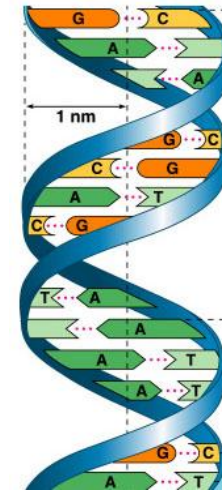


Wednesday, April 9<sup>th</sup>

# DNA The Genetic Material Replication

## Chapter 16



# Scientific History

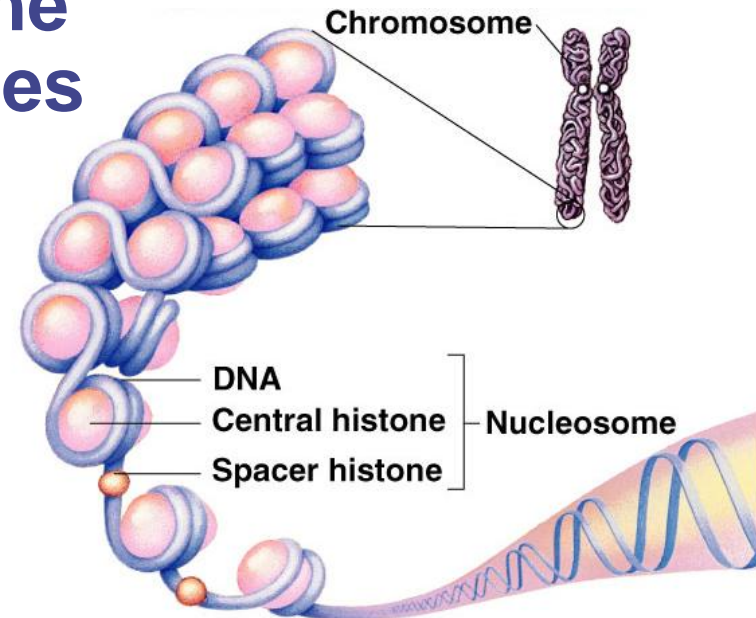
- **The march to understanding that DNA is the genetic material**
  - ◆ **T.H. Morgan (1908)**
  - ◆ **Frederick Griffith (1928)**
  - ◆ **Avery, McCarty & MacLeod (1944)**
  - ◆ **Hershey & Chase (1952)**
  - ◆ **Watson & Crick (1953)**
  - ◆ **Meselson & Stahl (1958)**

1908 | 1933

# Genes are on chromosomes

## ■ 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?**



1928

# The “Transforming Factor”

## ■ Frederick Griffith

- ◆ *Streptococcus pneumonia* bacteria
  - was working to find cure for pneumonia
- ◆ harmless live bacteria mixed with heat-killed infectious bacteria causes disease in mice
- ◆ substance passed from dead bacteria to live bacteria = “Transforming Factor”



# The “Transforming Factor”

live pathogenic strain of *bacteria*

live non-pathogenic strain of *bacteria*

heat-killed pathogenic *bacteria*

mix heat-killed pathogenic & non-pathogenic *bacteria*



## Transformation?

something in heat-killed bacteria could still transmit disease-causing properties

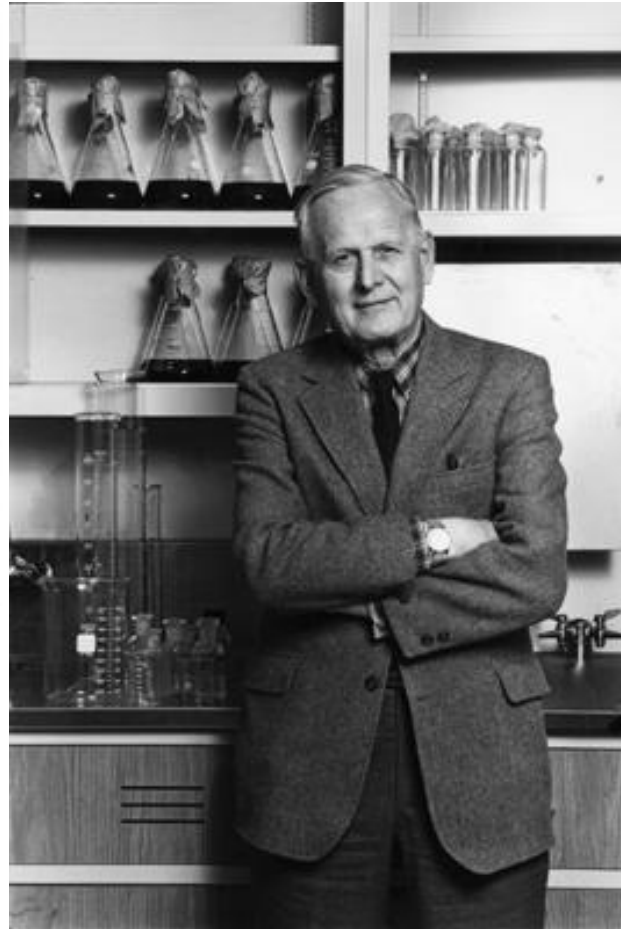
# DNA is the “Transforming Factor”<sup>1944</sup>

- **Avery, McCarty & MacLeod**
  - ◆ purified both DNA & proteins from *Streptococcus pneumoniae* bacteria
    - which will transform non-pathogenic bacteria?
  - ◆ injected protein into bacteria
    - no effect
  - ◆ injected DNA into bacteria
    - transformed harmless bacteria into virulent bacteria

# Avery, McCarty & MacLeod



**Oswald Avery**



**Maclyn McCarty**



**Colin MacLeod**

# Hershey and Chase

Confirmation of DNA: *animation*

[Hershey and Chase experiment](#)

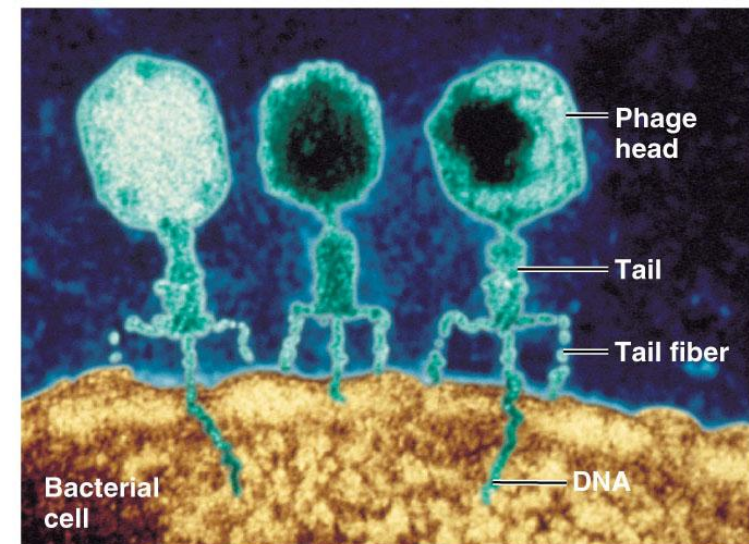
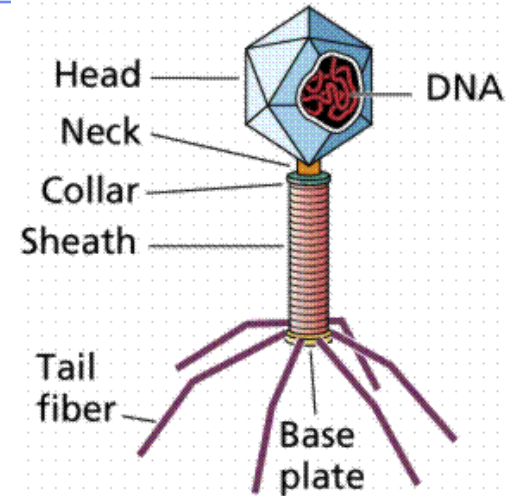


1952 | 1969

# Confirmation of DNA

## ■ Hershey & Chase

- ◆ classic “blender” experiment
- ◆ worked with **bacteriophage**
  - viruses that infect bacteria
- ◆ grew phage viruses in 2 media, radioactively labeled with either
  - $^{35}\text{S}$  in their proteins
  - $^{32}\text{P}$  in their DNA
- ◆ infected bacteria with labeled phages



# Hershey & Chase



# Thursday, April 10<sup>th</sup>

Please explain the experiment of **Frederick Griffith** to a peer at your table.

Today I will:

1. **Summarize** the work of Avery, McCarty & MacLeod.
2. **Describe** the Hershey-Chase “blender” experiment.
3. **State** Chargaff’s rules and **outline** the structure of a DNA nucleotide.

# Hershey & Chase

Protein coat labeled with  $^{35}\text{S}$

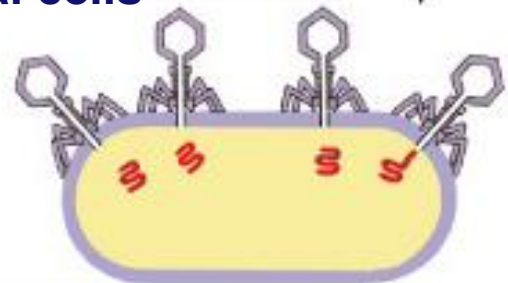
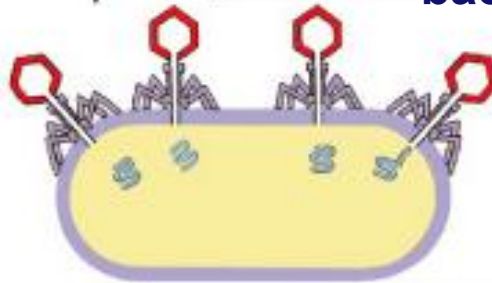


T2 bacteriophages are labeled with radioactive isotopes  
**S vs. P**

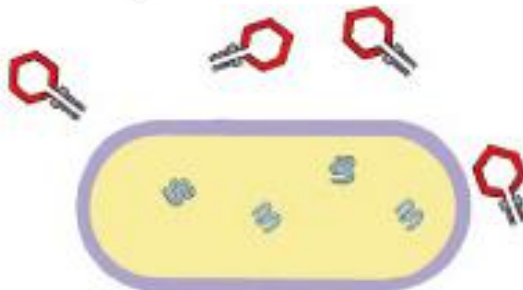
DNA labeled with  $^{32}\text{P}$



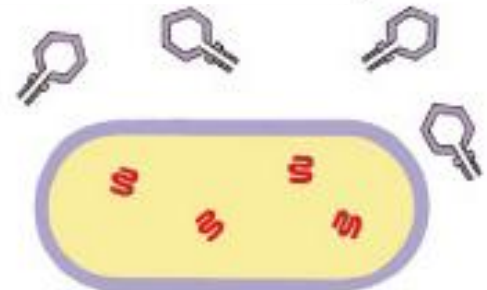
bacteriophages infect bacterial cells



bacterial cells are agitated to remove viral protein coats



$^{35}\text{S}$  radioactivity found in the medium

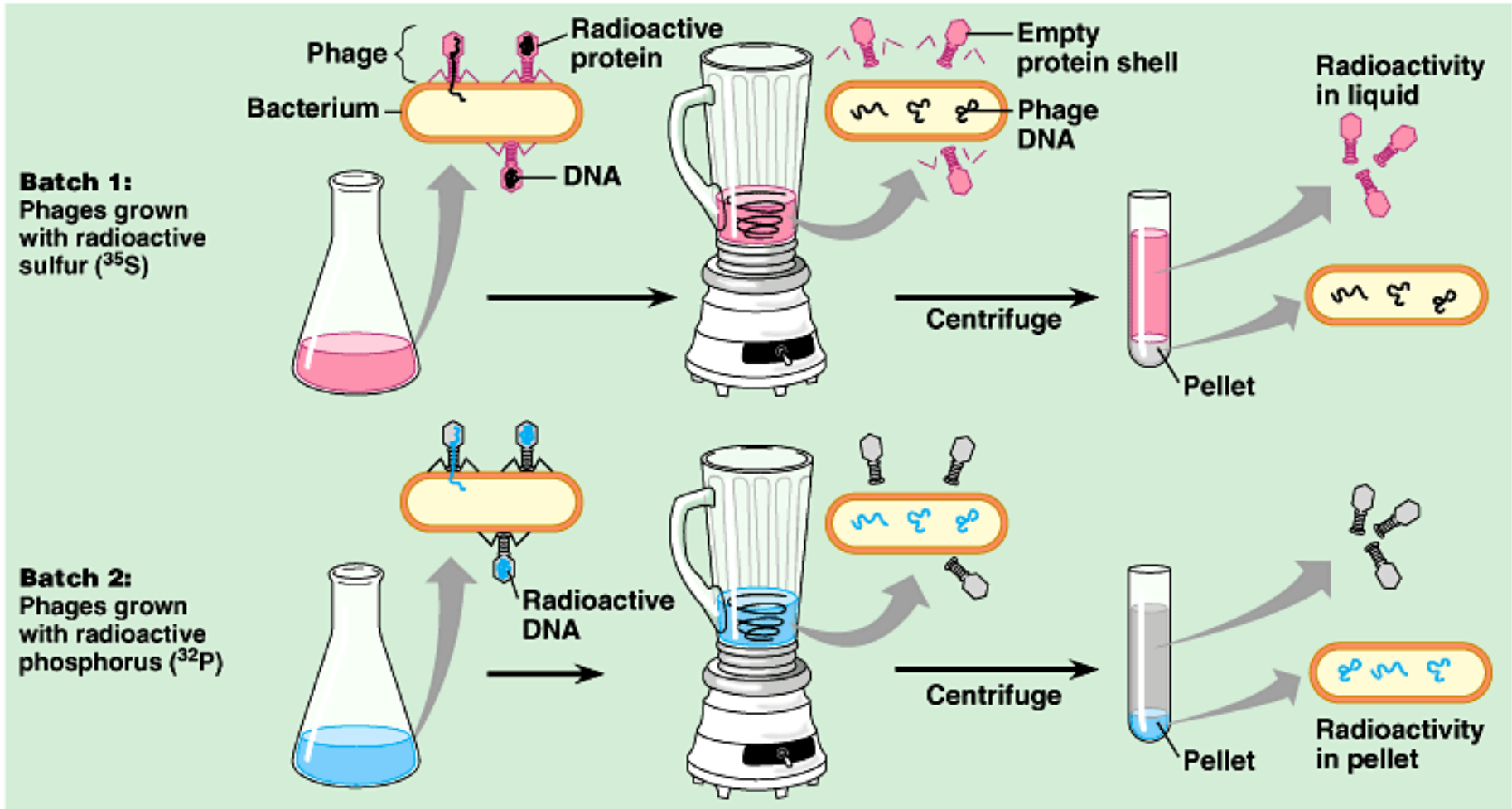


$^{32}\text{P}$  radioactivity found in the bacterial cells

Which radioactive marker is found inside the cell?

Which molecule carries viral genetic info?

- 1 Mix radioactively labeled phages with bacteria. The phages infect the bacterial cells.
- 2 Agitate in a blender to separate phages outside the bacteria from the cells and their contents.
- 3 Centrifuge the mixture so bacteria form a pellet at the bottom of the test tube.
- 4 Measure the radioactivity in the pellet and the liquid.



