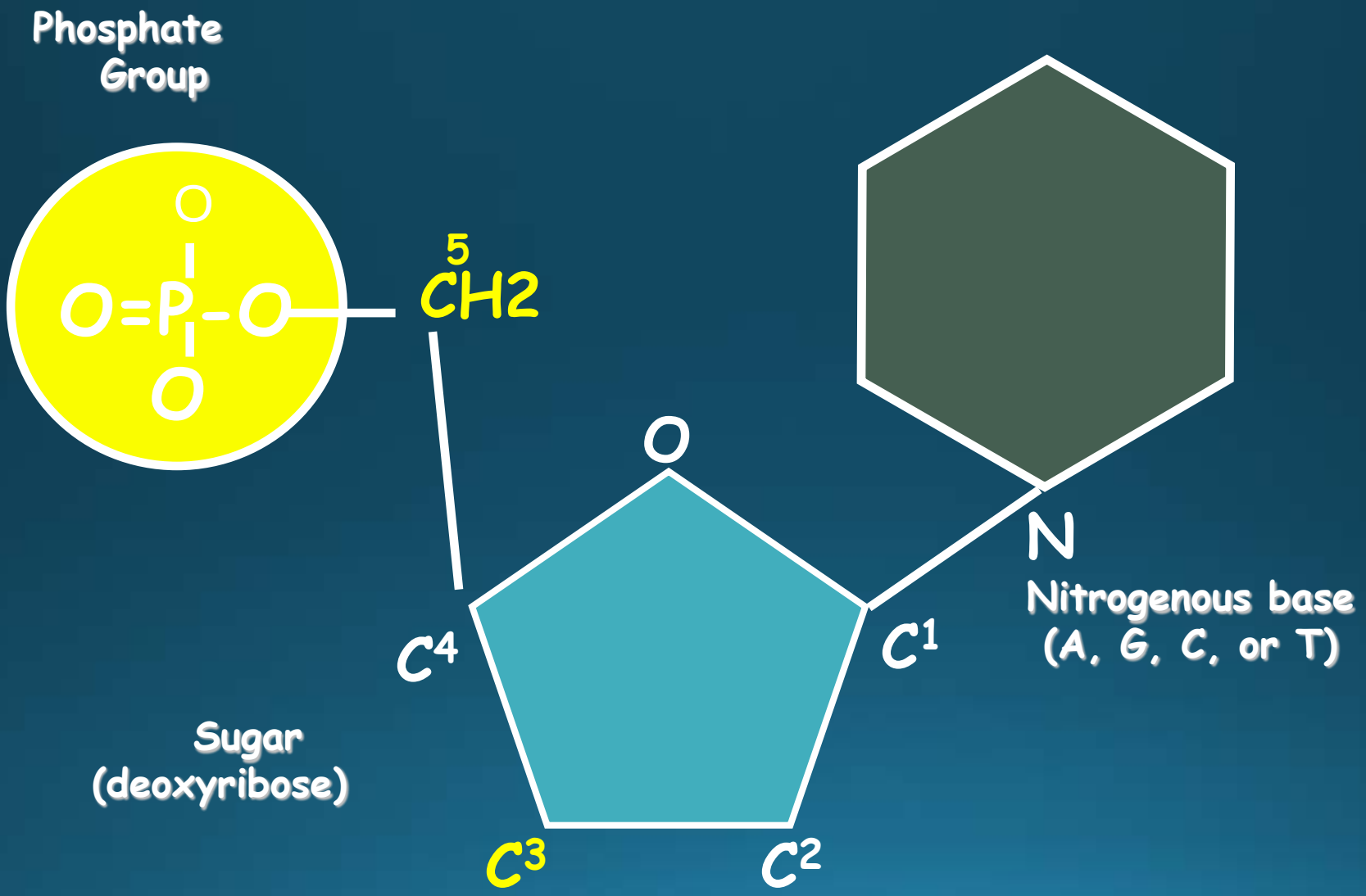
Helix

- Most DNA has a **right-hand twist** with **10 base pairs in a complete turn**
- Left twisted DNA is called Z-DNA or southpaw DNA
- Hot spots occur where right and left twisted DNA meet producing mutations

DNA

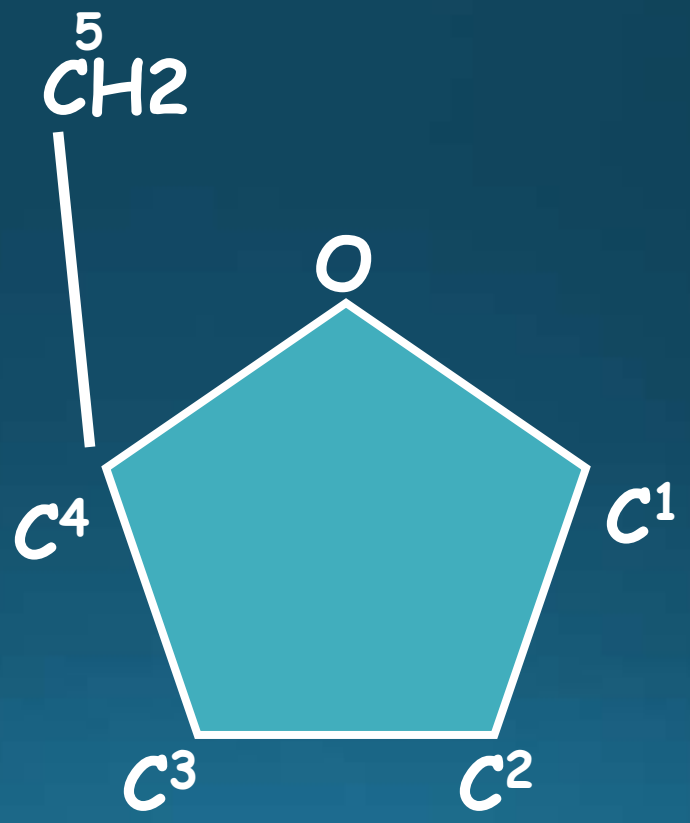
- Stands for Deoxyribonucleic acid
- Made up of subunits called nucleotides
- Nucleotide made of:
    1. Phosphate group
    2. 5-carbon sugar
    3. Nitrogenous base

DNA Nucleotide

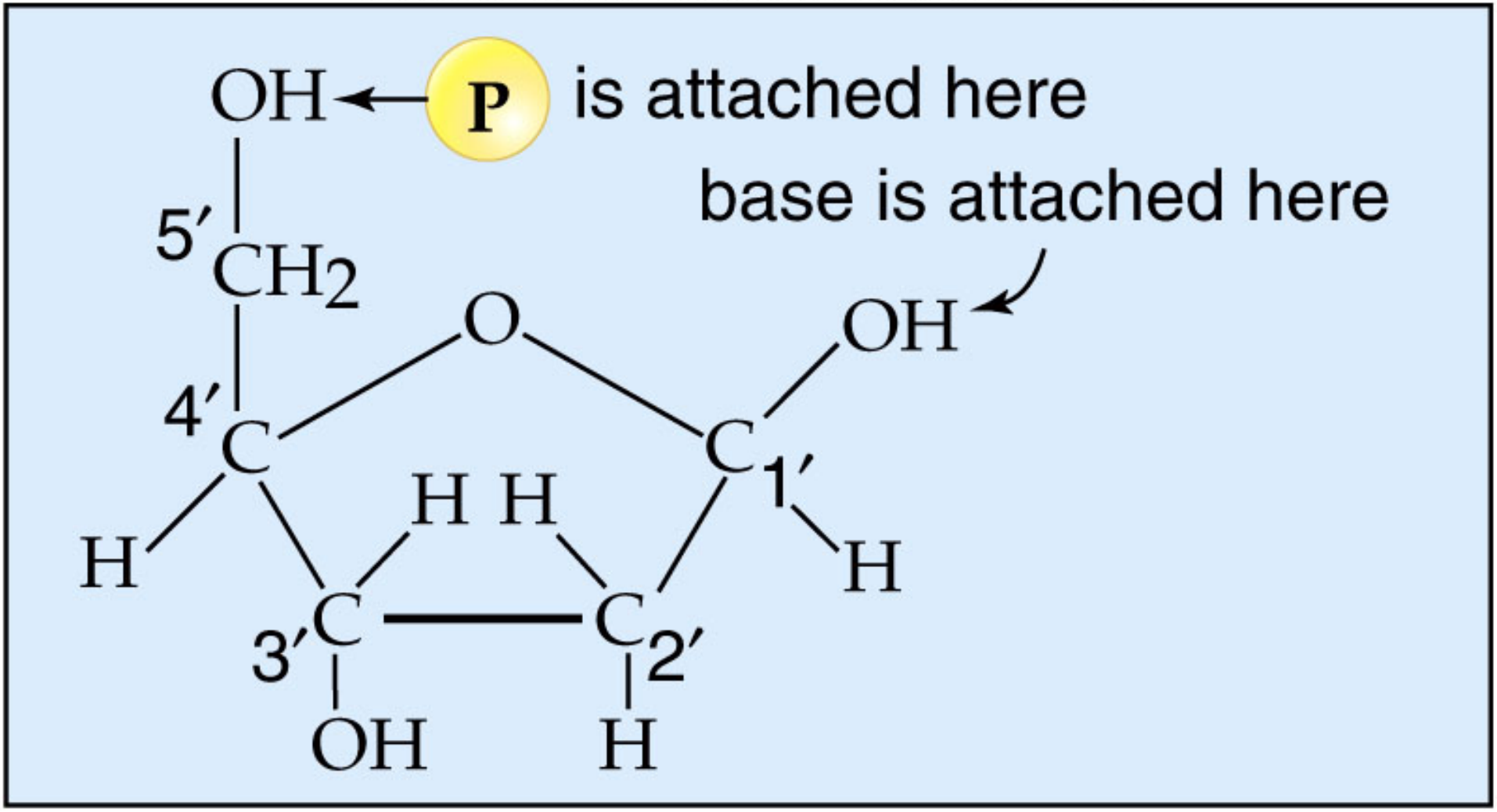


Pentose Sugar

- Carbons are numbered clockwise 1' to 5'



Sugar
(deoxyribose)



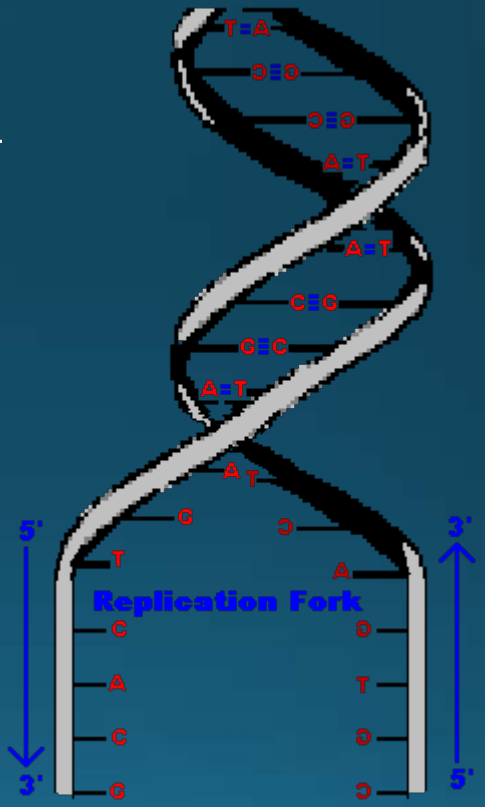
a.

DNA

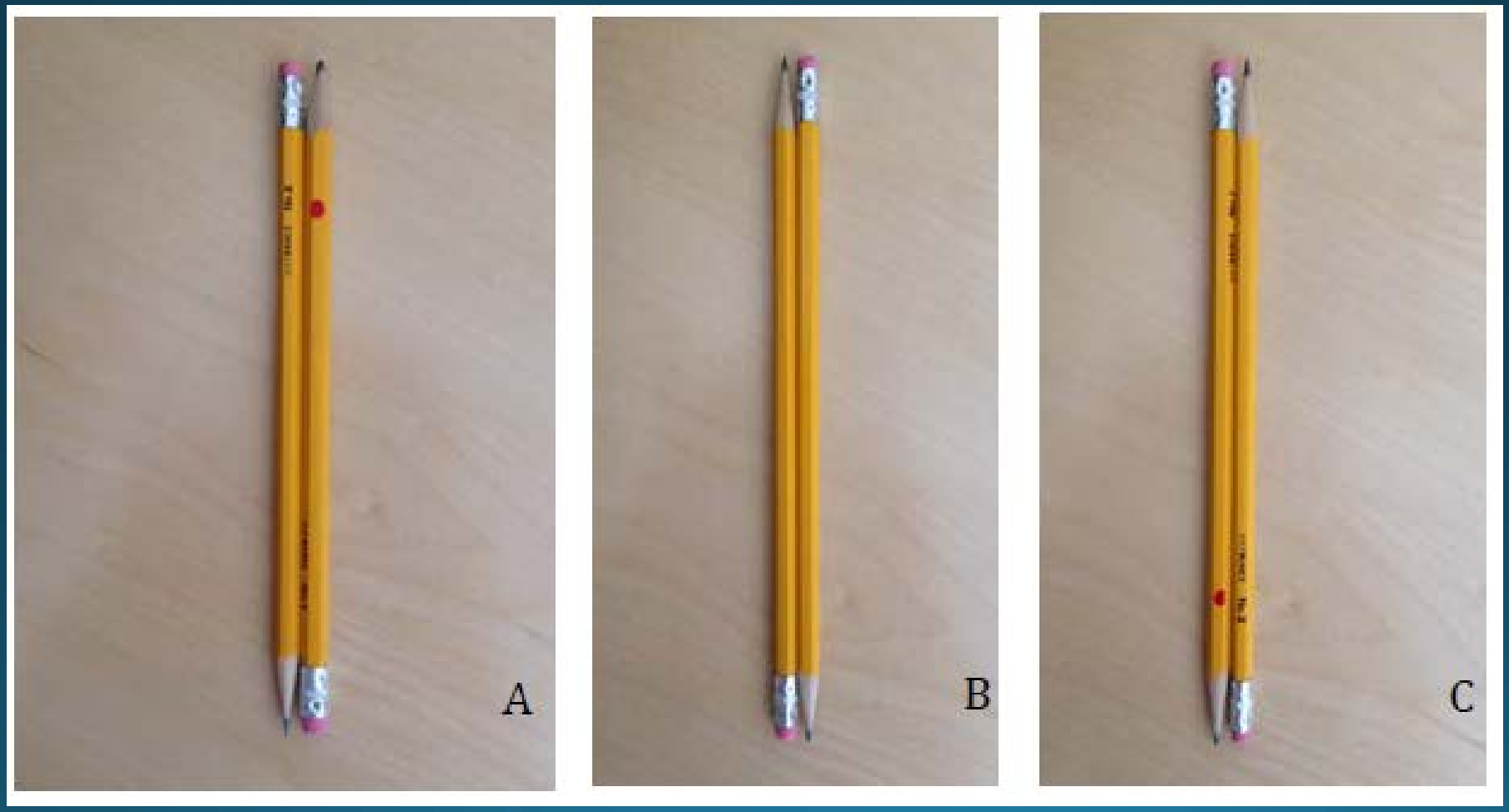
Antiparallel Strands

- One strand of DNA goes from 5’ to 3’ (sugars)

- The other strand is opposite in direction going 3’ to 5’ (sugars)

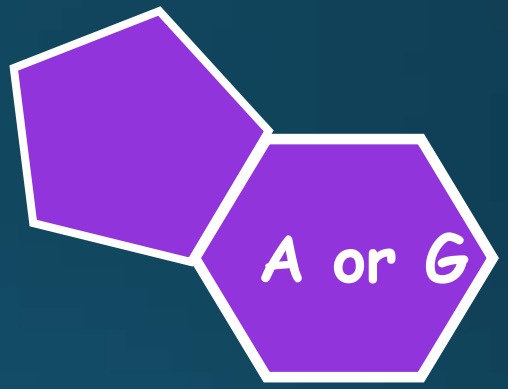


DNA strands have **DYAD symmetry**-pretend two pencils are two strands of DNA. When flipped upside down and backwards, it looks the same as the original.

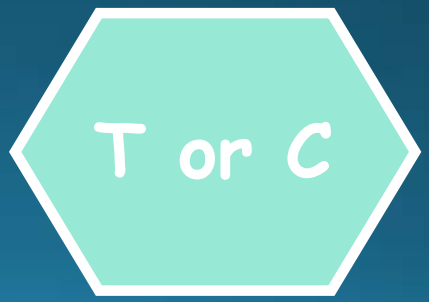


Nitrogenous Bases

- Double ring **PURINES**
  - Adenine (A)
  - Guanine (G)



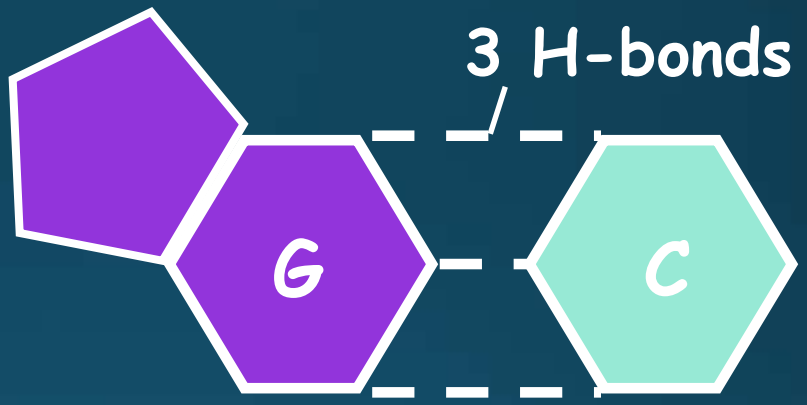
- Single ring **PYRIMIDINES**
  - Thymine (T)
  - Cytosine (C)



Base-Pairings

- **Purines only pair with Pyrimidines**

- Three hydrogen bonds required to bond Guanine & Cytosine



- Two hydrogen bonds are required to bond Adenine & Thymine

Question:

- **If there is 30% Adenine, how much Cytosine is present?**

Answer:

- There would be 20% Cytosine
- Adenine (30%) = Thymine (30%)
- Guanine (20%) = Cytosine (20%)
- Therefore, 60% A-T and 40% C-G

Your turn: On a sheet of paper

1. How many As if there are 23% Gs?
2. How many Cs if there are 44% Ts?
3. How many Ts if there are 31% As?
4. How many Gs if there are 16% Ts?

DNA Replication

Replication Facts

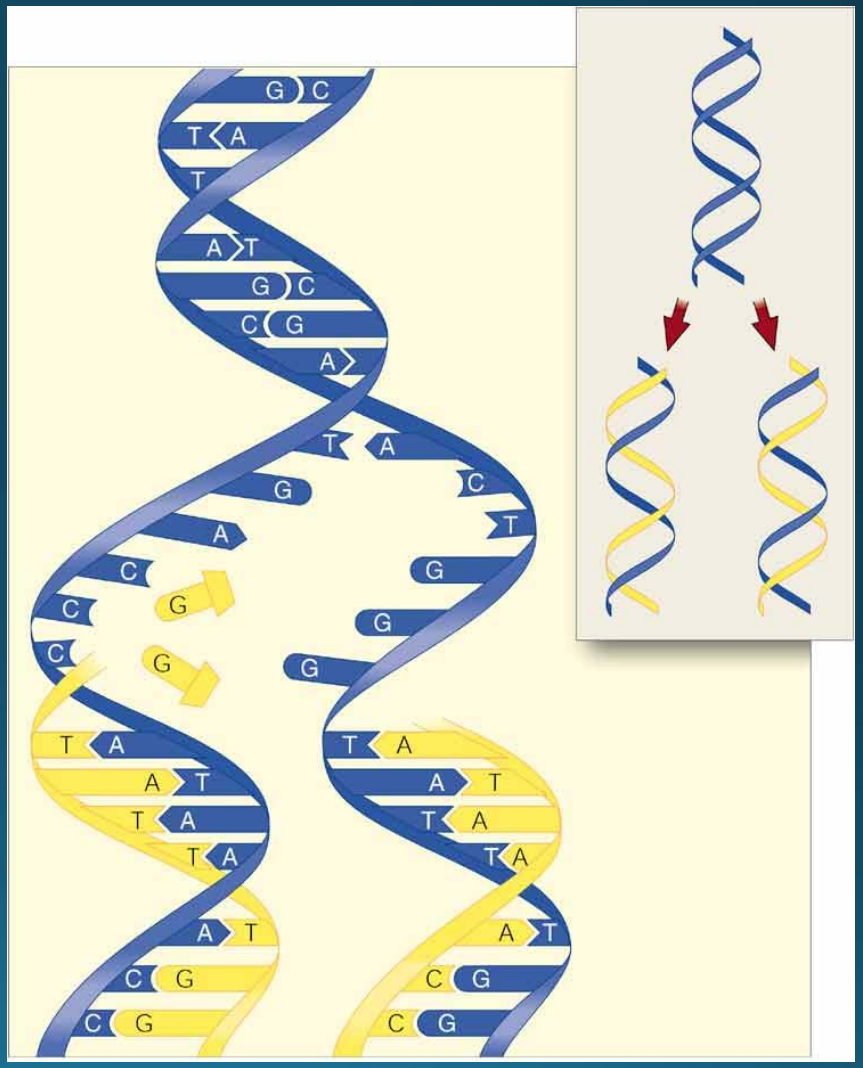
- DNA has to be copied before a cell divides
- New cells will need identical DNA strands

Semi-Conservative Replication of DNA

- **DNA Polymerase**

  catalyzes the synthesis of DNA using a template of DNA and nucleotides

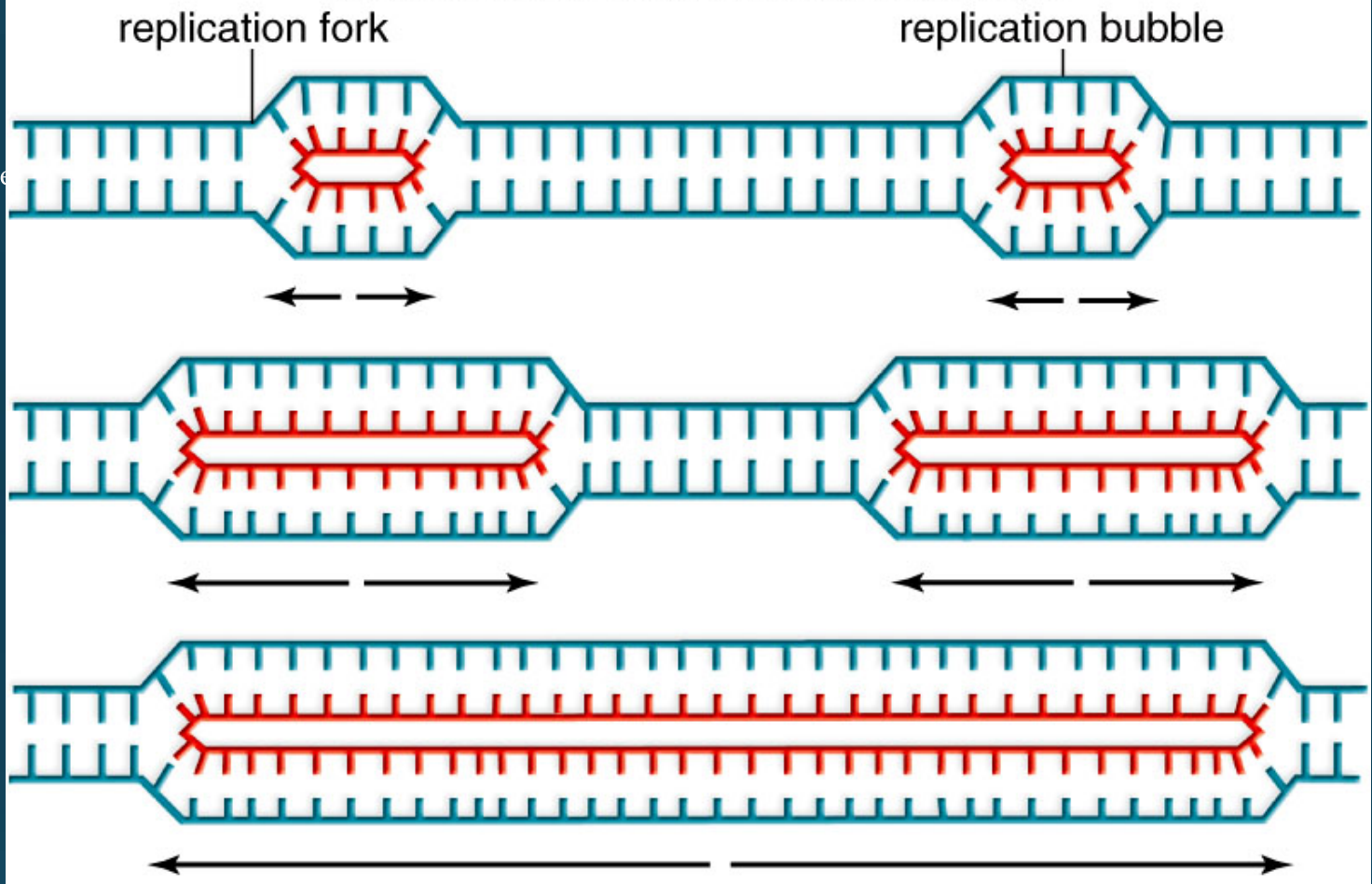
- One original strand is conserved in each daughter molecule