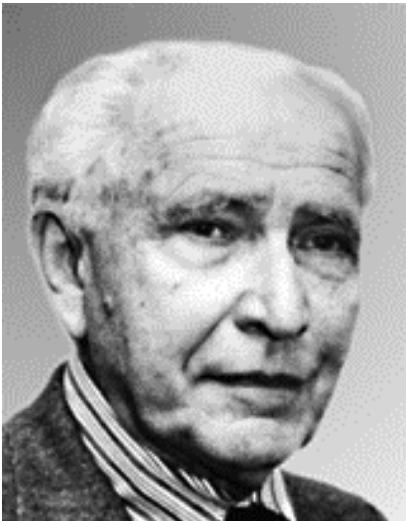
# Blender experiment

- Radioactive phage & bacteria in blender
  - ◆  $^{35}\text{S}$  phage
    - radioactive proteins stayed in supernatant
    - therefore protein did NOT enter bacteria
  - ◆  $^{32}\text{P}$  phage
    - radioactive DNA stayed in pellet
    - therefore DNA did enter bacteria
  - ◆ **Confirmed DNA is “transforming factor”**

1947

# Chargaff

- DNA composition: “Chargaff’s rules”
  - ◆ varies from species to species
  - ◆ all 4 bases not in equal quantity
  - ◆ bases present in characteristic ratio
    - humans:



Erwin Chargaff

**A = 30.9%**

**T = 29.4%**

**G = 19.9%**

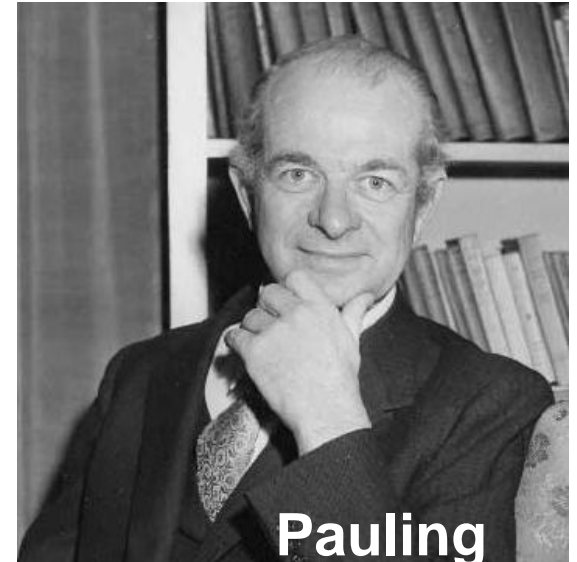
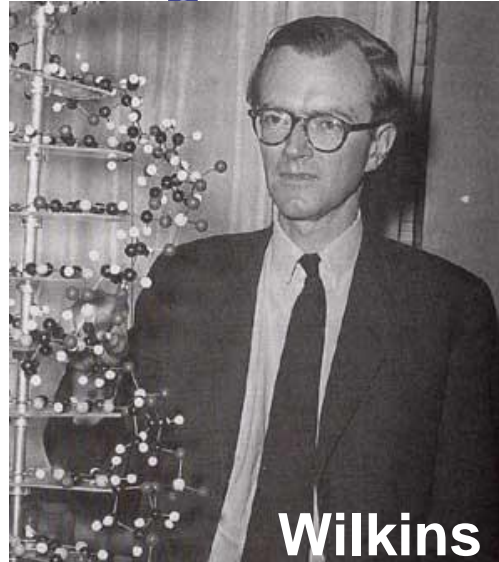
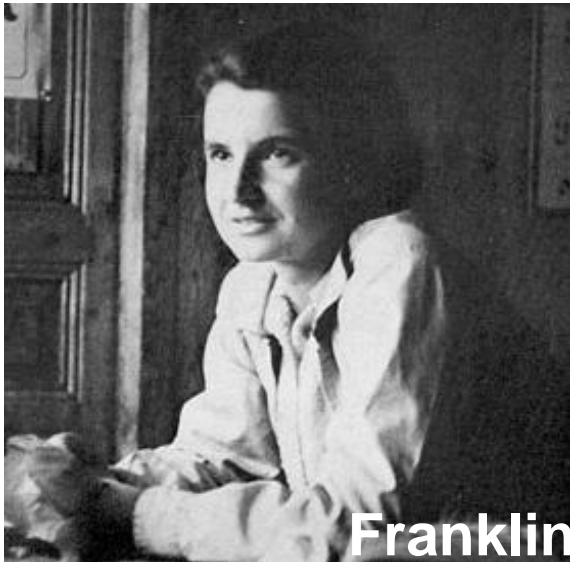
**C = 19.8%**



1953 | 1962

# Structure of DNA

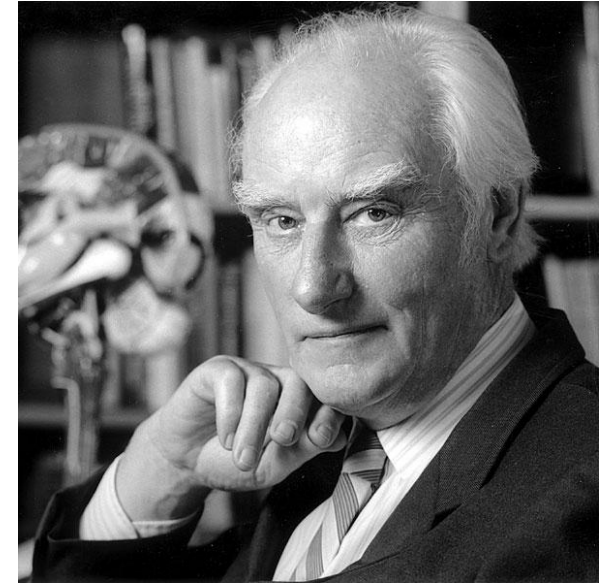
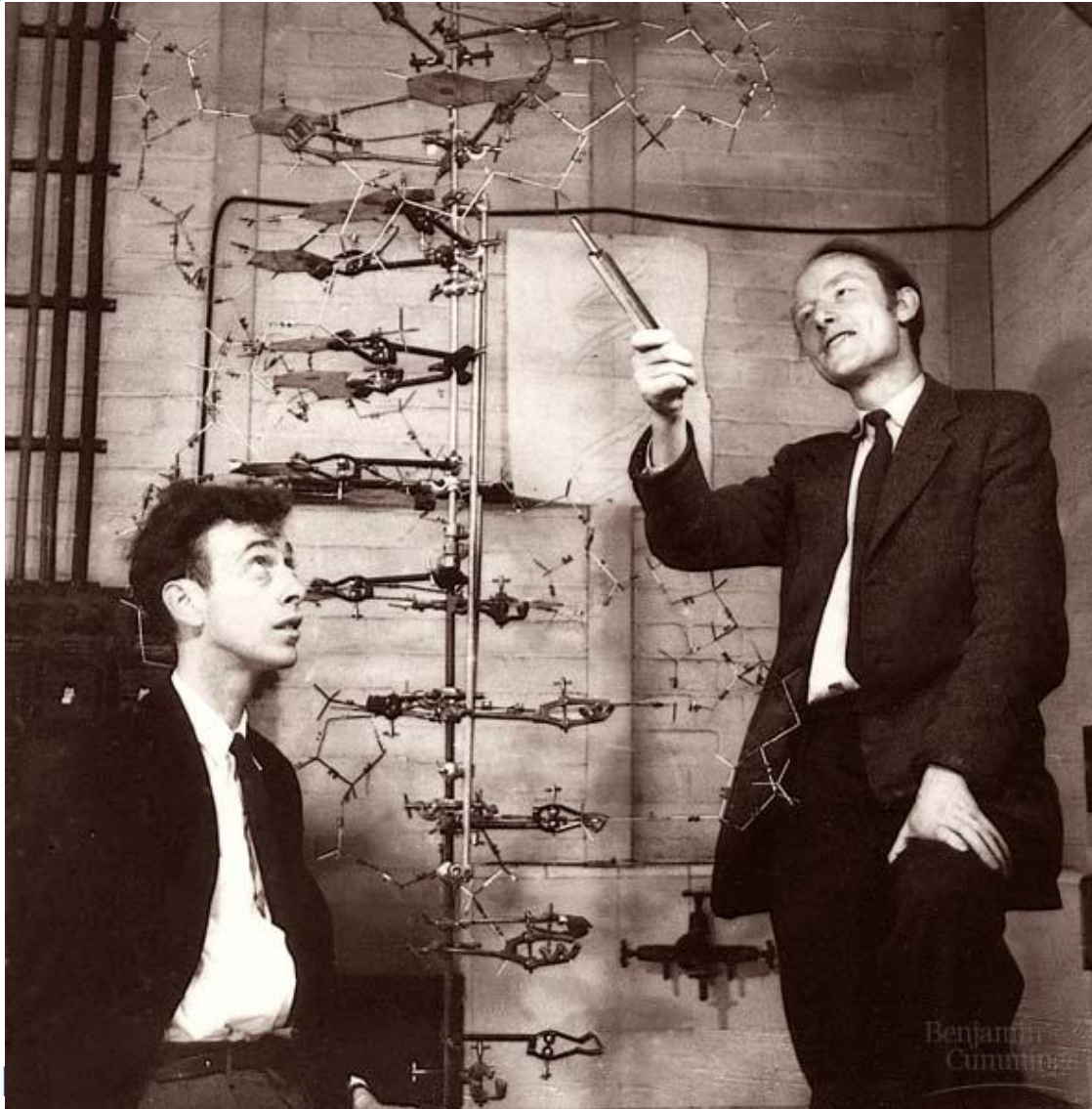
- **Watson & Crick**
  - ◆ developed double helix model of DNA
    - other scientists working on question:
      - ◆ Rosalind Franklin
      - ◆ Maurice Wilkins
      - ◆ Linus Pauling



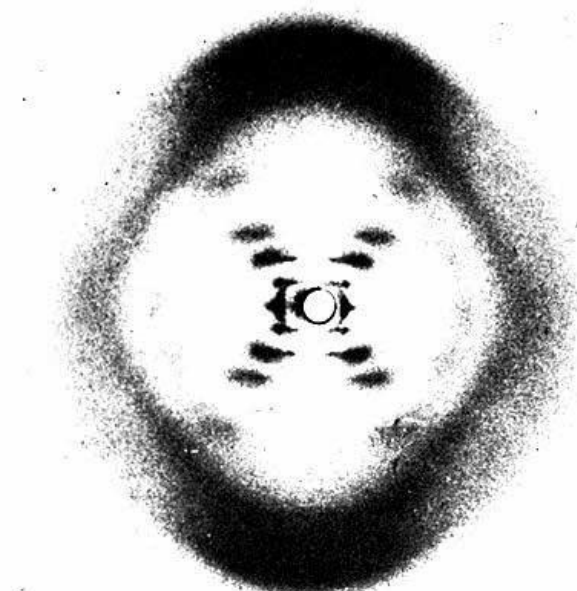
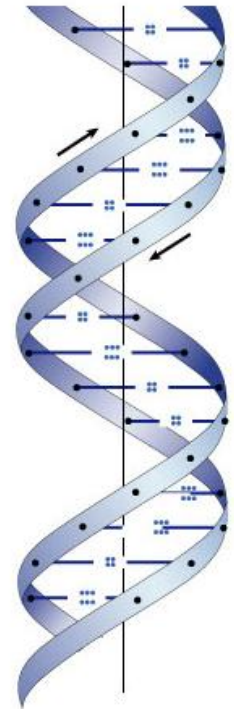
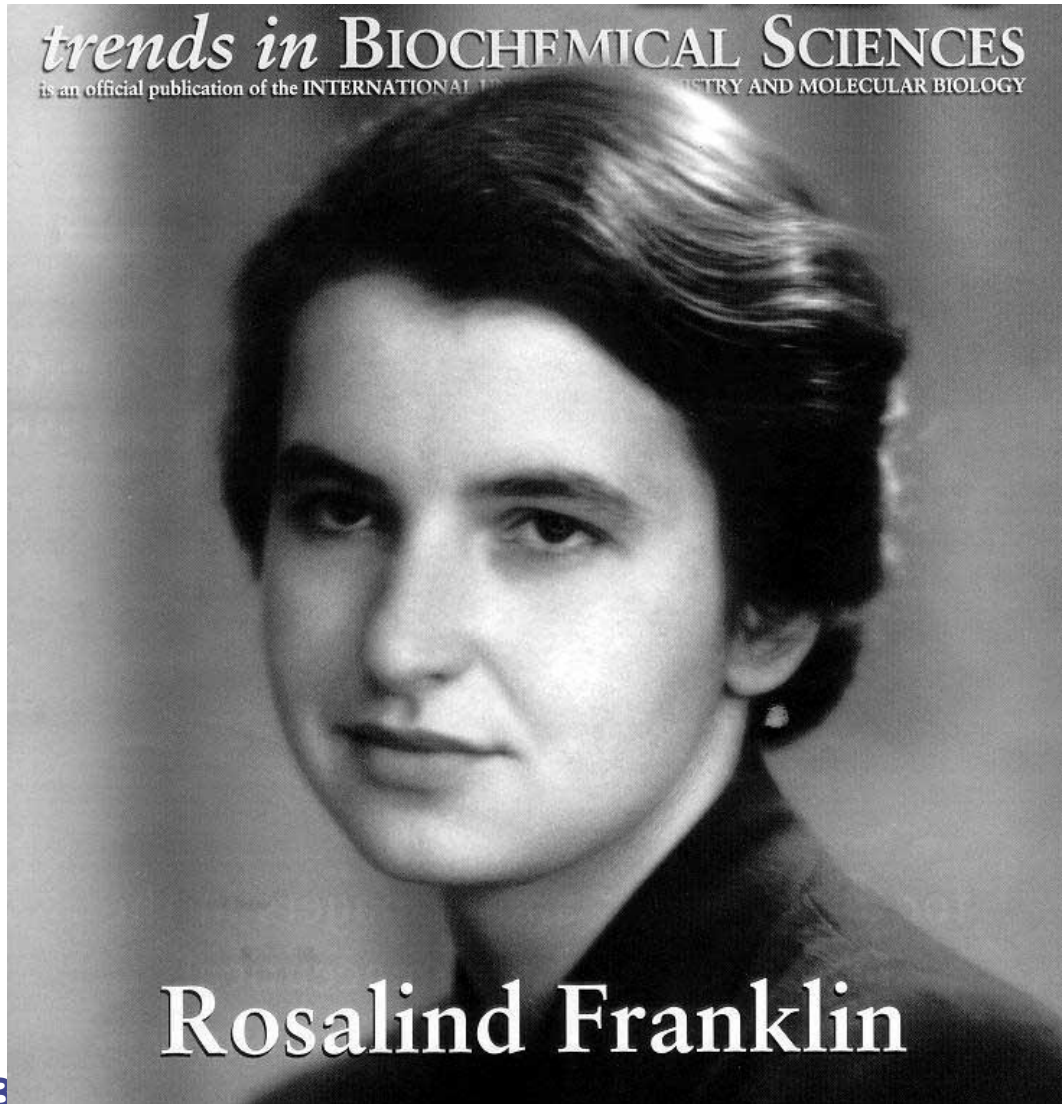


# Watson and Crick

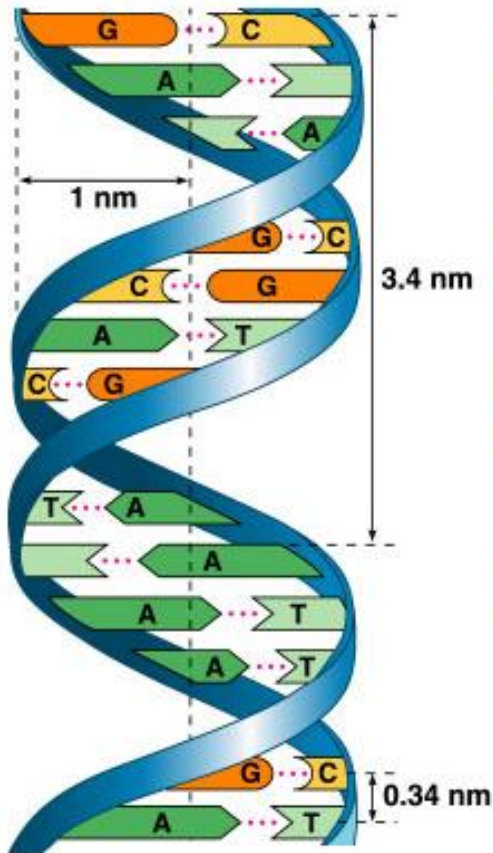
1953 article in Nature



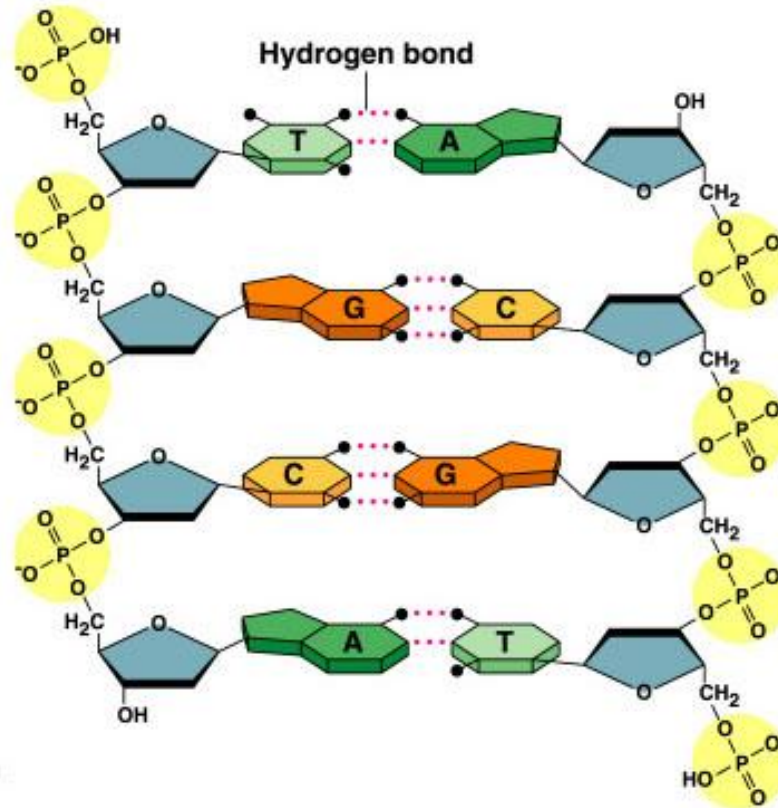
# Rosalind Franklin (1920-1958)