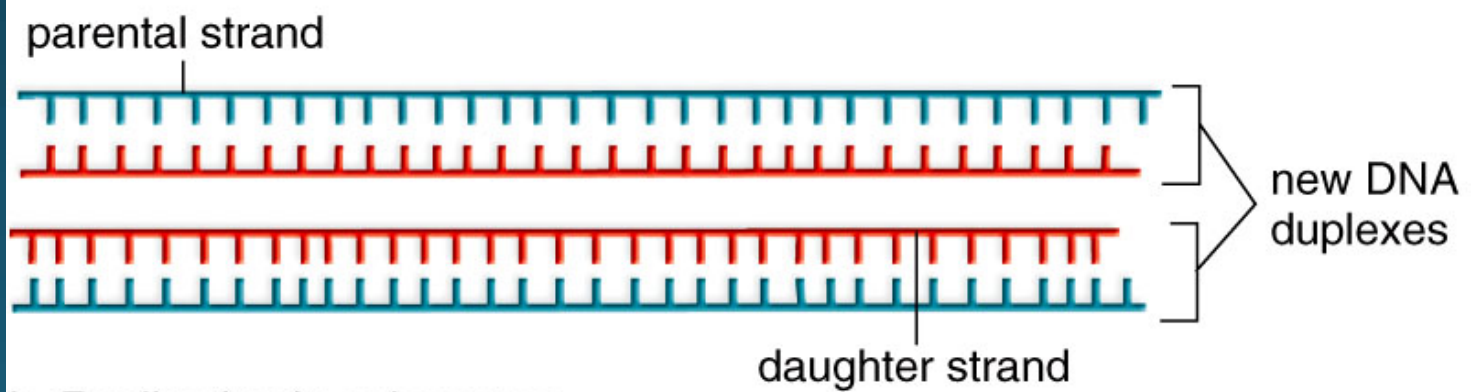


Replication: Prokaryotic vs. Eukaryotic

- Eukaryotic Replication
  - DNA replication begins at numerous points along linear chromosome
  - DNA Unwinds and unzips into two strands
  - Old strand of DNA serves as template for new strand
  - Complementary base-pairing forms new strand on each old strand
  - Replication bubbles spread bi-directionally until they meet

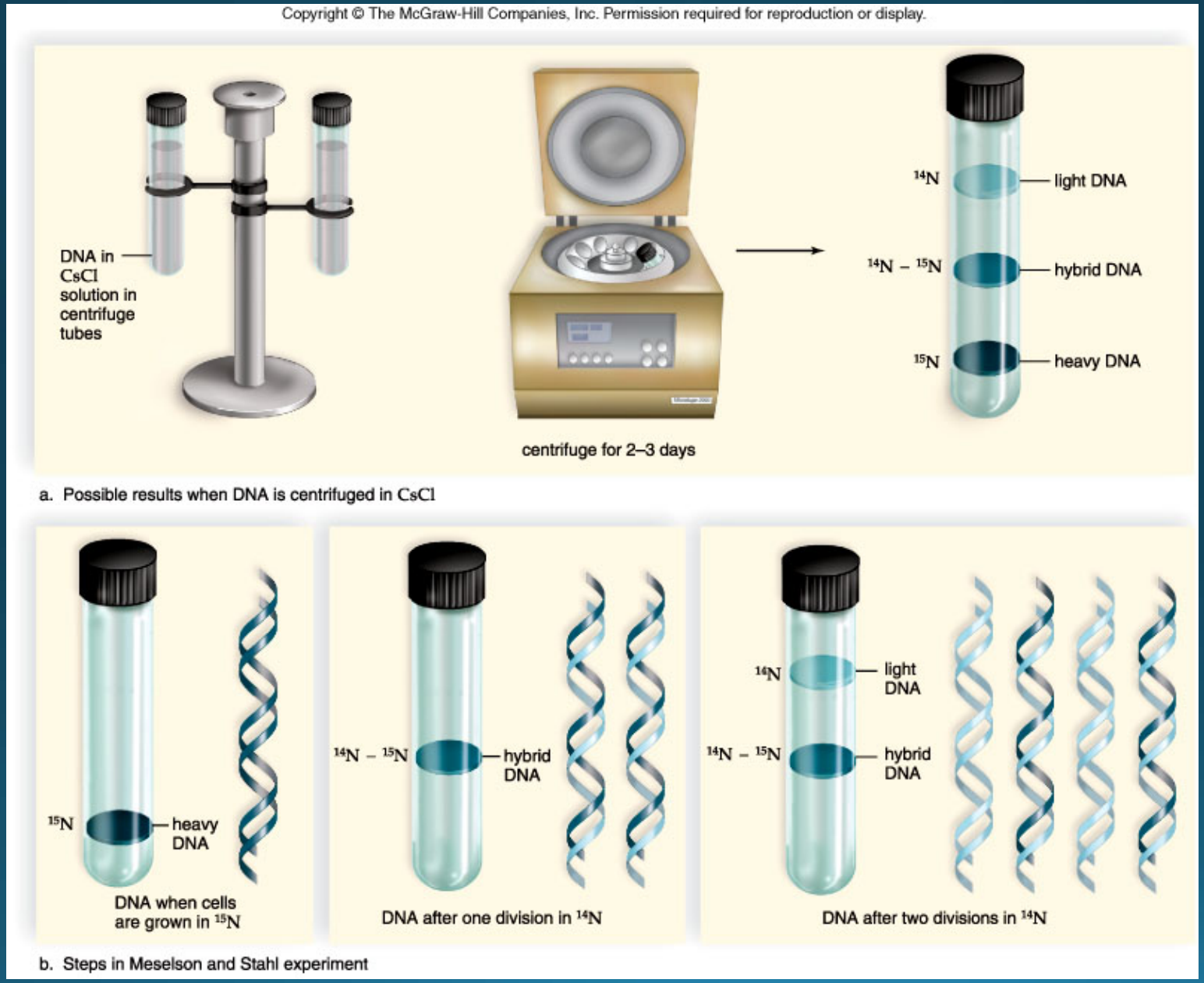
Figure





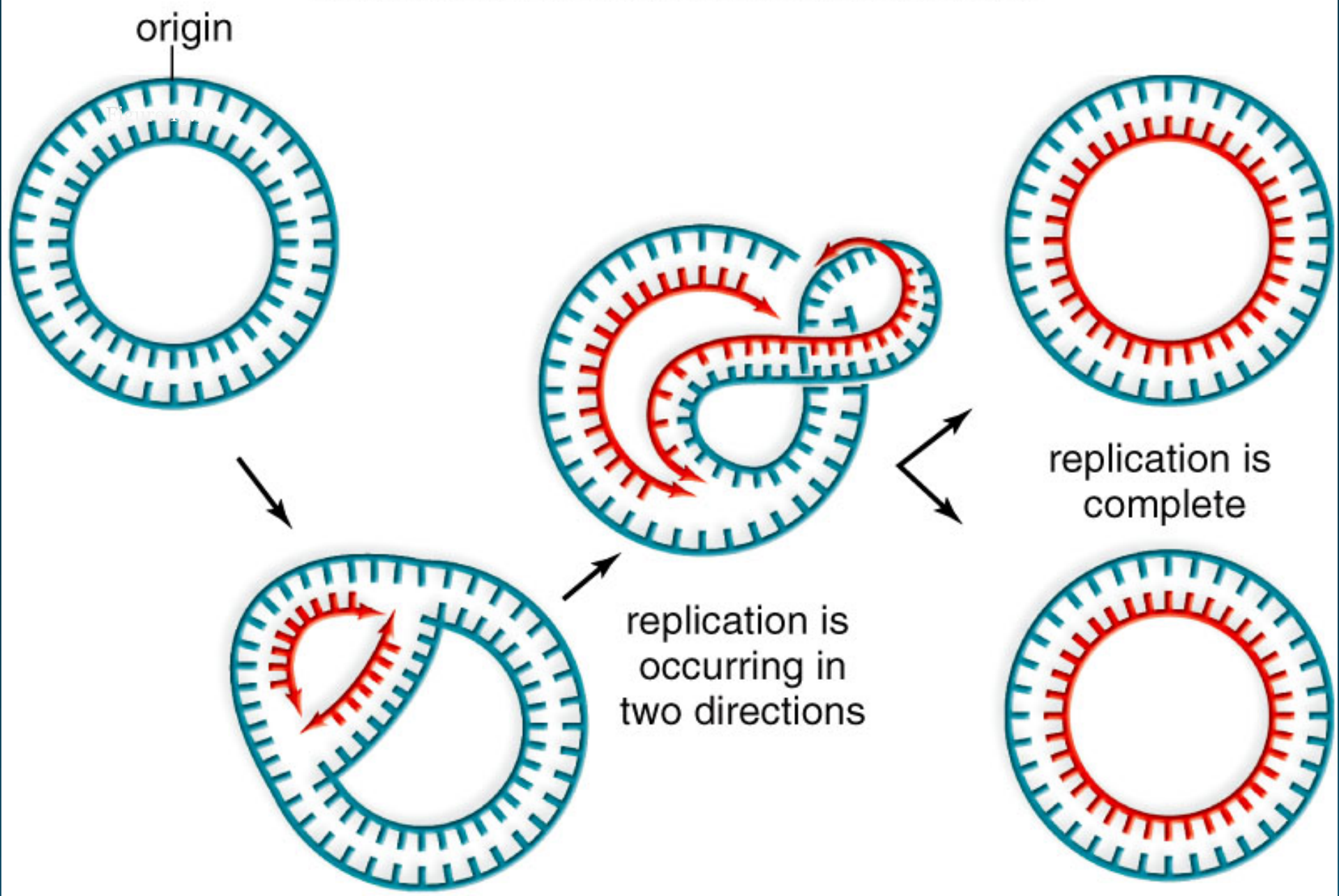
b. Replication in eukaryotes

Meselson and Stahl's DNA replication experiment



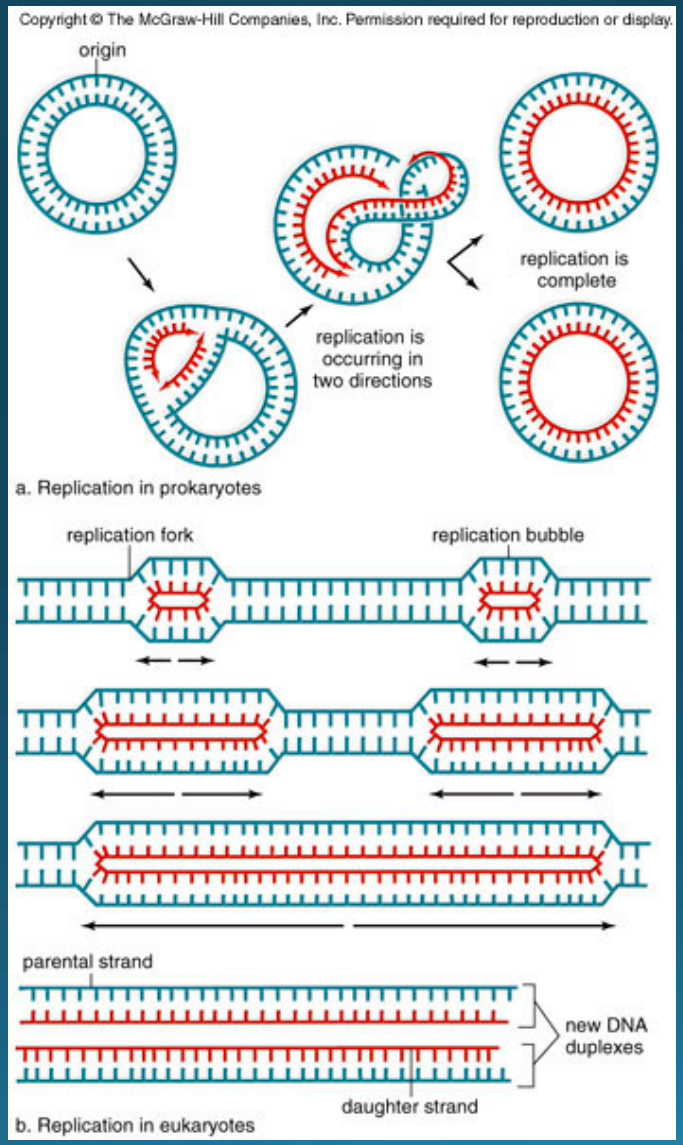
Replication: Prokaryotic vs. Eukaryotic

- Prokaryotic Replication
  - Bacteria have a single circular loop
  - Replication moves around the circular DNA molecule in both directions
  - Produces two identical circles
  - Cell divides between circles, as fast as every 20 minutes



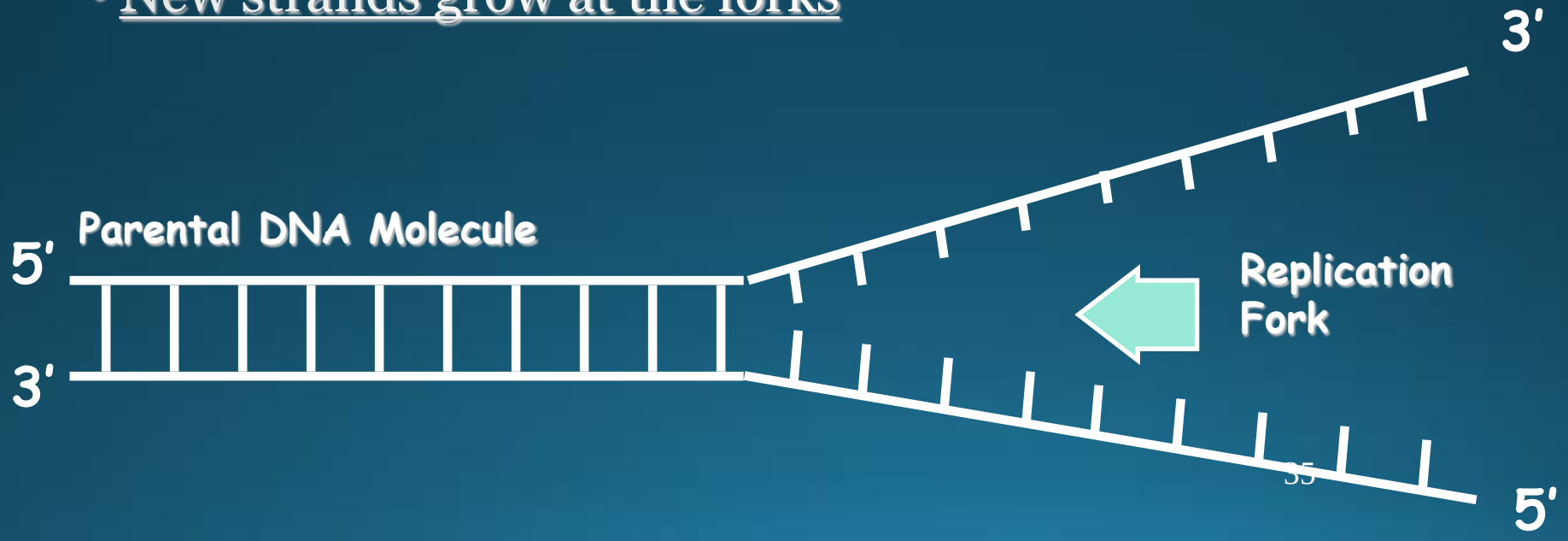
a. Replication in prokaryotes

Replication: Prokaryotic vs. Eukaryotic



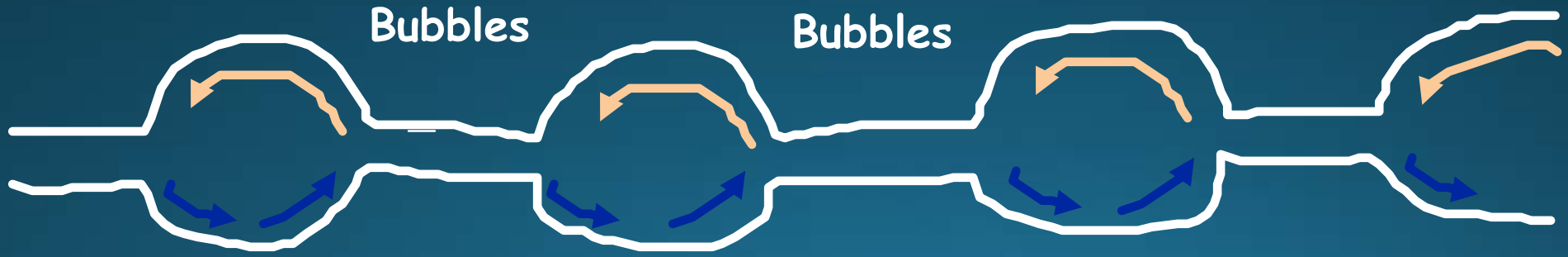
DNA Replication

- Begins at Origins of Replication
- Two strands open forming Replication Forks (Y-shaped region)
- New strands grow at the forks



DNA Replication

- As the 2 DNA strands open at the origin, Replication Bubbles form
- Eukaryotic chromosomes have MANY bubbles
- Prokaryotes (bacteria) have a single bubble



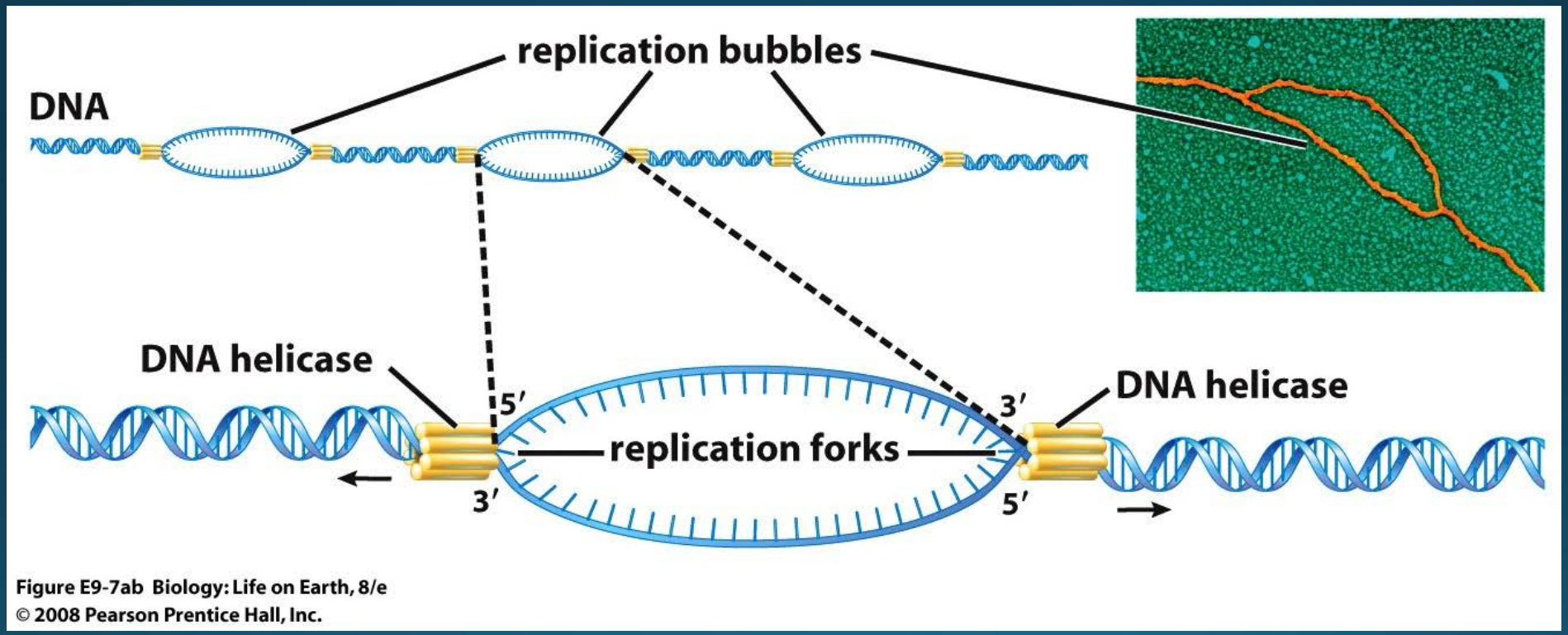


Figure E9-7ab Biology: Life on Earth, 8/e

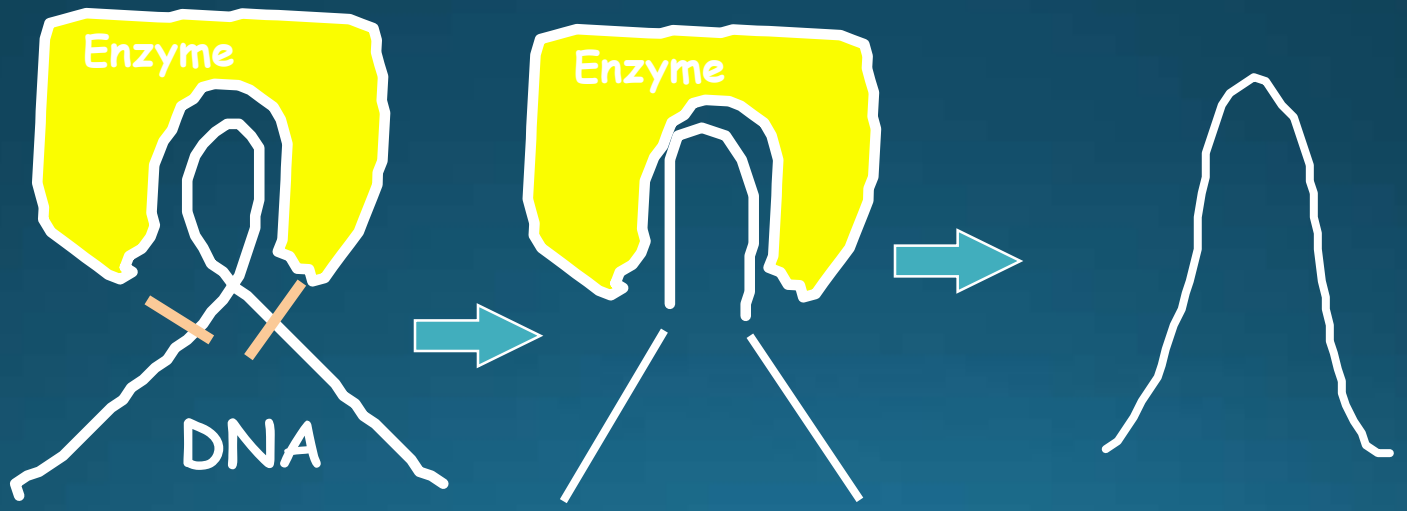
DNA Replication

- Enzyme **DNA Helicase** unwinds and separates the 2 DNA strands by breaking the weak hydrogen bonds