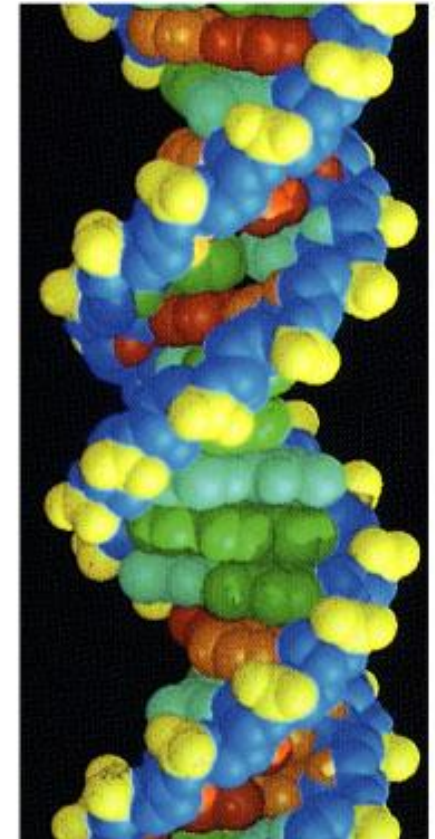
# Double helix structure of DNA



(a) Key features of DNA structure



(b) Partial chemical structure

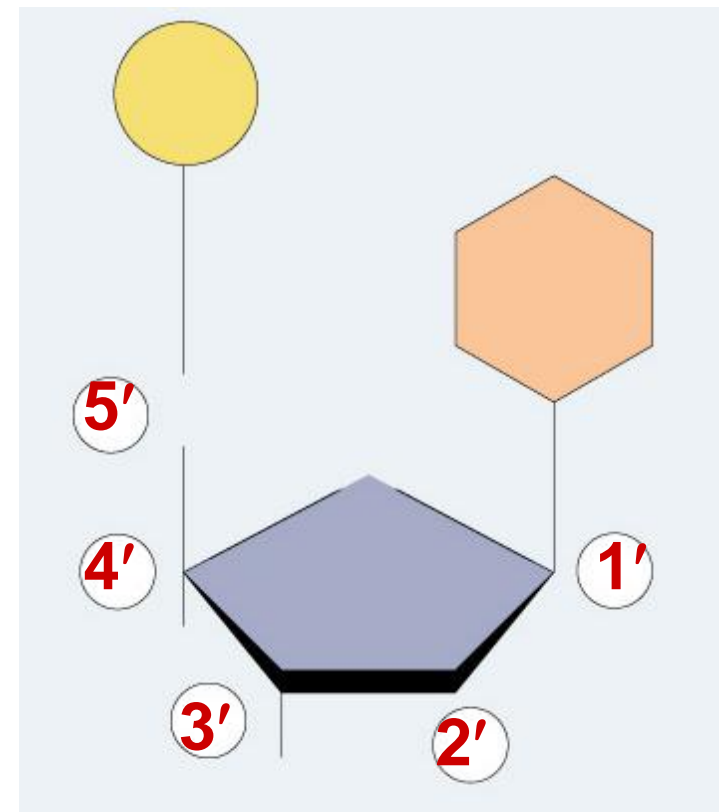


(c) Space-filling model

the structure of DNA suggested a mechanism for how DNA is copied by the cell

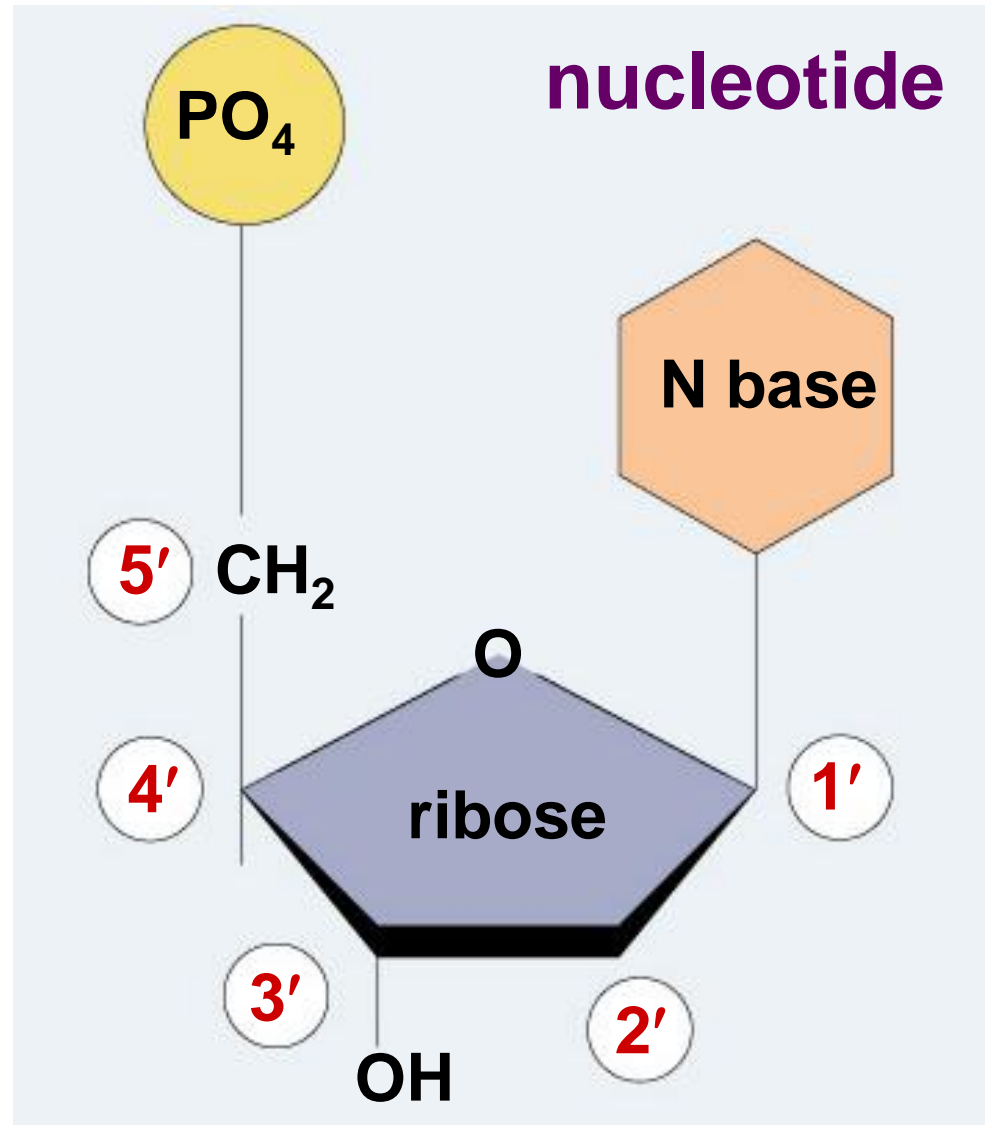
Friday, April 11<sup>th</sup>

Let's review the NUMBERING of carbons in a **deoxyribose** sugar molecule:



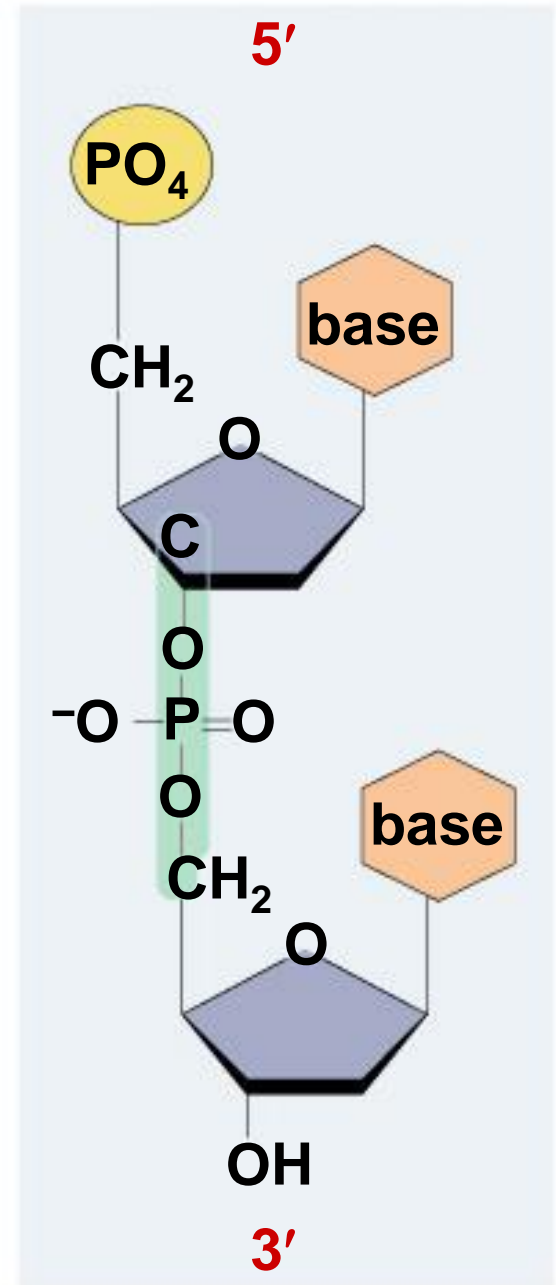
# Directionality of DNA

- You need to number the carbons!
  - ◆ it matters!



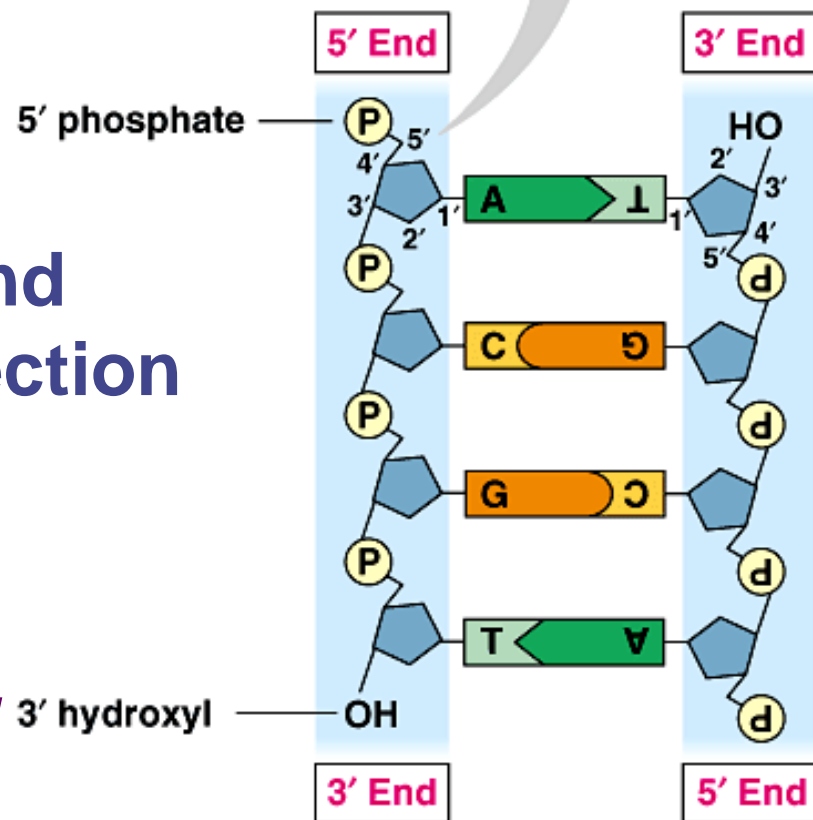
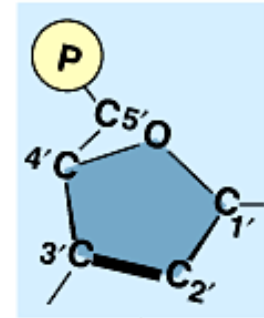
# The DNA backbone

- Putting the DNA backbone together
  - ◆ refer to the 3' and 5' ends of the DNA
    - the last trailing carbon



# Anti-parallel strands

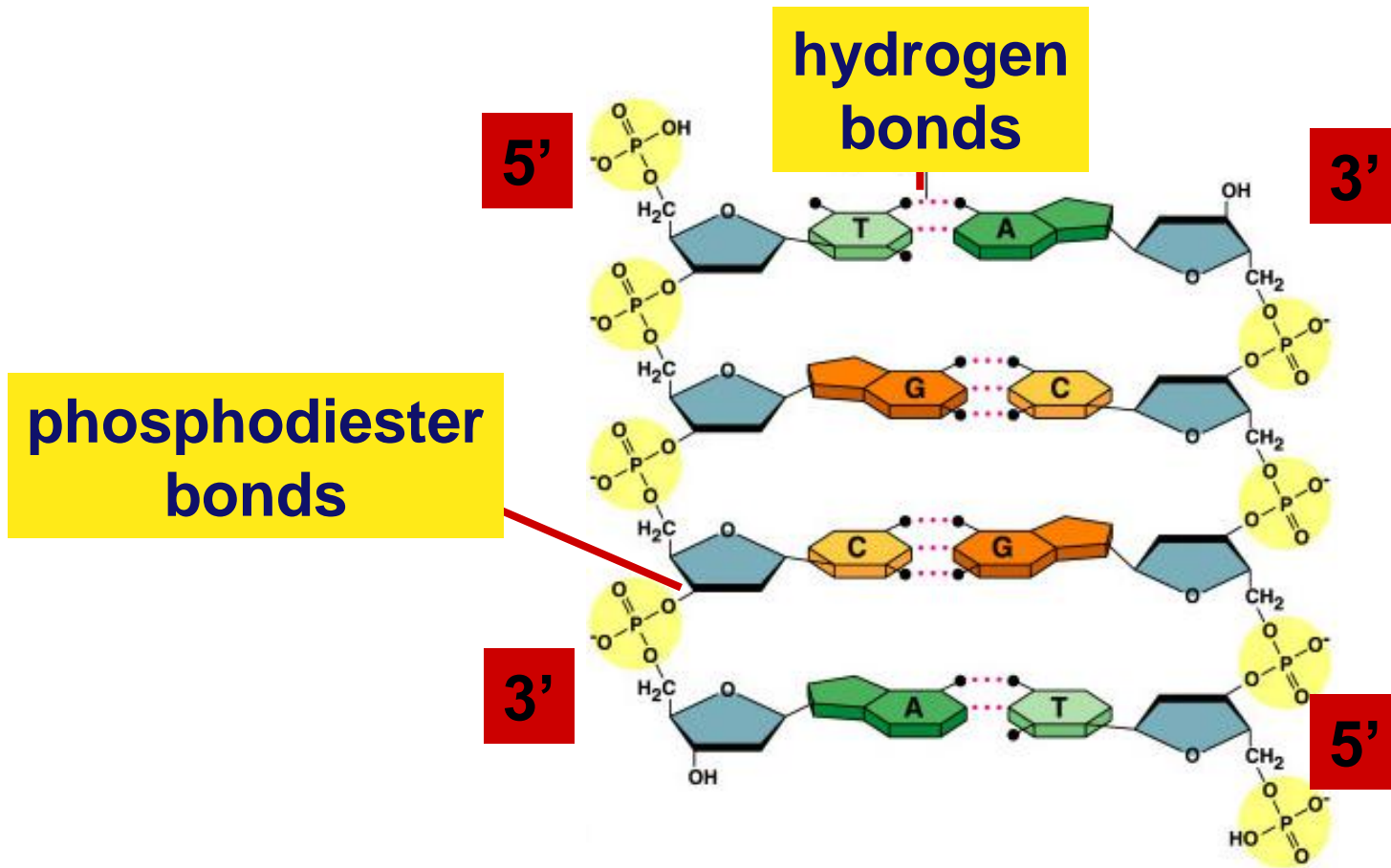
- Phosphate to sugar bond involves carbons in 3' & 5' positions
  - ◆ DNA molecule has “direction”
  - ◆ complementary strand runs in opposite direction



*“It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.”*

**Watson & Crick**

# Bonding in DNA





# Base pairing in DNA

## ■ Purines

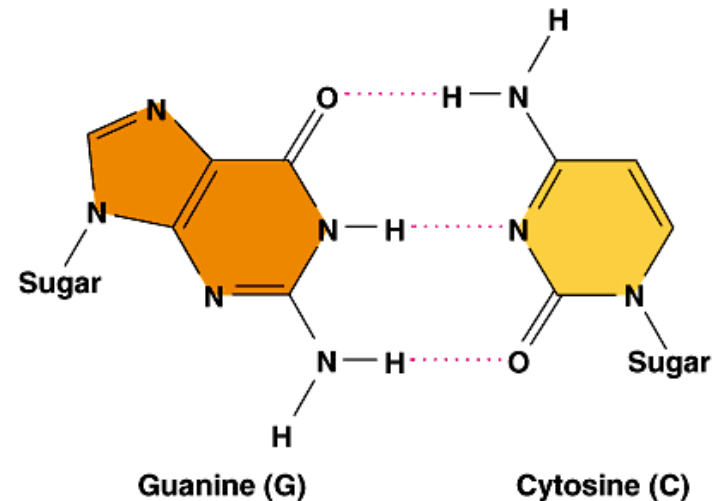
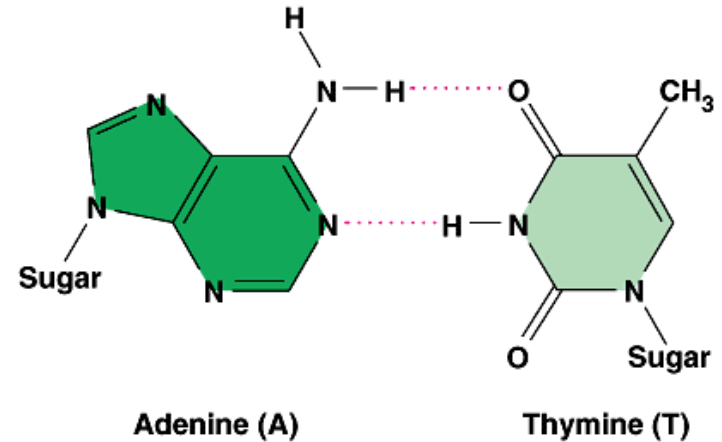
- ◆ adenine (A)
- ◆ guanine (G)