- Single-Strand Binding Proteins (SSBs) attach and keep the 2 DNA strands separated and untwisted

DNA Replication

- Enzyme **Topoisomerase** attaches to the 2 forks of the bubble to **relieve stress** on the DNA molecule as it separates

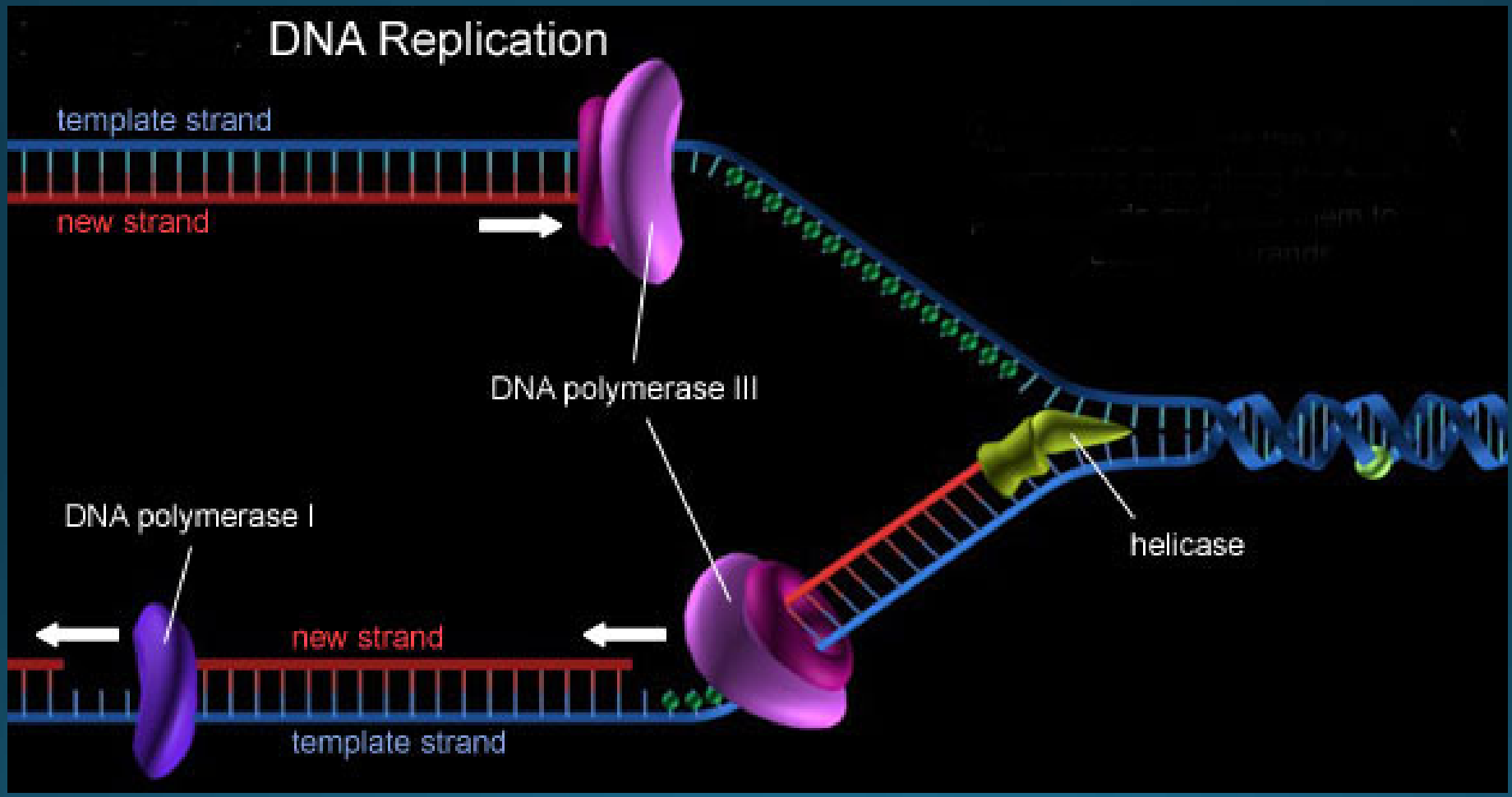


DNA Replication

- **Primase** is an enzyme that synthesizes a complimentary RNA Primer

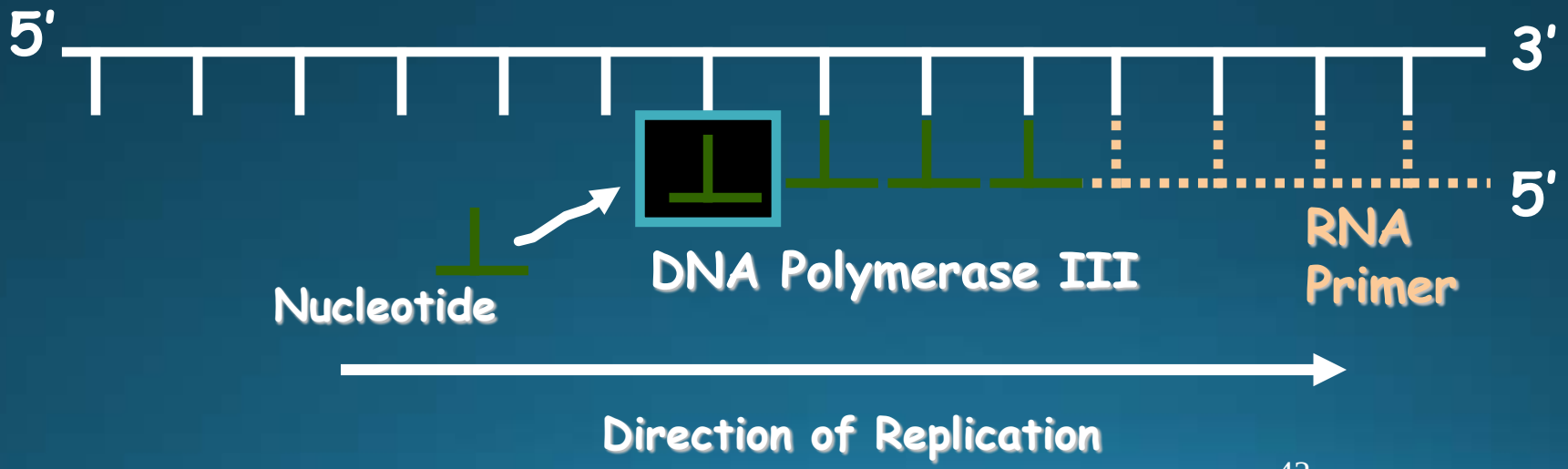
- **RNA primers** bind to serve as a starting point for the addition of new nucleotides

- **DNA polymerase III** can then add the new nucleotides

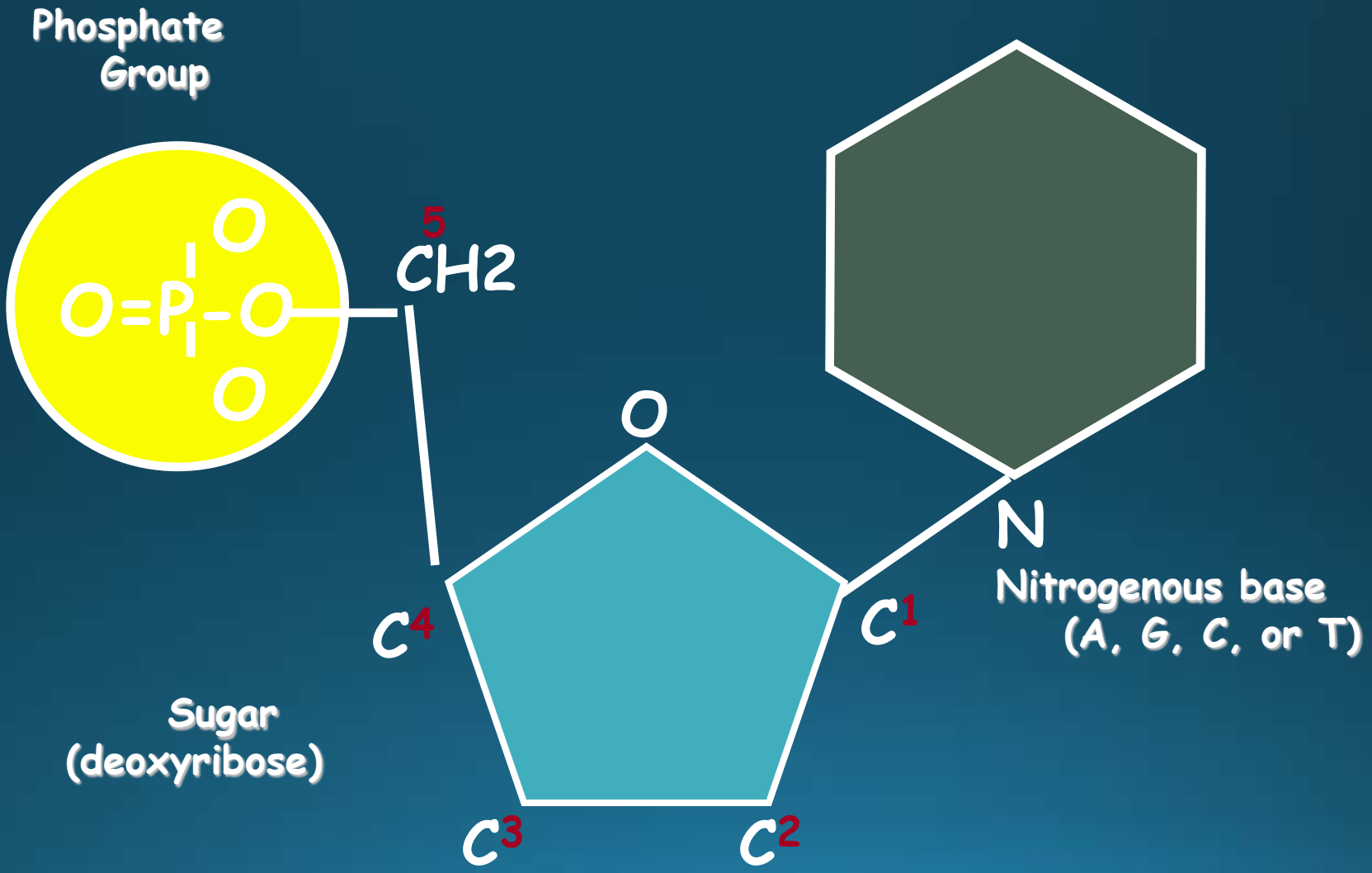

DNA Replication
template strand
new strand
DNA polymerase III
DNA polymerase I
helicase
new strand
template strand