## ■ Pyrimidines

- ◆ thymine (T)
- ◆ cytosine (C)

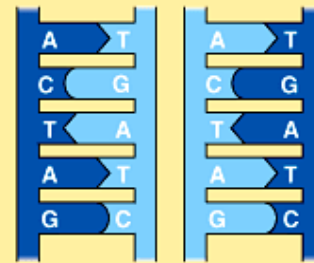
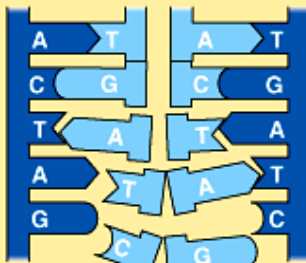
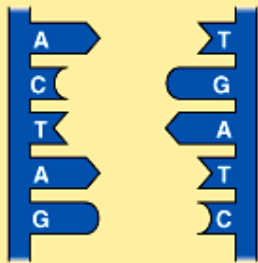
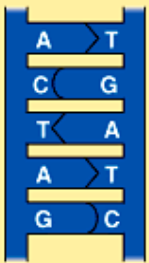
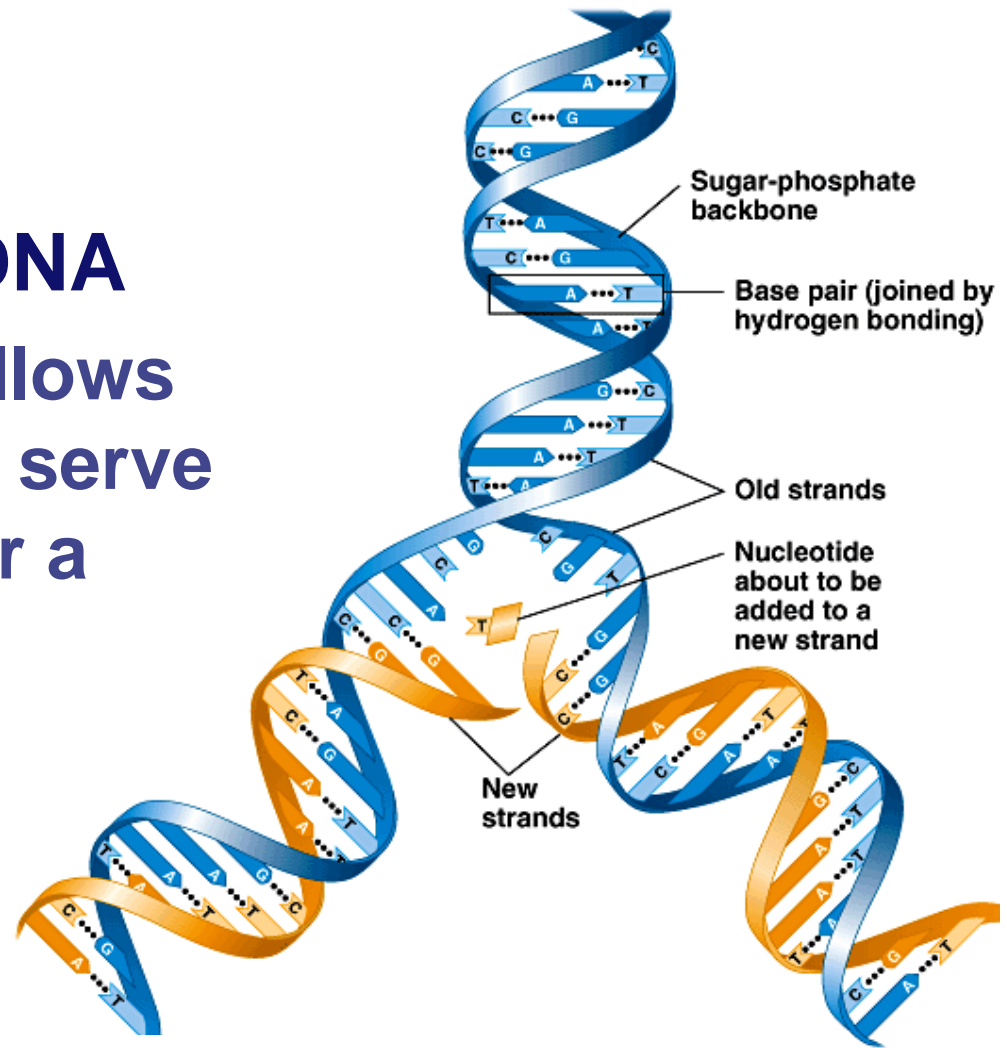
## ■ Pairing

- ◆ A : T
- ◆ C : G



# Copying DNA

- **Replication of DNA**
  - ◆ base pairing allows each strand to serve as a pattern for a new strand



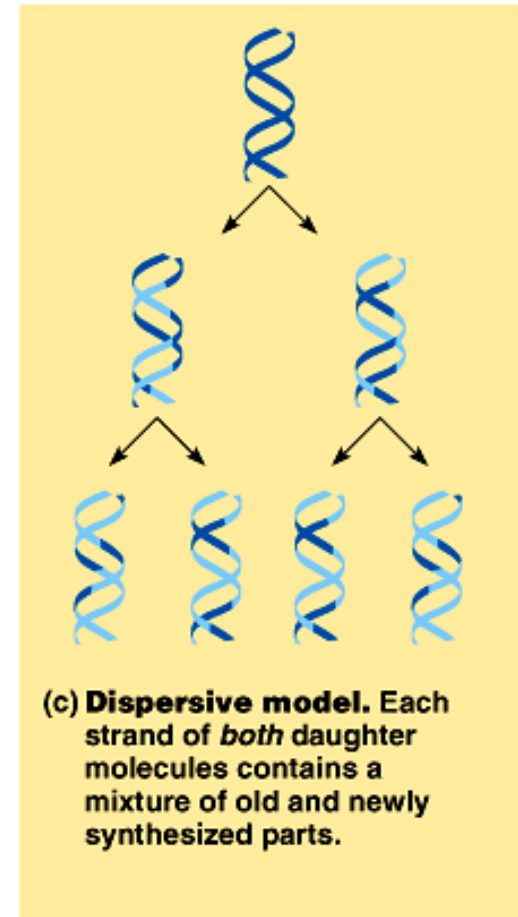
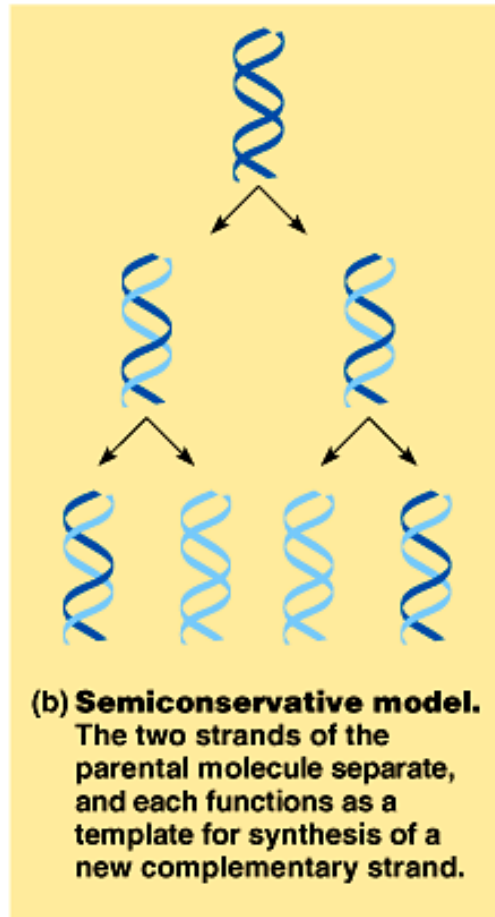
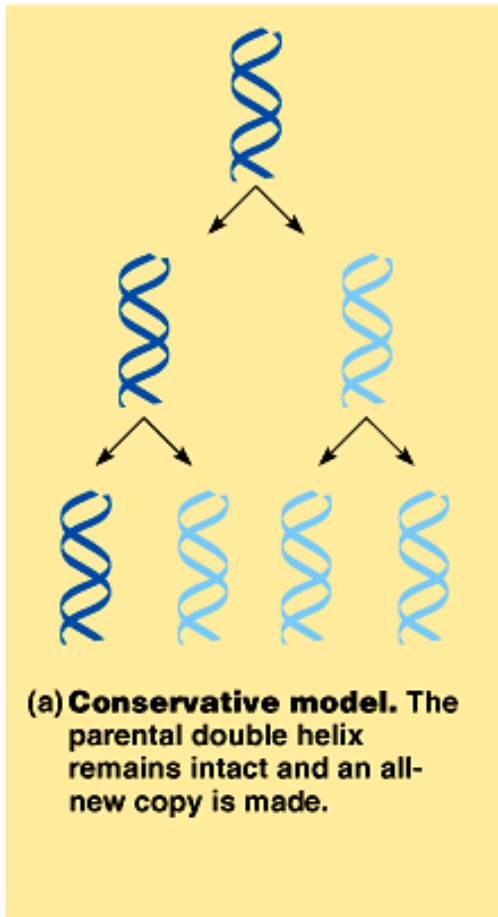
# Models of DNA Replication

- Alternative models
  - so how is DNA copied?

Parent cell

First replication

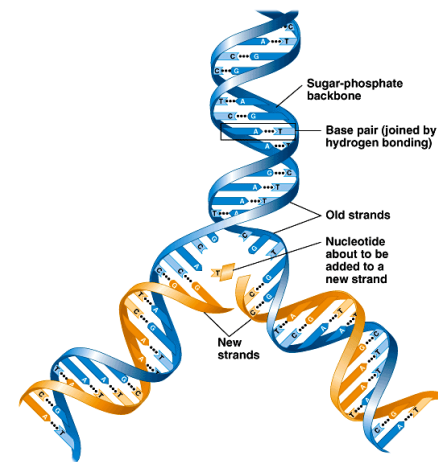
Second replication



# Models of DNA Replication

- Meselson and Stahl

*Animation: Models of DNA Replication*

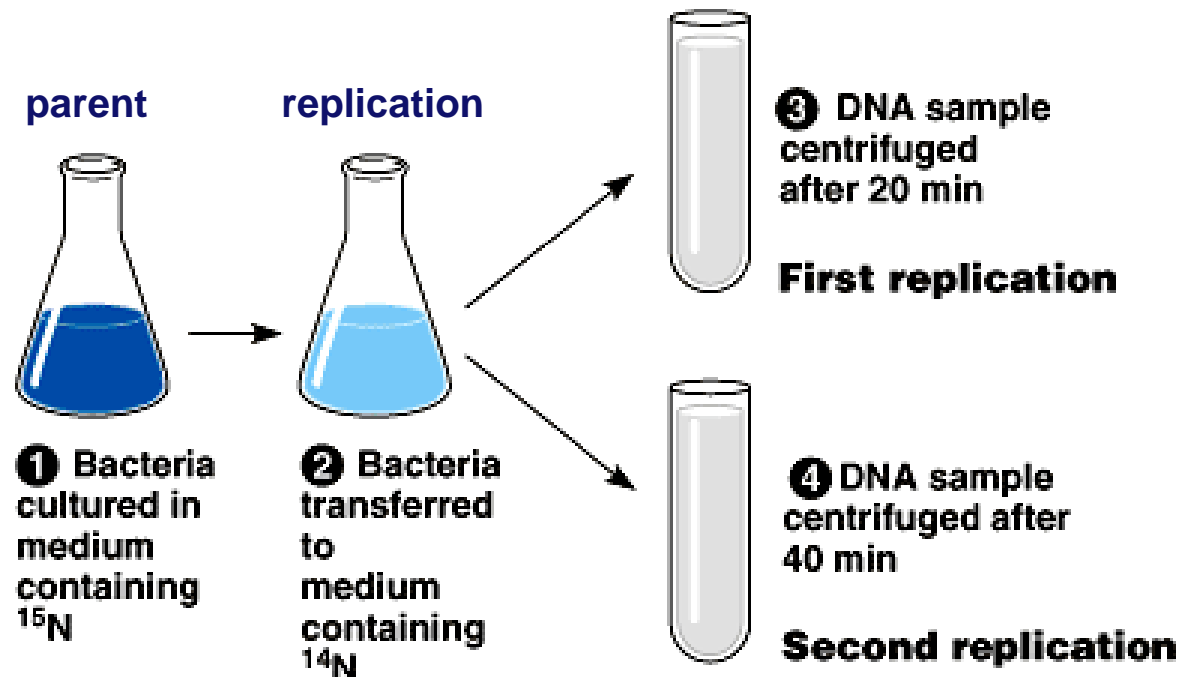


# Semi-conservative replication

## ■ Meselson & Stahl

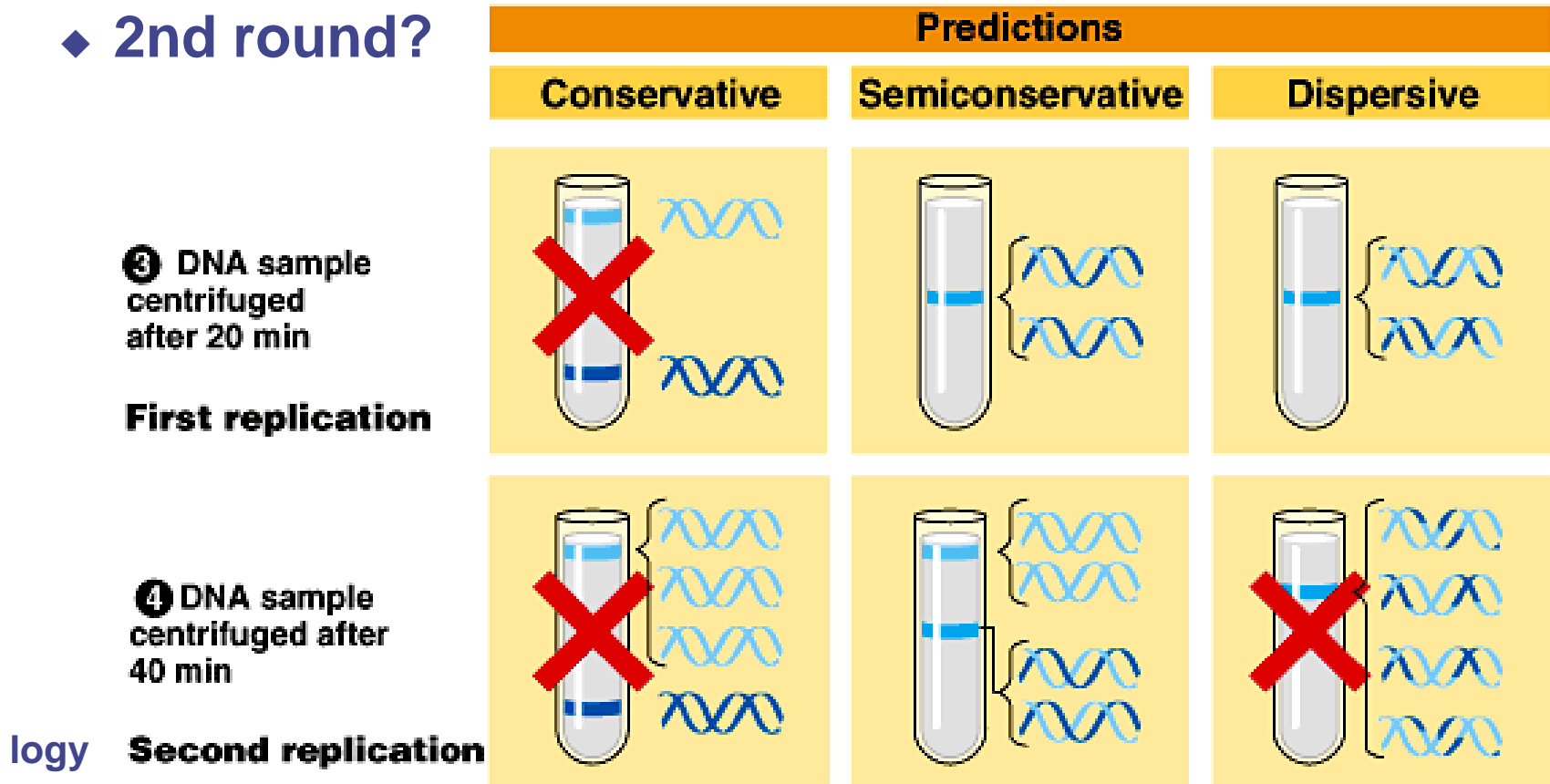
- ◆ label nucleotides of “parent” DNA strands with heavy nitrogen =  $^{15}\text{N}$
- ◆ label new nucleotides with lighter isotope =  $^{14}\text{N}$

*“The Most Beautiful Experiment in Biology”*



# Semi-conservative replication

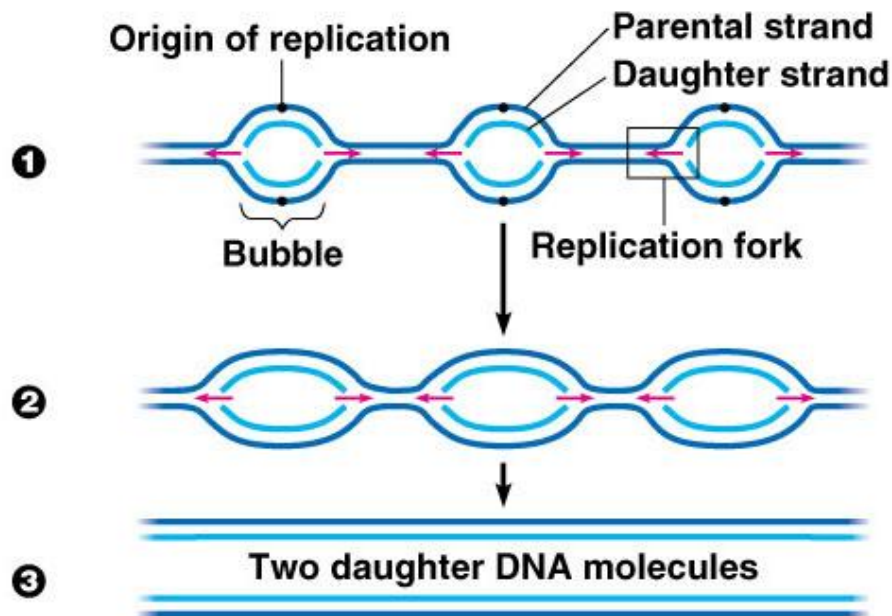
- Make predictions...
  - ◆  $^{15}\text{N}$  strands replicated in  $^{14}\text{N}$  medium
  - ◆ 1st round of replication?
  - ◆ 2nd round?