DNA Replication

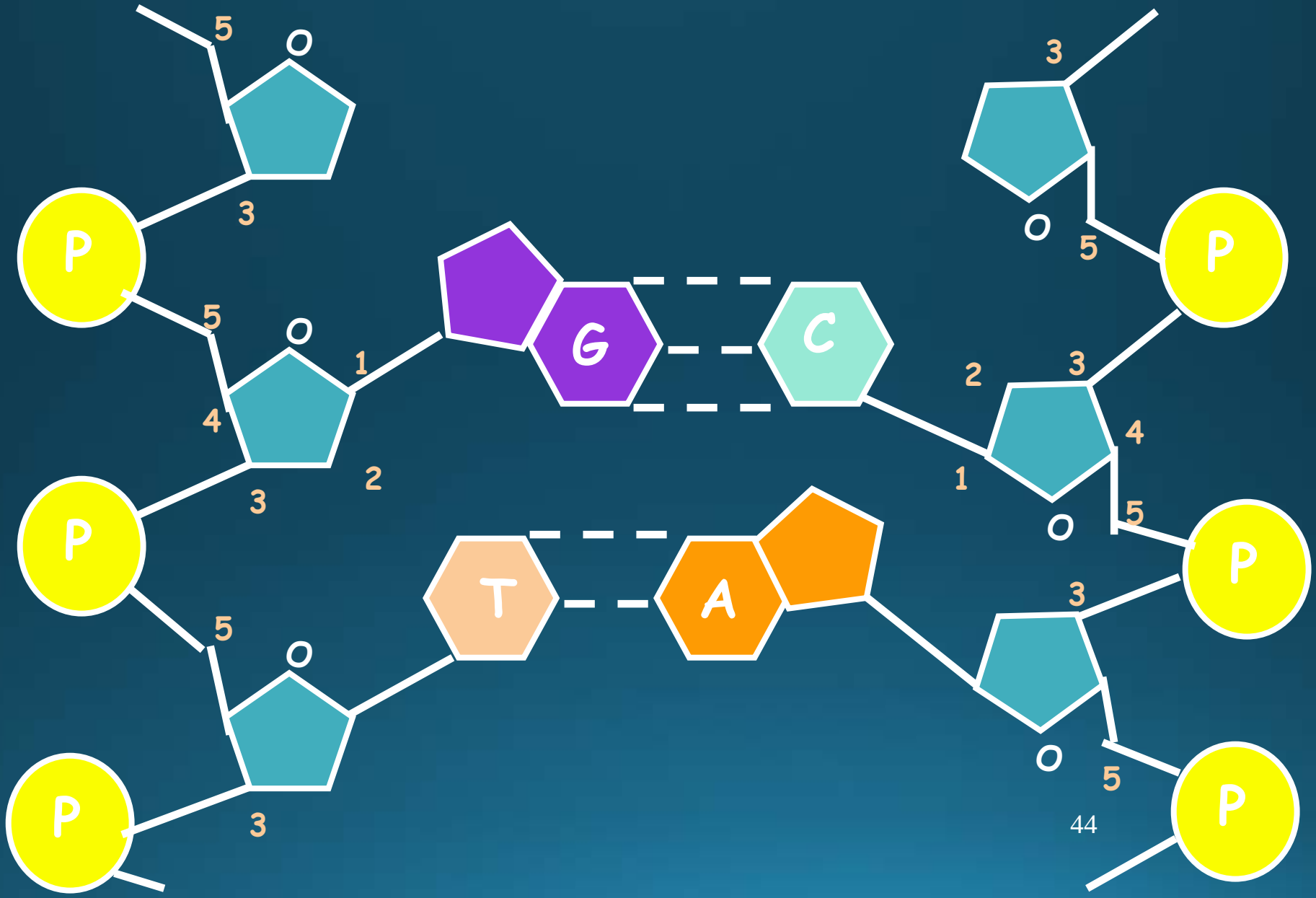
- DNA polymerase III can only add nucleotides to the 3' end of the DNA
- This causes the NEW strand to be built in a 5' to 3' direction



Remember HOW the Carbons Are Numbered!

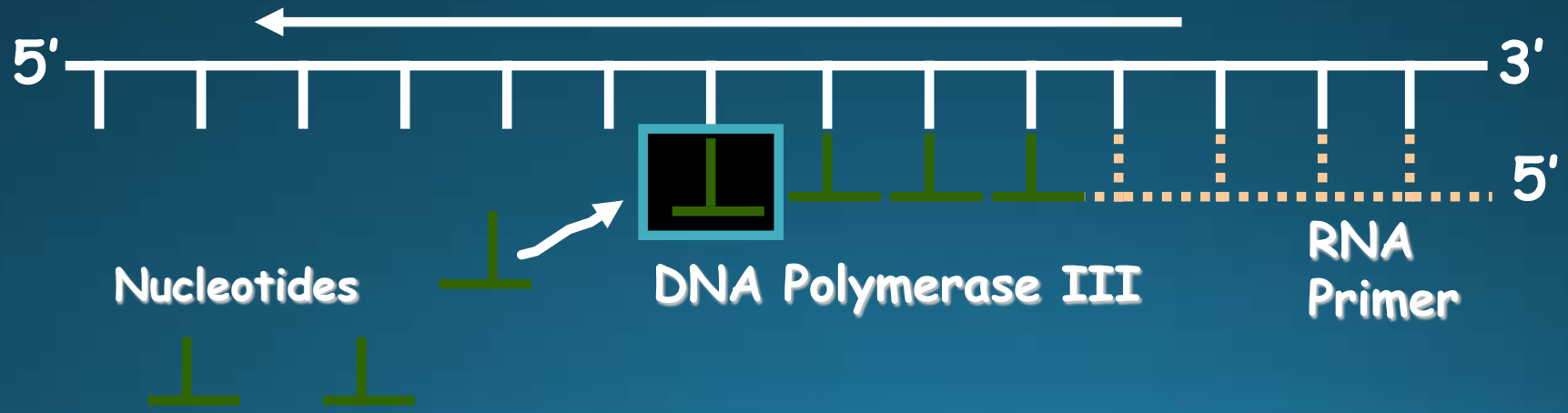


Remember the Strands are Antiparallel



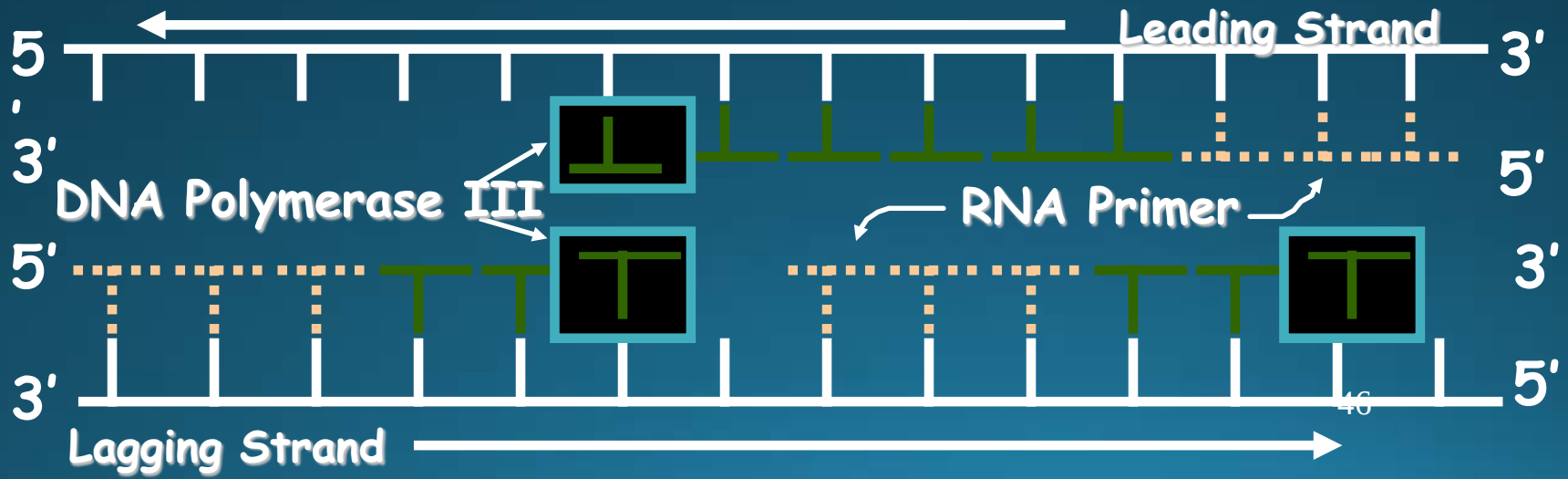
Synthesis of the New DNA Strands

- The **Leading Strand** is synthesized as a single continuous strand from the point of origin toward the opening replication fork



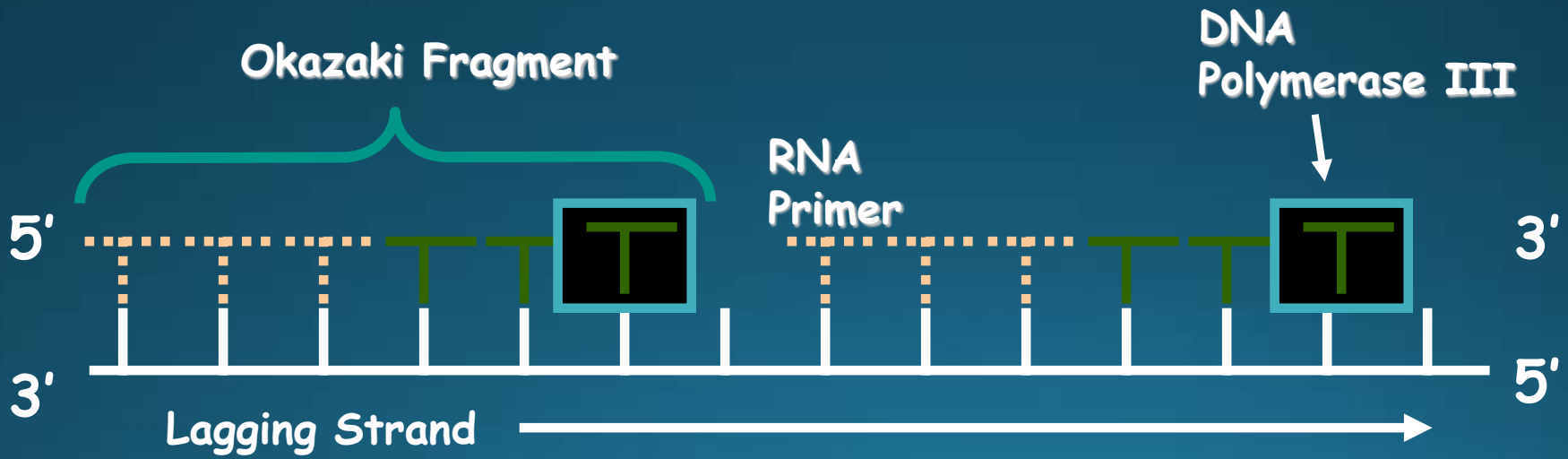
Synthesis of the New DNA Strands

- The **Lagging Strand** is synthesized discontinuously against overall direction of replication
- This strand is made in MANY short segments It is replicated from the replication fork toward the origin