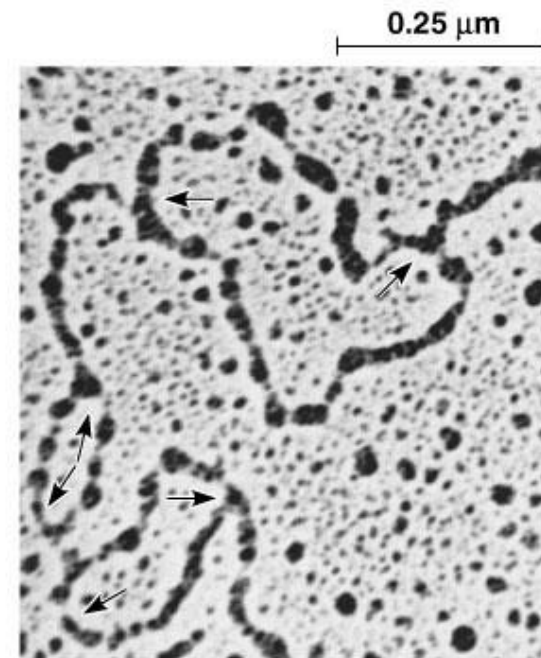
logy

# DNA Replication

- Large team of enzymes coordinates replication



(a) In eukaryotes, DNA replication begins at many sites along the giant DNA molecule of each chromosome.



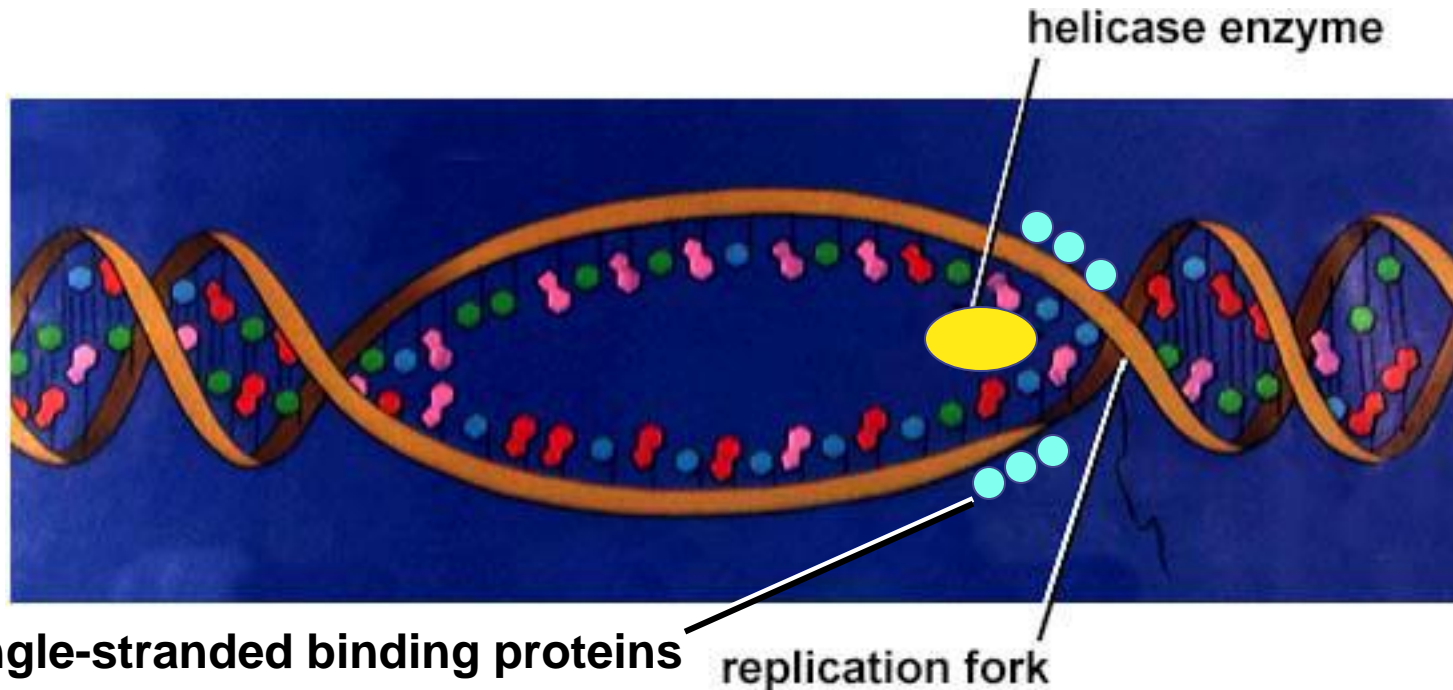
(b) In this micrograph, three replication bubbles are visible along the DNA of cultured Chinese hamster cells. The arrows indicate the direction of DNA replication at the two ends of each bubble (TEM).

# Replication: 1st step

- Unwind DNA

- ◆ helicase enzyme

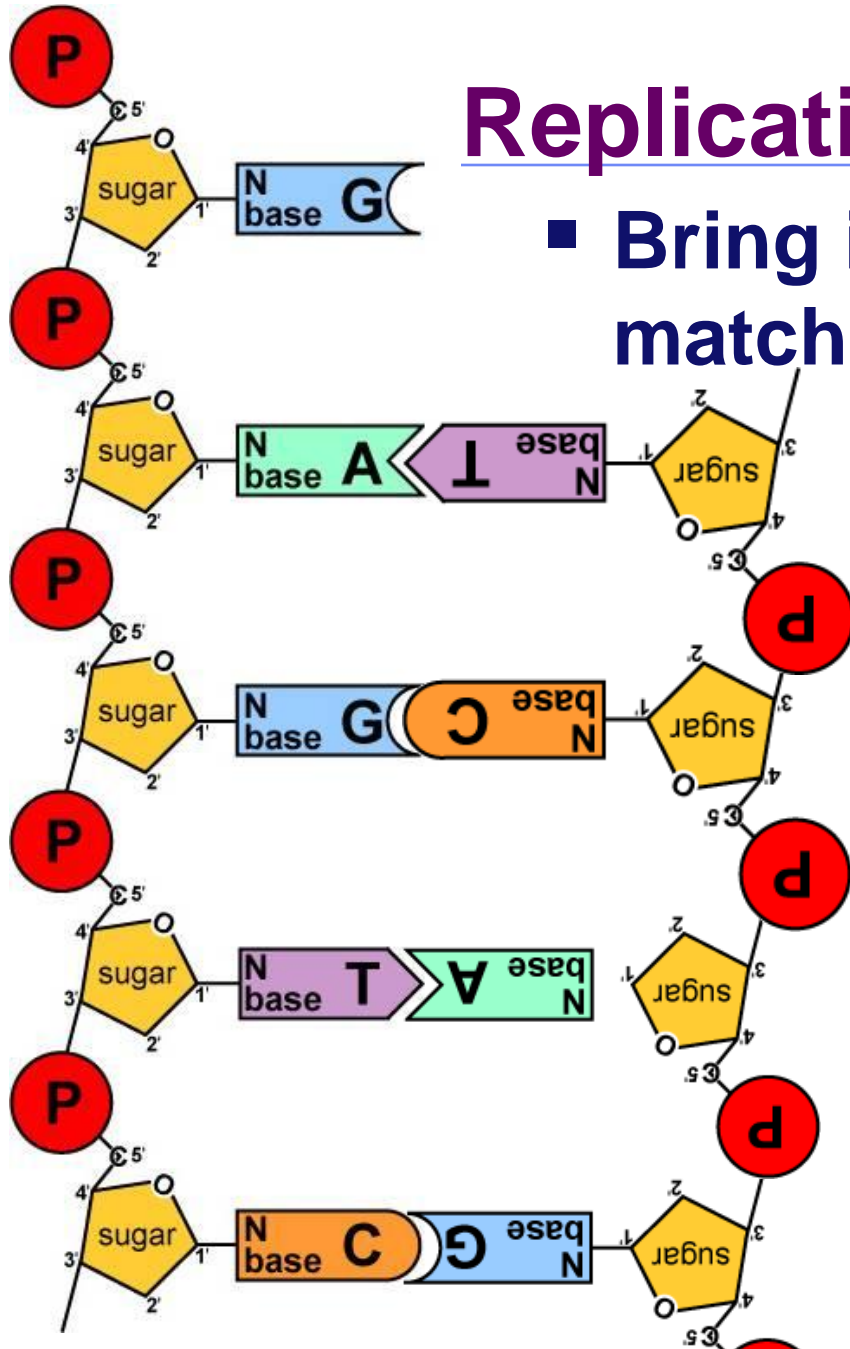
- unwinds part of DNA helix
    - stabilized by single-stranded binding proteins





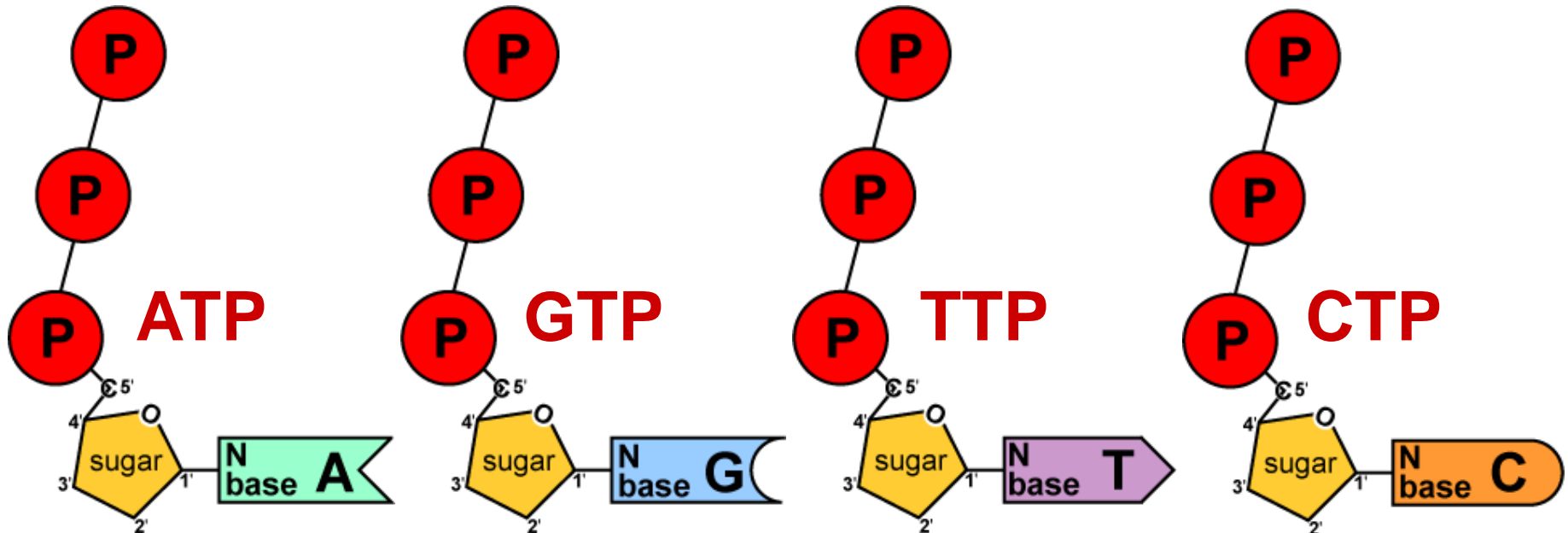
# Replication: 2nd step

- Bring in new nucleotides to match up to template strands



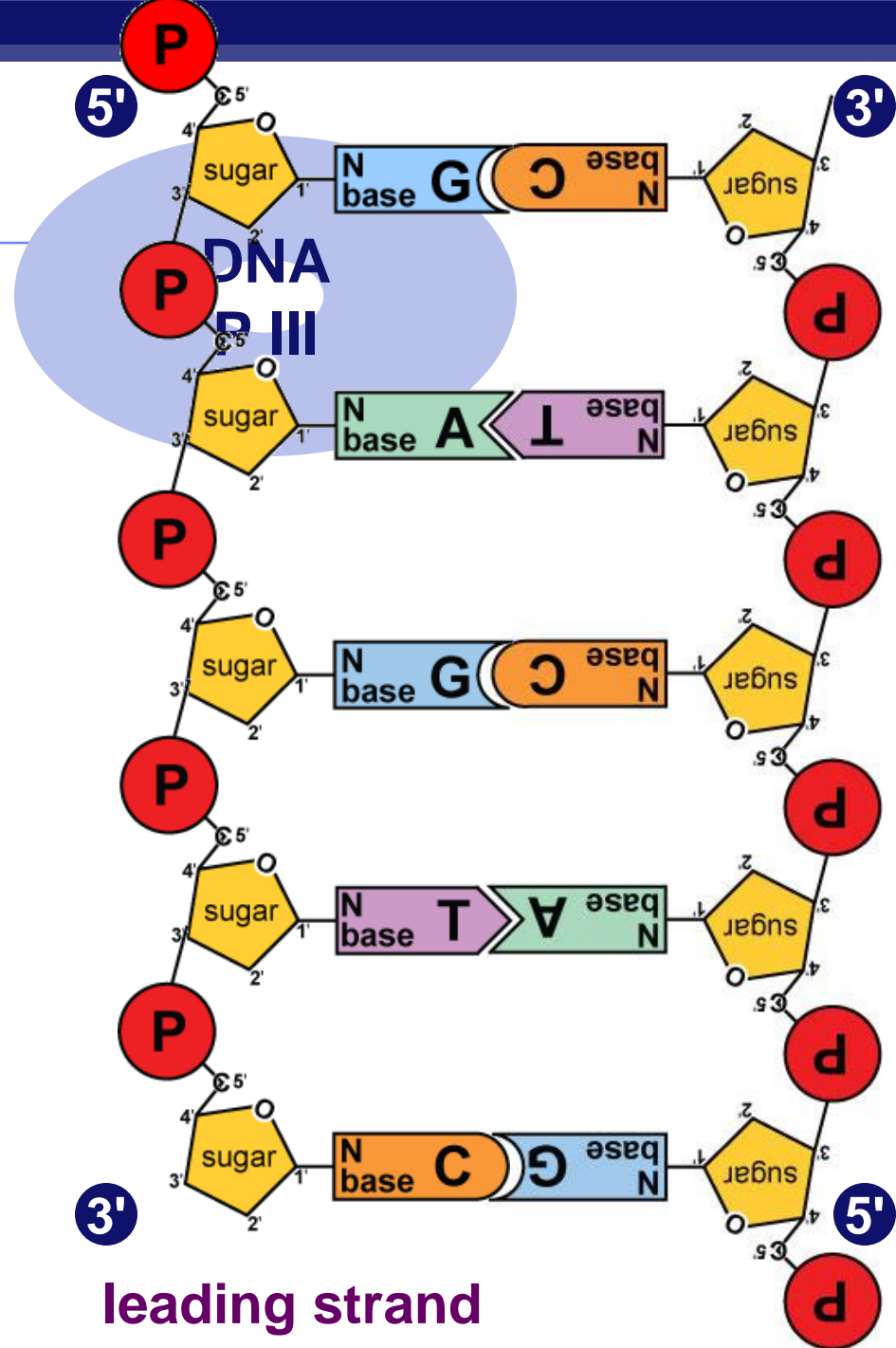
# Energy of Replication

- The nucleotides arrive as nucleosides
  - ◆ DNA bases with **P-P-P**
  - ◆ DNA bases arrive with their own energy source for bonding
  - ◆ bonded by DNA polymerase III