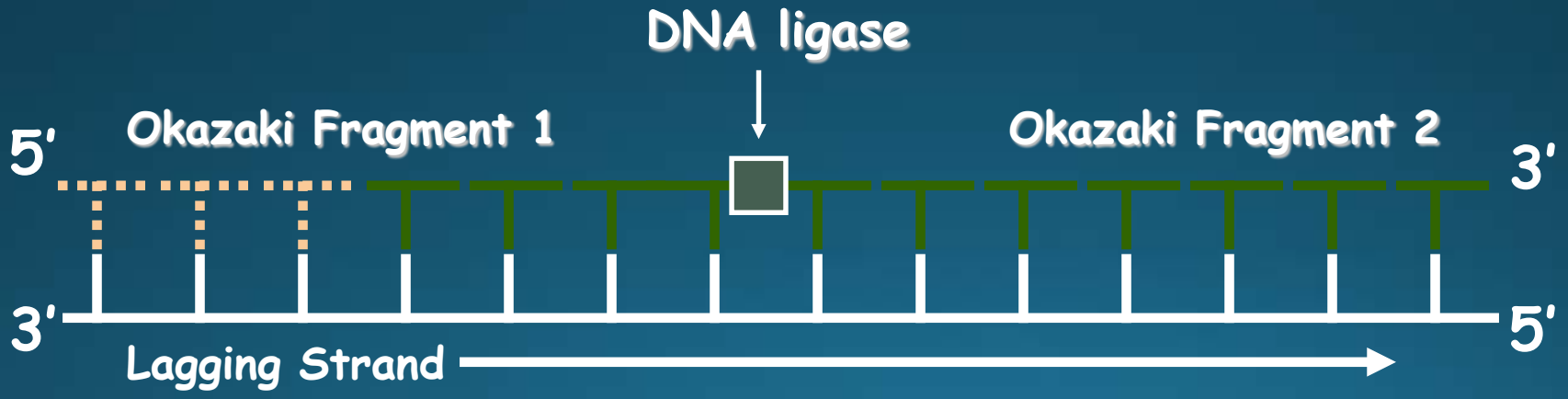
Lagging Strand Segments

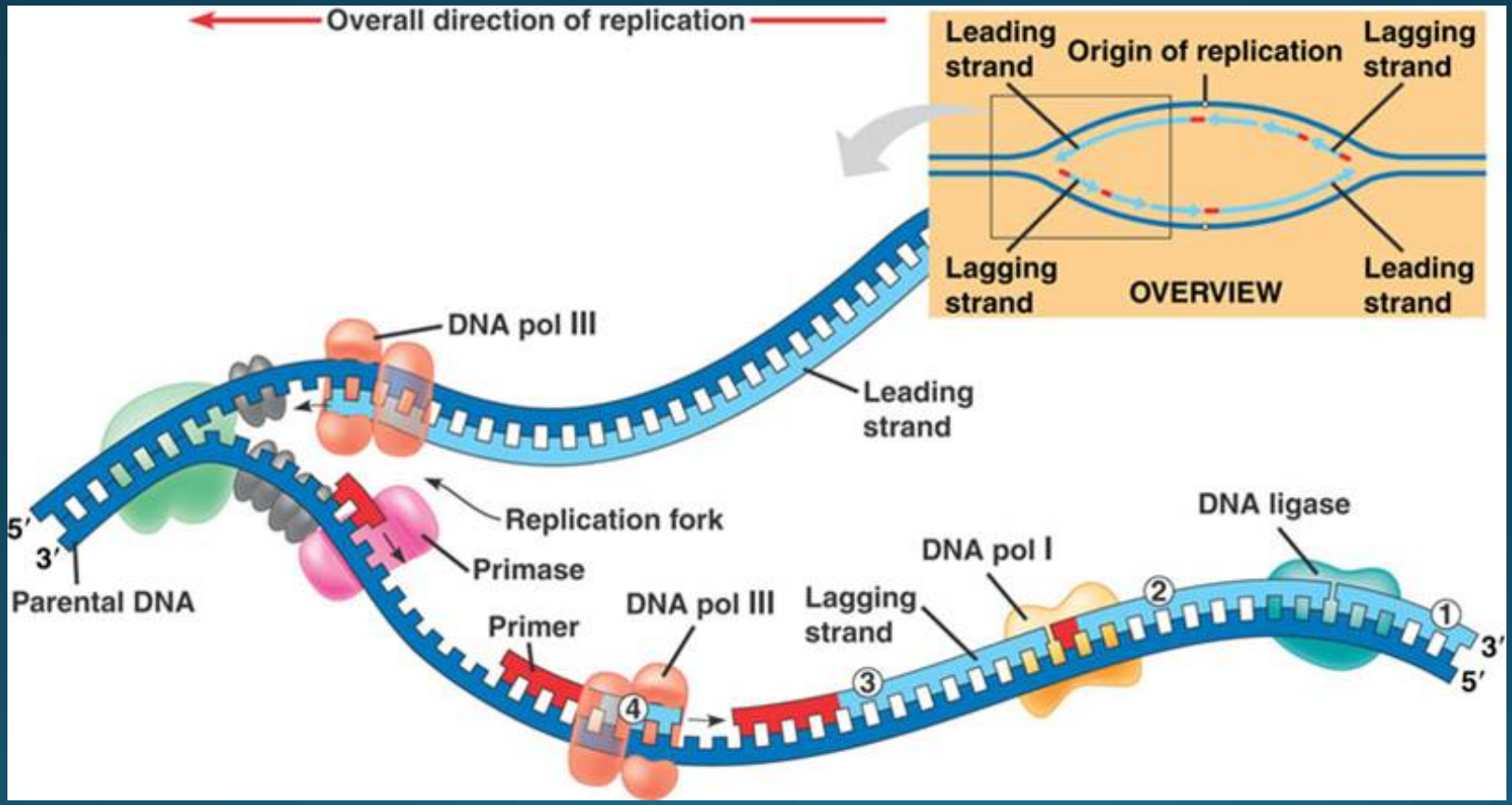
- **Okazaki Fragments** - series of short segments on the lagging strand
- Leaves GAPS between fragments



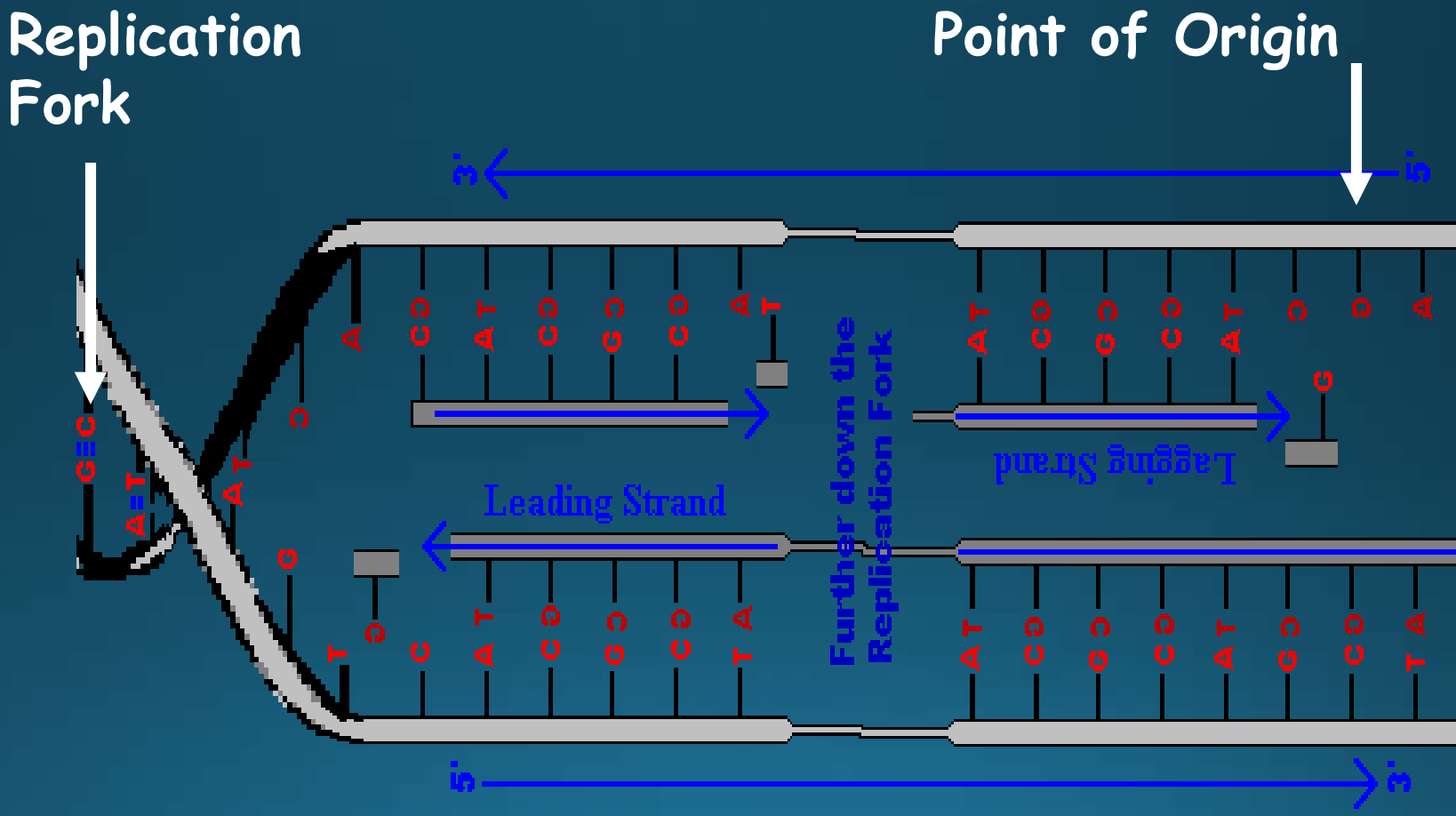
Joining of Okazaki Fragments

- **DNA Polymerase I** – fills in the DNA nucleotides where RNA primers have been removed.
- The enzyme **Ligase** joins the Okazaki fragments together to make one strand