# Replication

- Adding bases
  - ◆ can only add nucleotides to 3' end of a growing DNA strand
  - ◆ strand grow 5'→3'

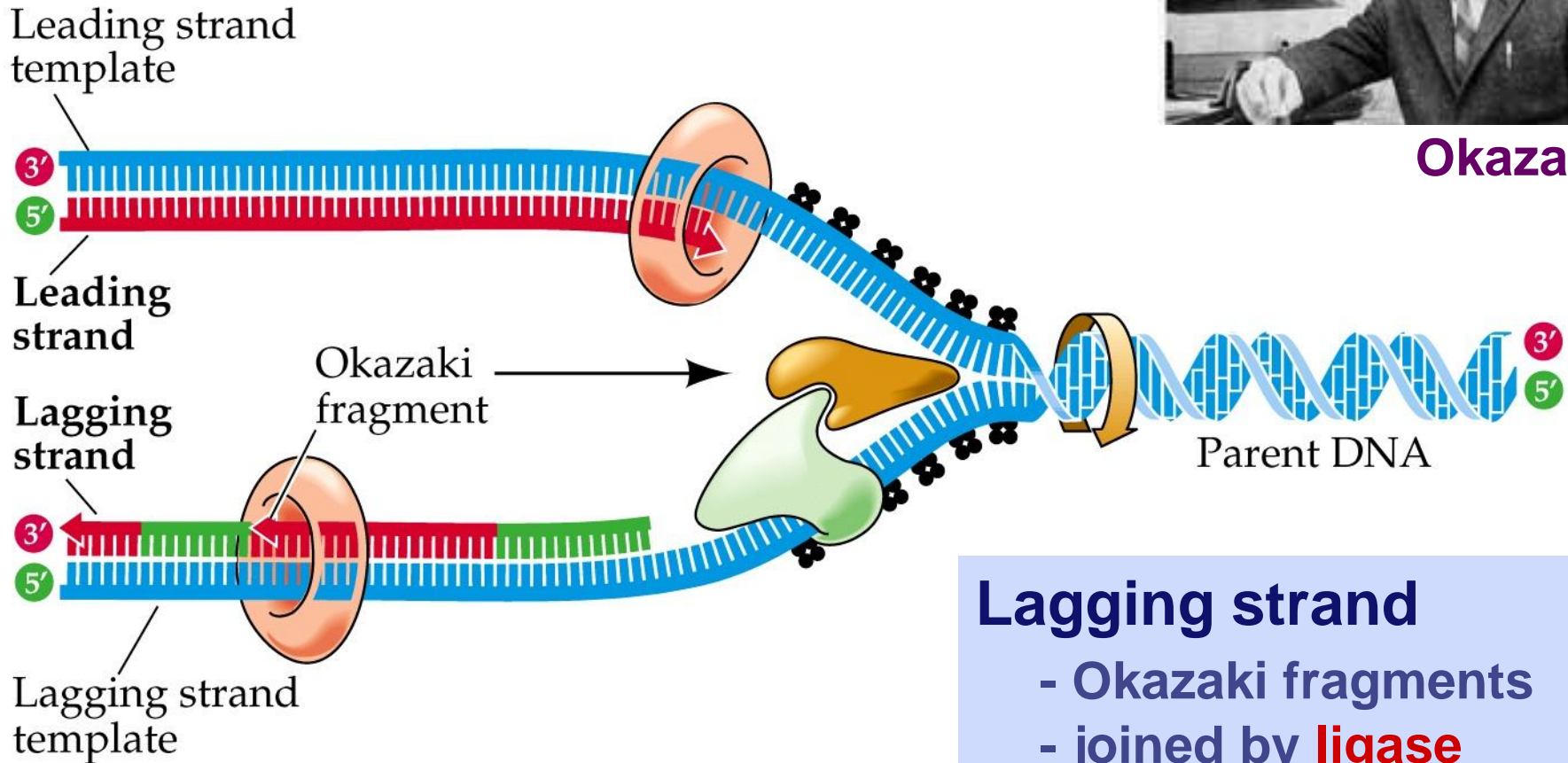


# Leading & Lagging strands

**Leading strand**  
- continuous synthesis



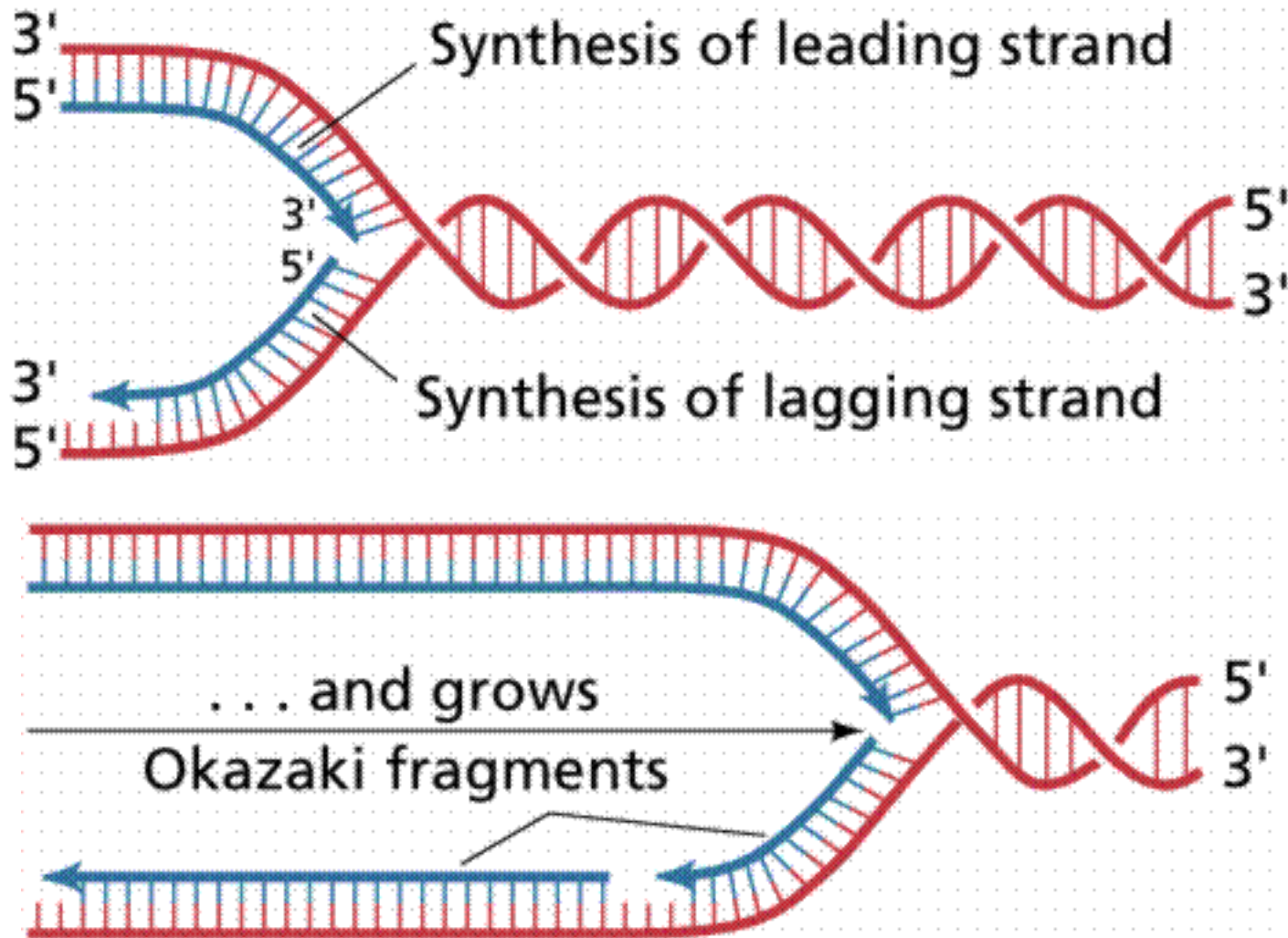
**Okazaki**



## Lagging strand

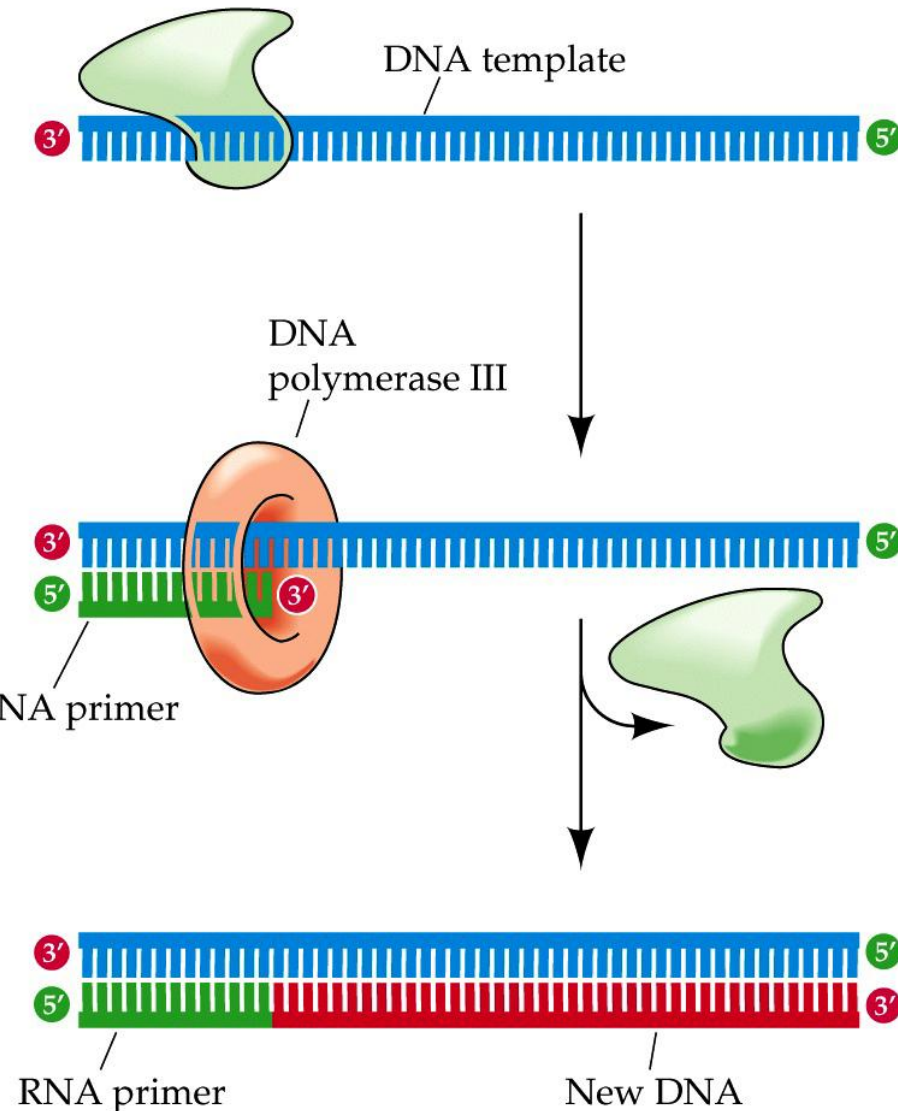
- Okazaki fragments
- joined by **ligase**
- “spot welder” enzyme

# Okazaki fragments



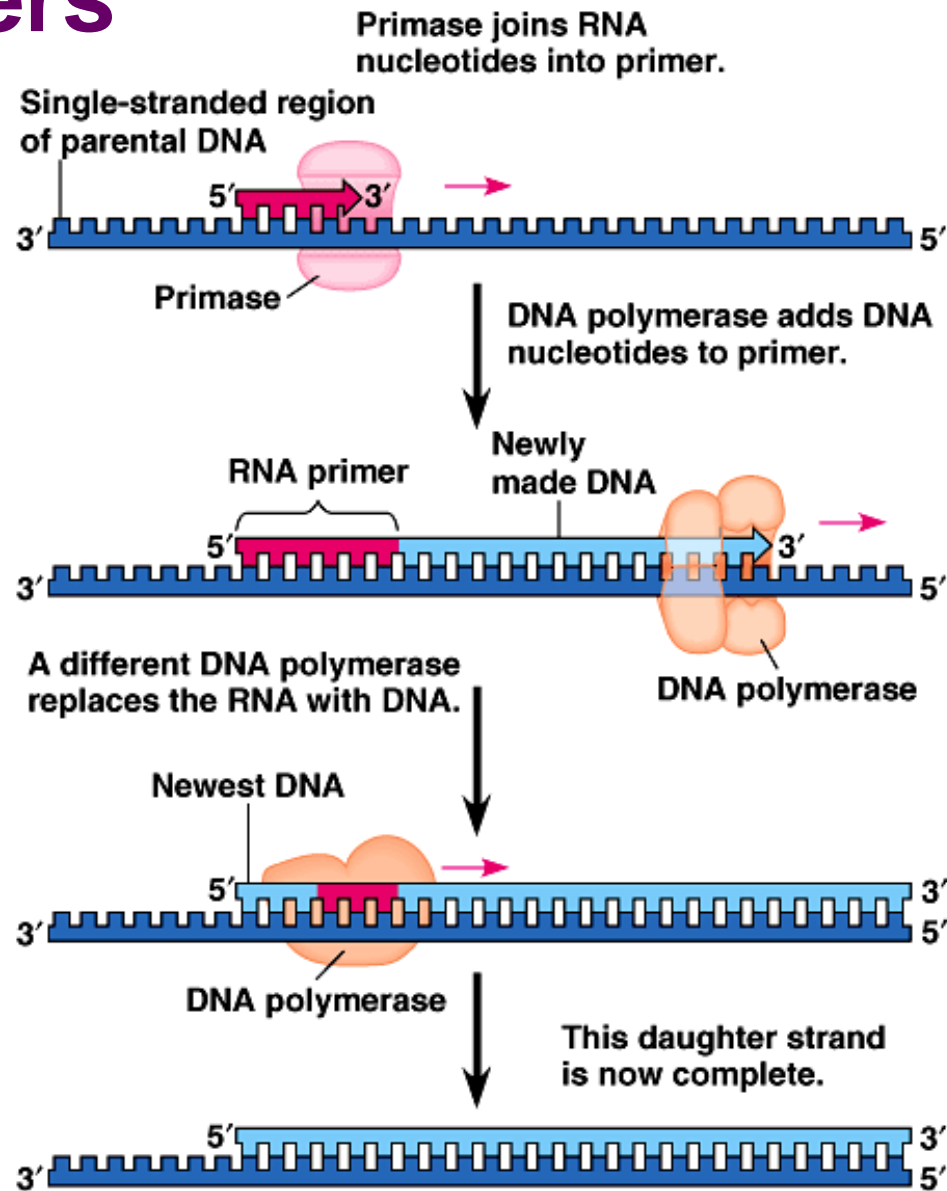
# Priming DNA synthesis

- DNA polymerase III can only extend an existing DNA molecule
  - ◆ cannot start new one
    - cannot place first base
  - ◆ short RNA primer is built first by primase
    - starter sequences
    - DNA polymerase III can now add nucleotides to RNA primer



# Cleaning up primers

**DNA polymerase I** removes sections of RNA primer and replaces with DNA nucleotides



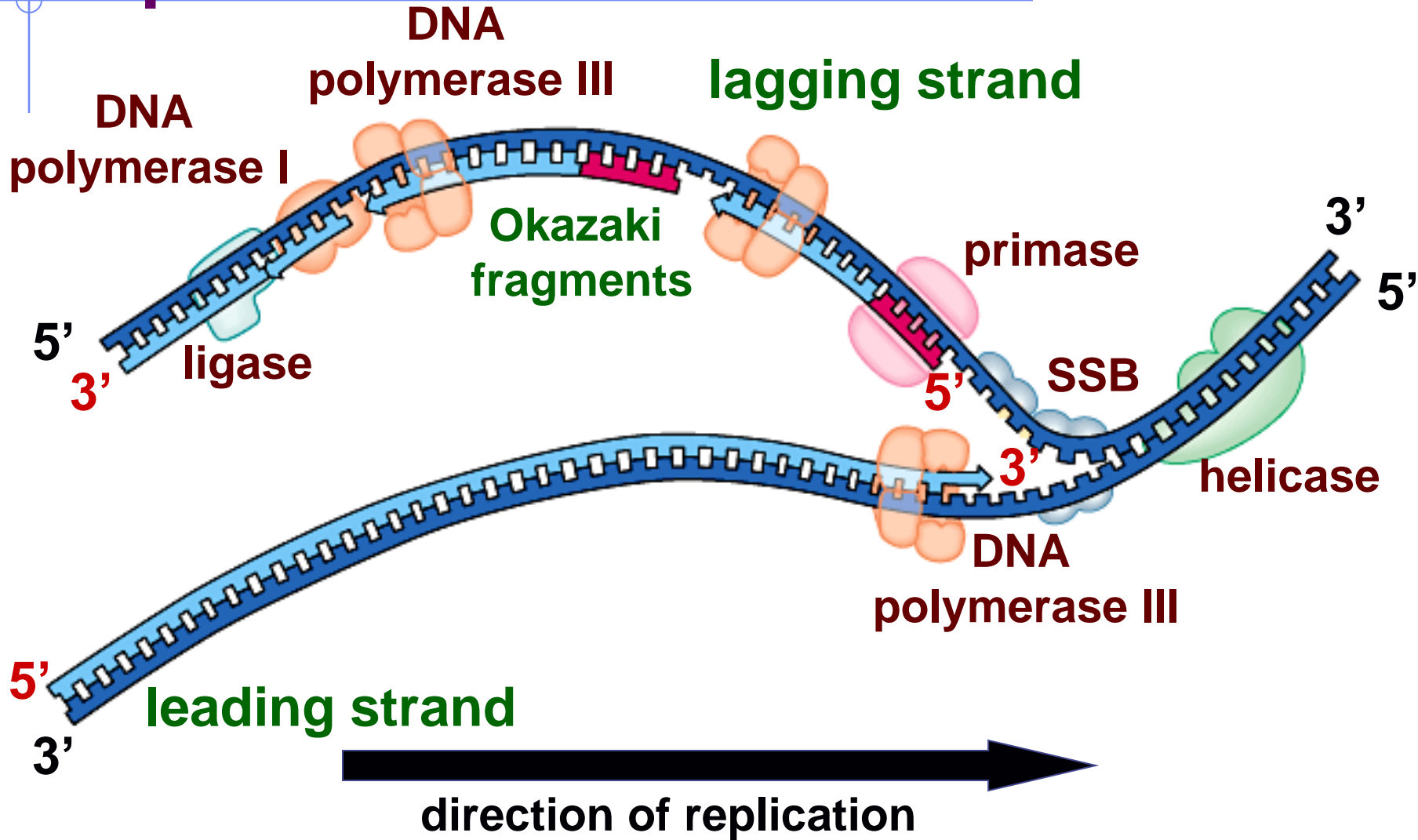
# McGraw-Hill Replication Fork

A decorative graphic consisting of a horizontal blue line extending from the left edge of the slide to the right. A vertical blue line extends from the top edge of the slide down to the horizontal line. At the intersection of these two lines, there is a small white circle with a blue outline. A second horizontal blue line is positioned lower on the slide, extending from the left edge to the right edge. A vertical blue line extends from the bottom edge of the slide up to the second horizontal line. At the intersection of these two lines, there is another small white circle with a blue outline.

[Replication Fork animation](#)



# Replication fork

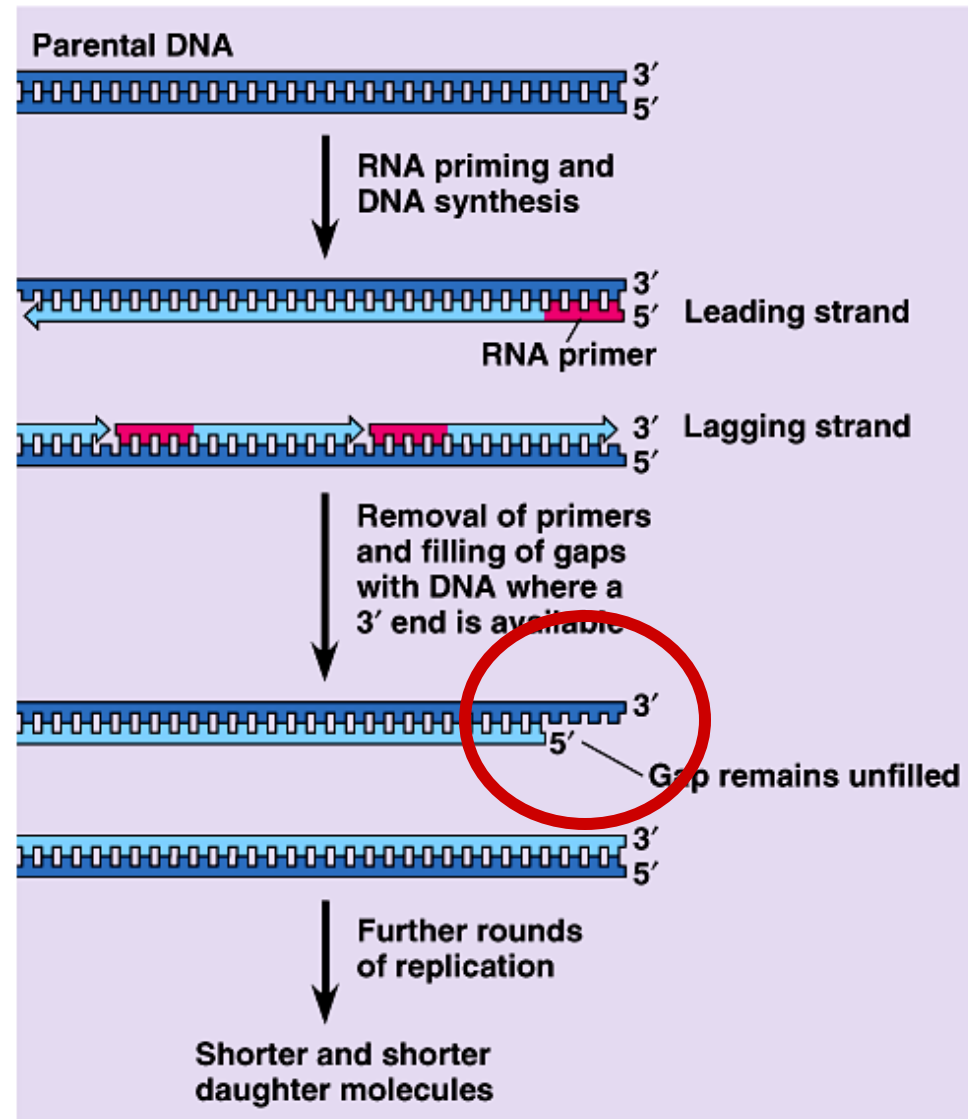


# Animation: Replication

- <http://www.youtube.com/watch?v=teV62zrm2P0>

# And in the end...

- Ends of chromosomes are eroded with each replication
  - ◆ an issue in aging?
  - ◆ ends of chromosomes are protected by telomeres



# Telomeres

- Expendable, non-coding sequences at ends of DNA

- ◆ short sequence of bases repeated 1000s times

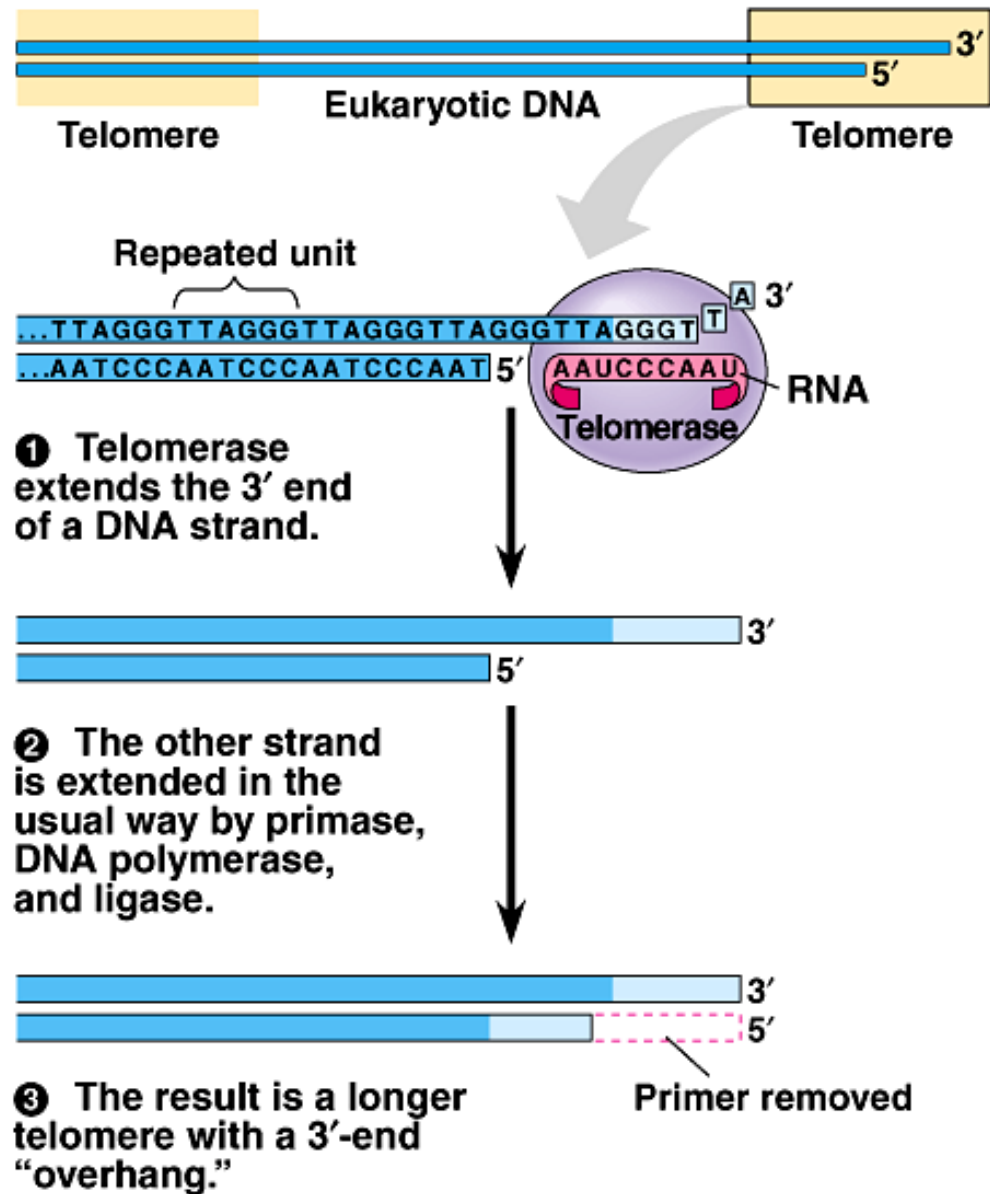
- ◆ TTAGGG in humans

- Telomerase enzyme in certain cells

- ◆ enzyme extends telomeres

- ◆ prevalent in cancers

- Why?

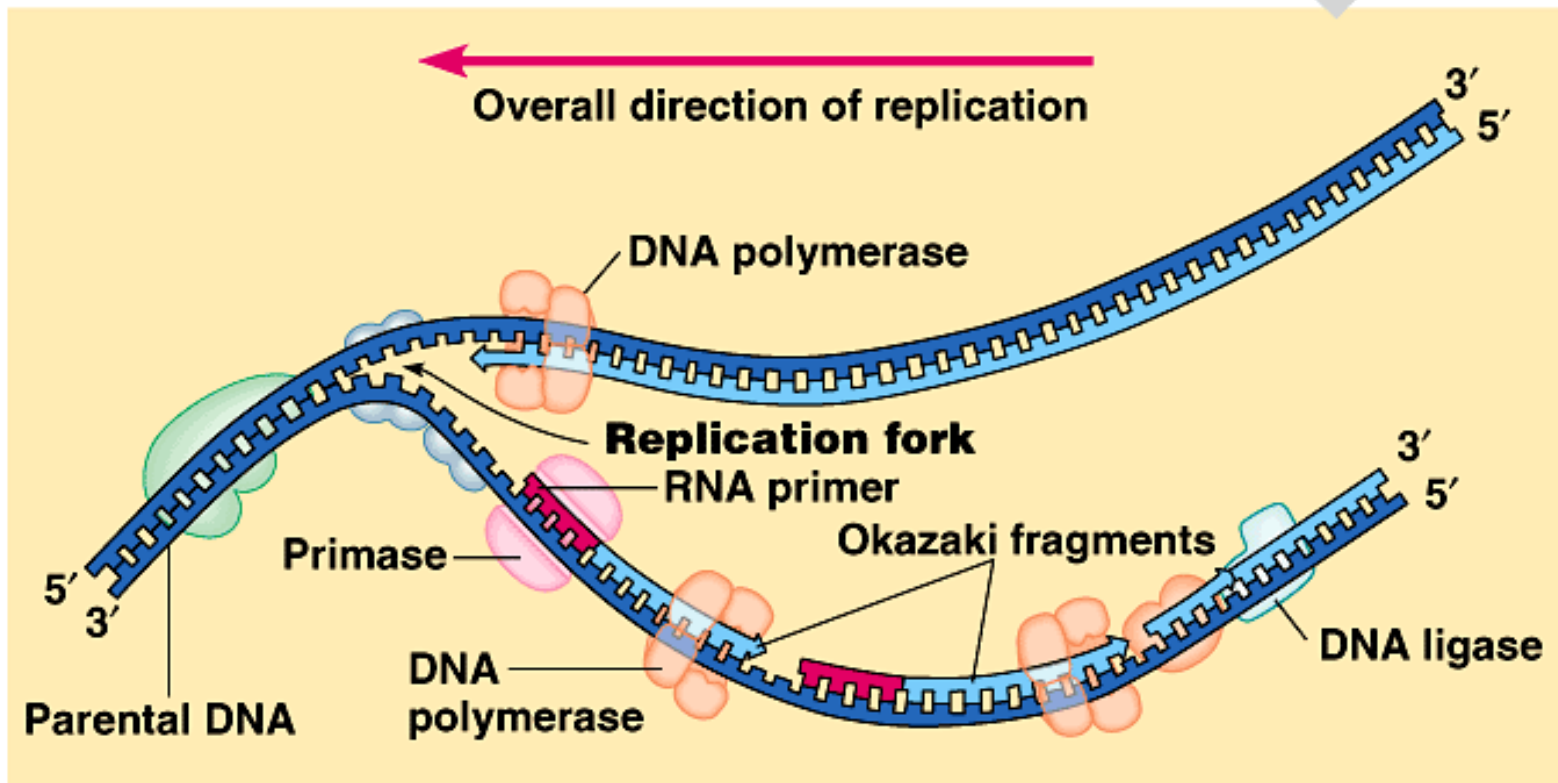
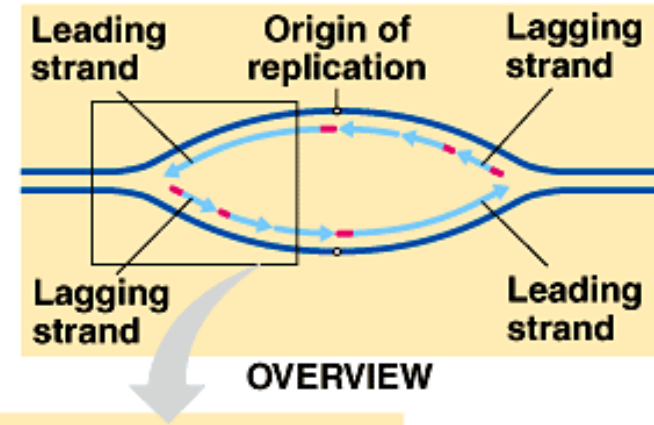


(b)

# Replication bubble

Adds 1000 bases/second!