Replication of Strands

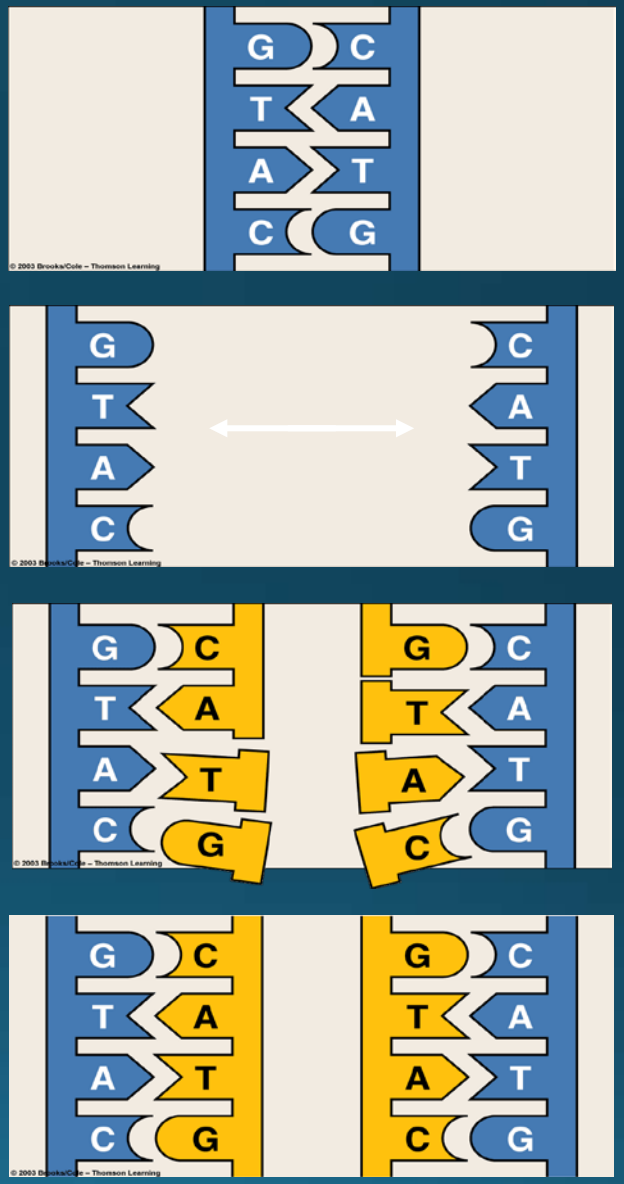


DNA Replication

- Strands are unwound and separate
- New bases pair

  G with C

  T with A
- New DNA composed of one “old” strand and one “new” strand



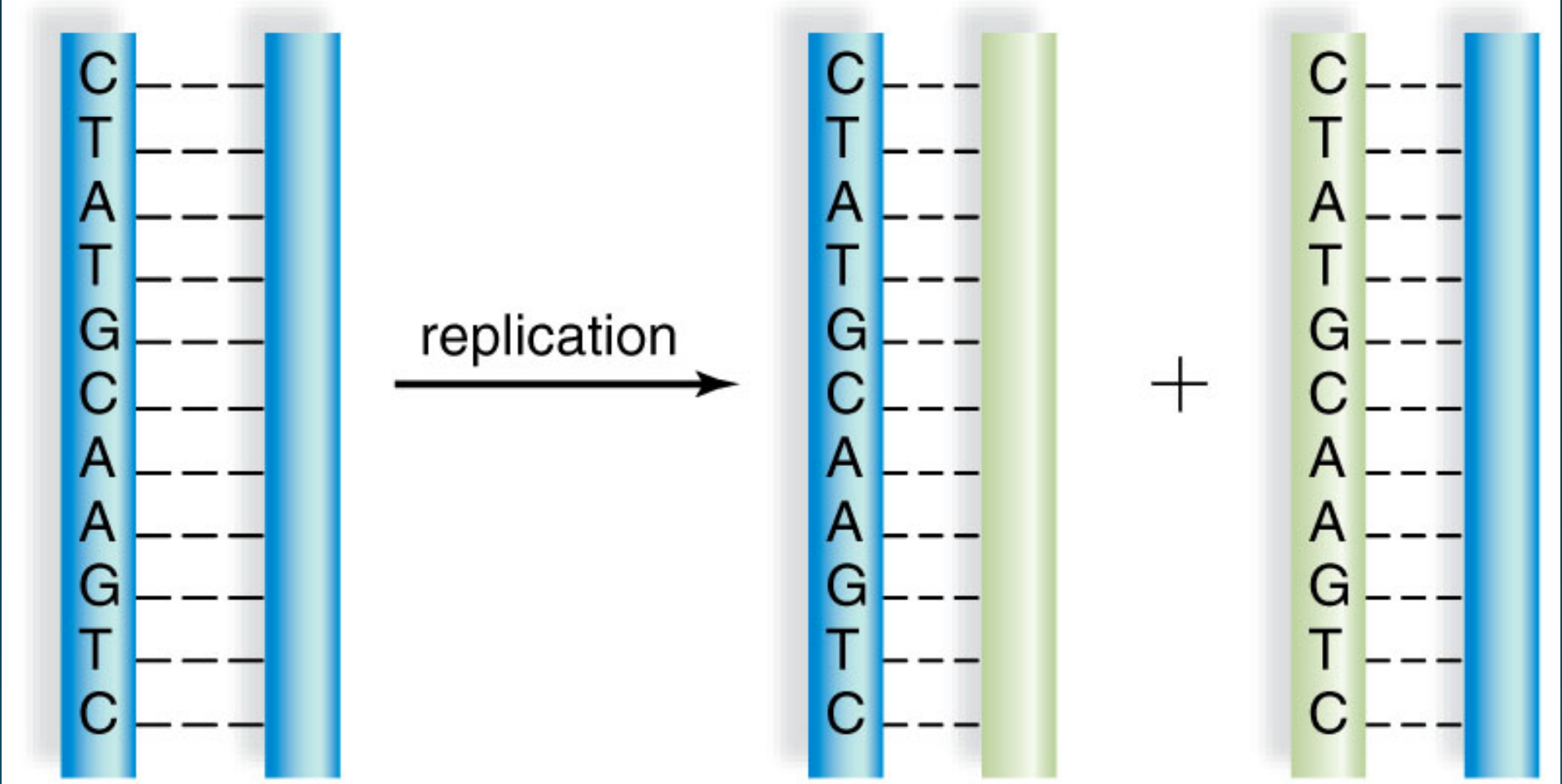


Figure 13Ab

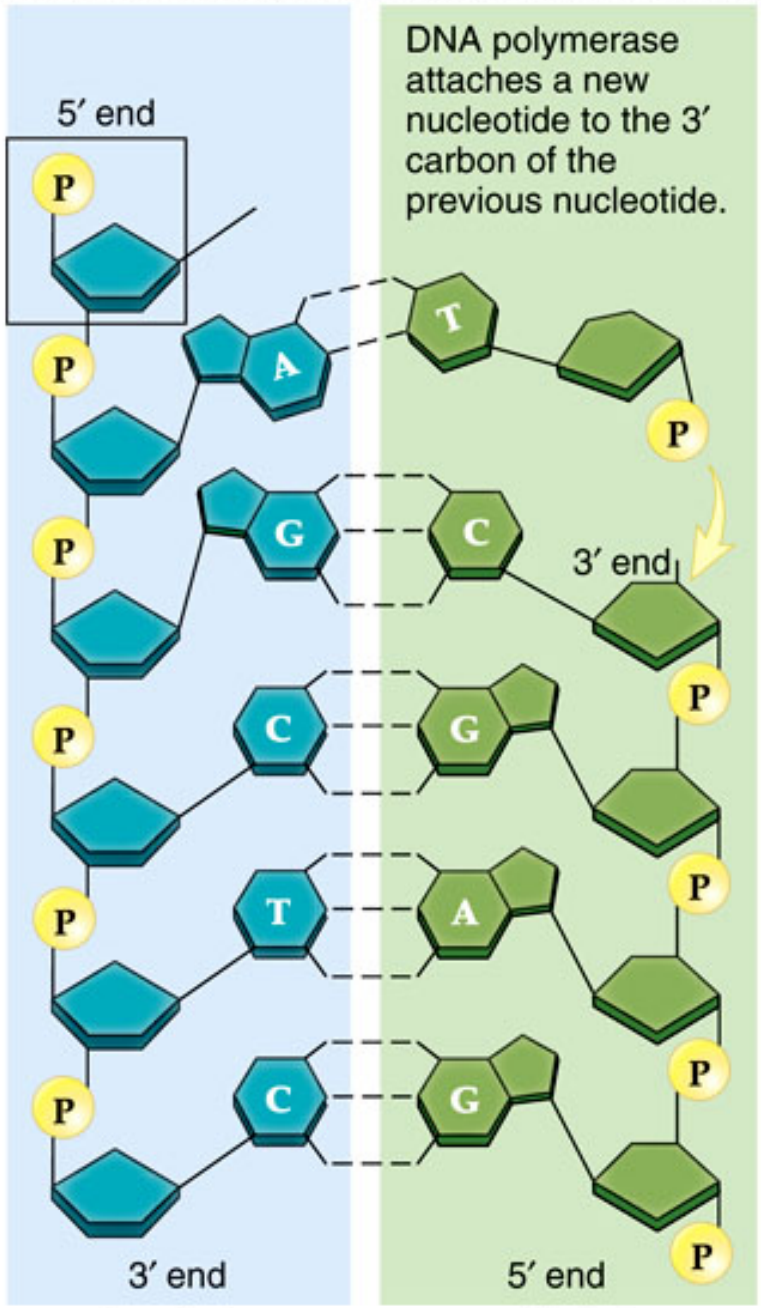
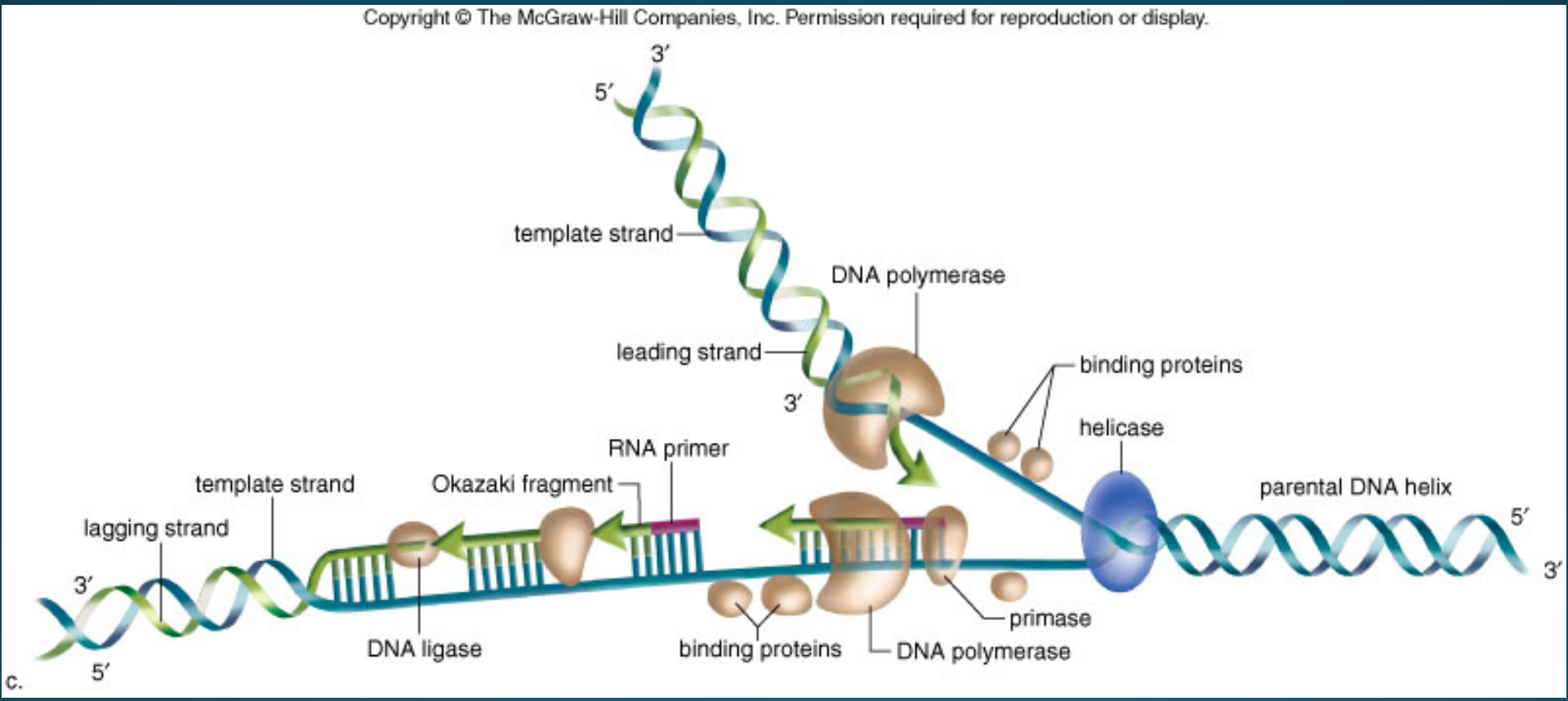


Figure 13Ac


Copyright © The McGraw-Hill Companies, Inc. Permission required for reproduction or display.
3′
5′
template strand
DNA polymerase
leading strand
3′
binding proteins
helicase
RNA primer
template strand
Okazaki fragment
parental DNA helix
5′
lagging strand
3′
3′
primase
DNA ligase
binding proteins
DNA polymerase
5′
c.

Replication Errors

- Genetic variations are the raw material for evolutionary change
- Mutation:
  - A permanent (but unplanned) change in base-pair sequence
    - Some due to errors in DNA replication
    - Others are due to DNA damage
  - DNA repair enzymes are usually available to reverse most errors

Proofreading New DNA

- DNA polymerase initially makes about 1 in 10,000 base pairing errors
- Enzymes proofread and correct these mistakes
- The new error rate for DNA that has been proofread is 1 in 1 billion base pairing errors

DNA Damage & Repair

- Chemicals & ultraviolet radiation damage the DNA in our body cells
- Cells must continuously repair DAMAGED DNA
- Excision repair occurs when any of over 50 repair enzymes remove damaged parts of DNA
- DNA polymerase and DNA ligase replace and bond the new nucleotides together

Semiconservative Model of Replication

- Idea presented by Watson & Crick
- The two strands of the parental molecule separate, and each acts as a template for a new complementary strand
- New DNA consists of 1 PARENTAL (original) and 1 NEW strand of DNA

Question:

- What would be the complementary DNA strand for the following DNA sequence?

DNA 5'-CGTATG-3'

Answer:

DNA 5’-GCGTATG-3’

DNA 3’-CGCATAC-5’

Now you do these AND calculate the percentage of A/Ts and G/Cs:

1.5′-ATCGGATTTATA-3′

2.5′-ATCGTCAGGCTT-3′

3.5′-CGGCACCTCCGCAGG-3′

4.5′-ATTTACGATTCATTG-3′

5.5′-GGGCGATACGTACATT-3′