- Which direction does DNA build?
- List the enzymes & their role

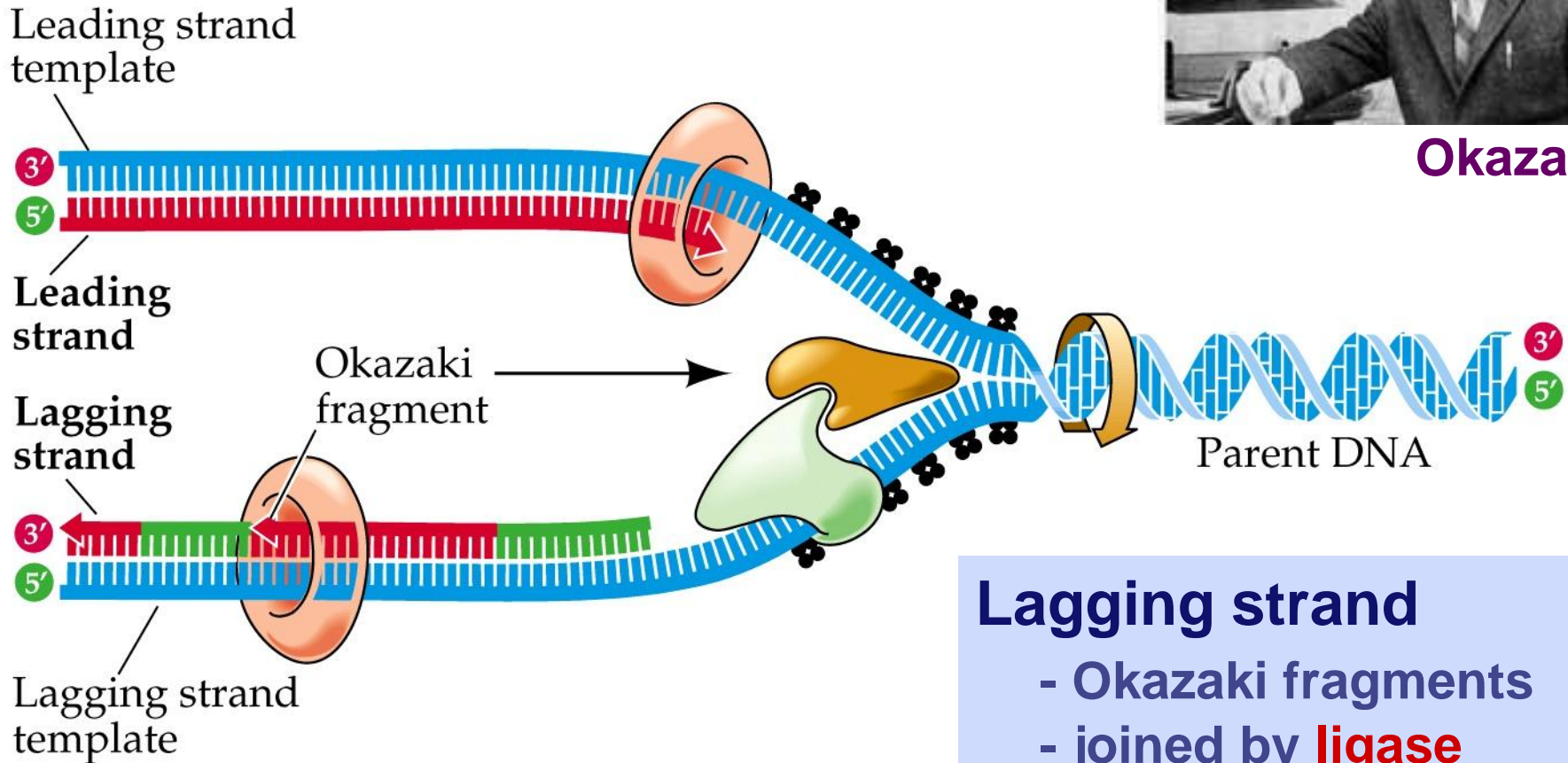


# Replication: A Review

**Leading strand**  
- continuous synthesis



**Okazaki**

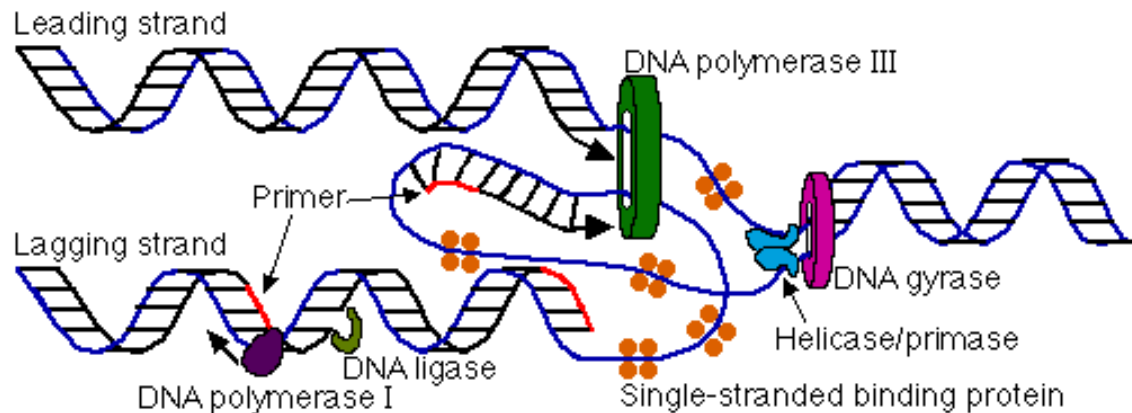


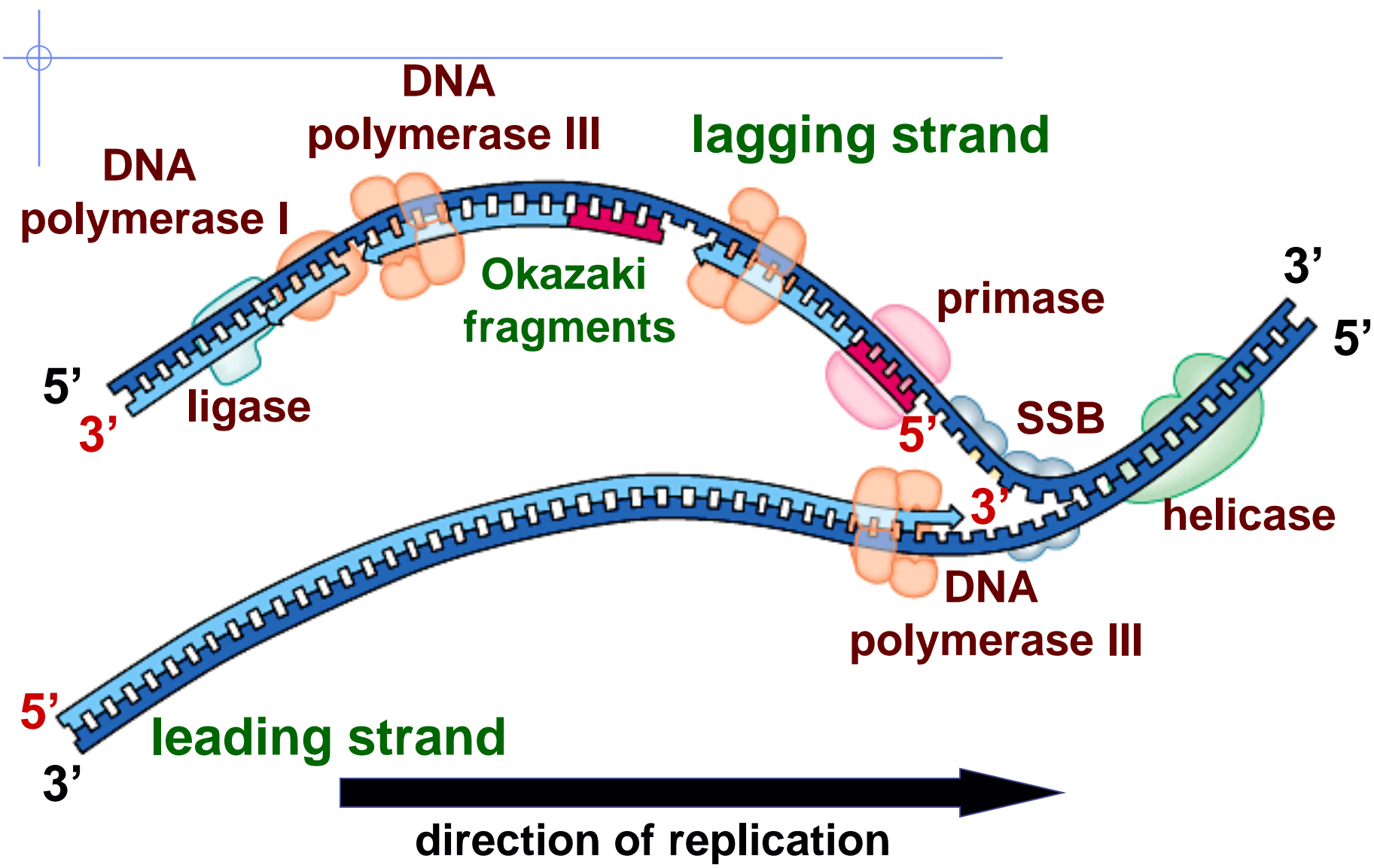
## Lagging strand

- Okazaki fragments
- joined by **ligase**
- “spot welder” enzyme

# Replication enzymes

- helicase
- DNA polymerase III
- primase
- DNA polymerase I
- ligase
- single-stranded binding proteins



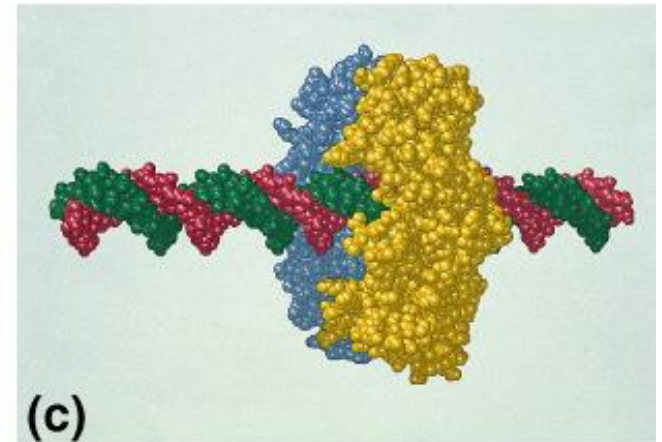
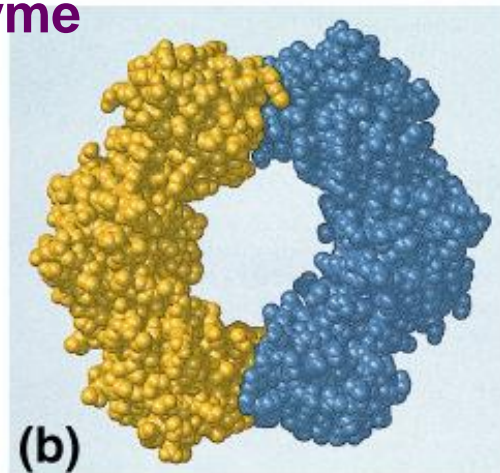
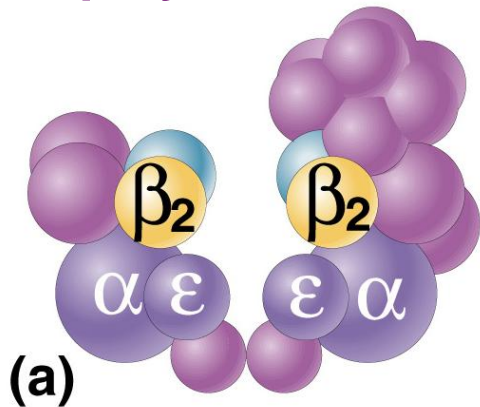




# DNA polymerases

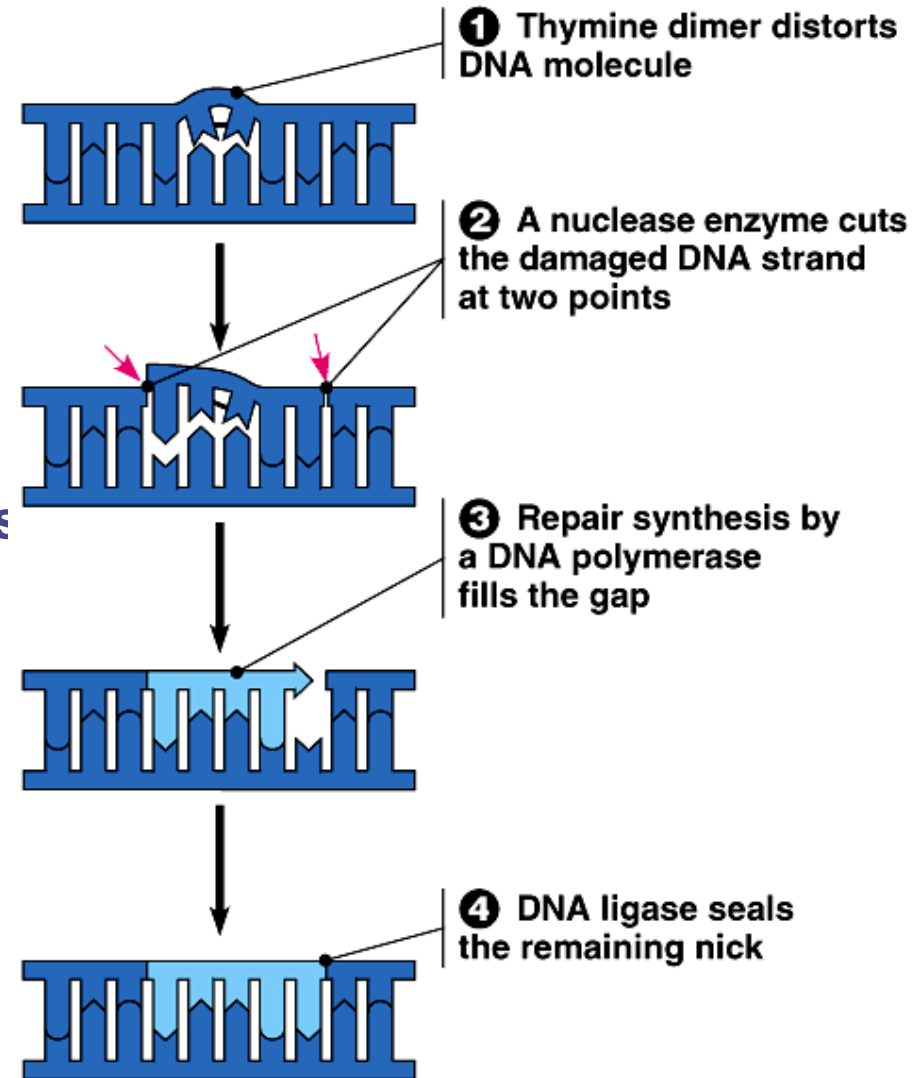
- DNA polymerase III
  - ◆ 1000 bases/second
  - ◆ main DNA building enzyme
- DNA polymerase I
  - ◆ 20 bases/second
  - ◆ editing, repair & primer removal

## DNA polymerase III enzyme



# Editing & proofreading DNA

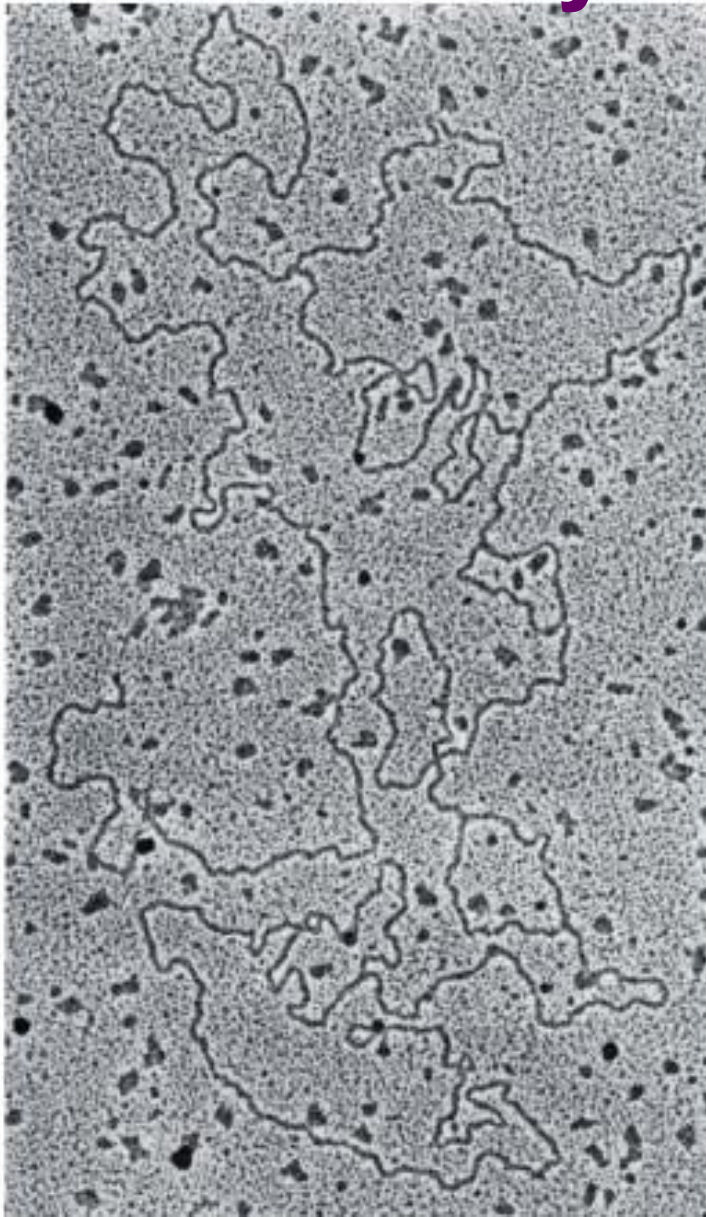
- 1000 bases/second = lots of typos!
- DNA polymerase I
  - ◆ proofreads & corrects typos
  - ◆ repairs mismatched bases
  - ◆ excises abnormal bases
    - repairs damage throughout life
  - ◆ reduces error rate from 1 in 10,000 to 1 in 100 million bases



## Fast & accurate!

- It takes *E. coli* <1 hour to copy 5 million base pairs in its single chromosome
  - ◆ divide to form 2 identical daughter cells
- Human cell copies its 6 billion bases & divide into daughter cells in only few hours
  - ◆ remarkably accurate
  - ◆ only ~1 error per 100 million bases
  - ◆ ~30 errors per cell cycle

# What's it really look like?



# The “Central Dogma”

- flow of genetic information within a cell

