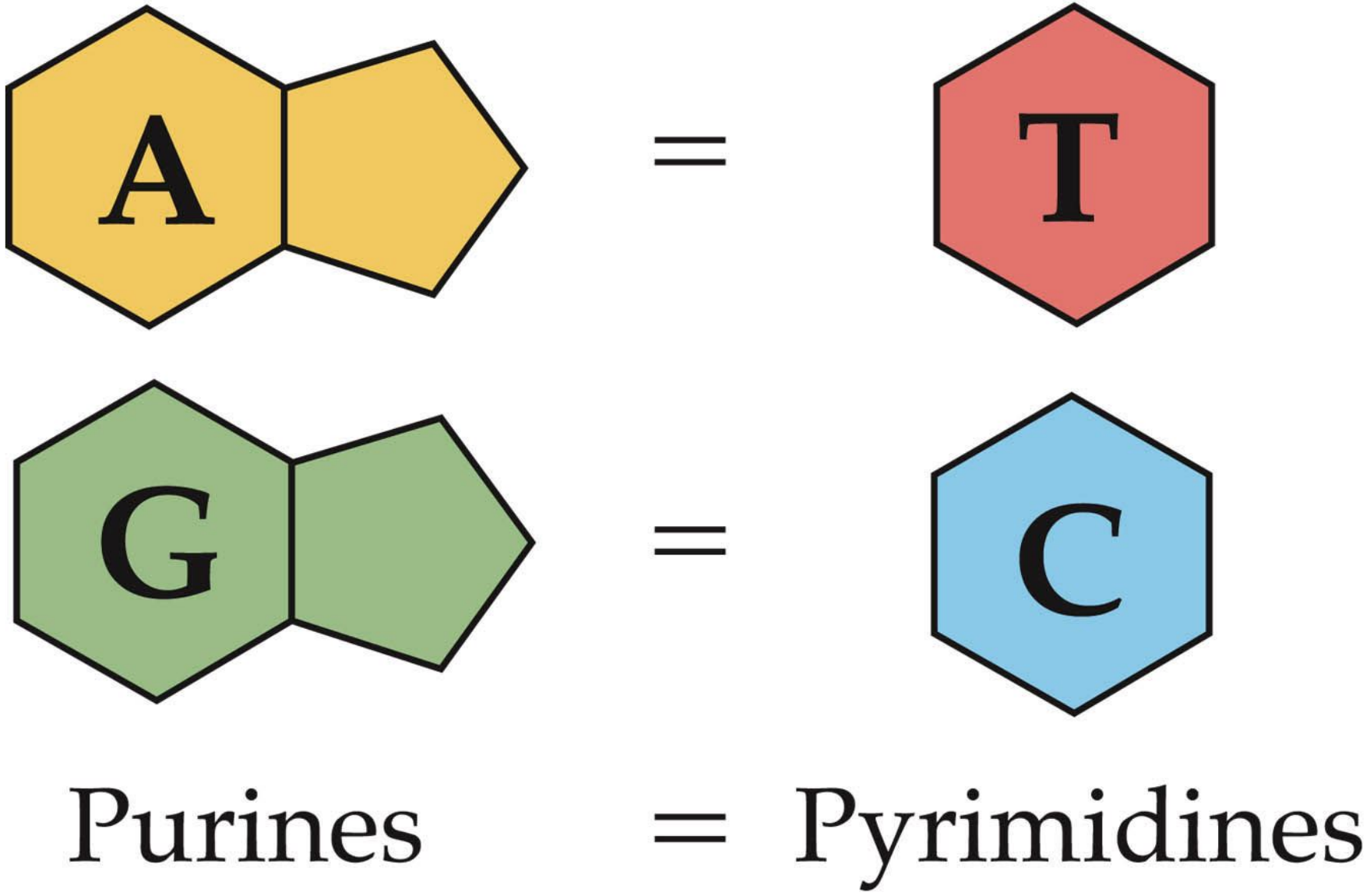

Erwin Chargaff

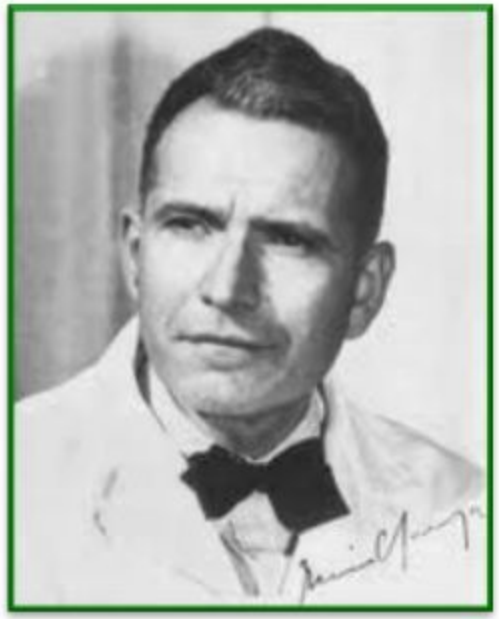
Chargaff rules

Success criteria

- Can apply Chargaff's rule to calculate a correct number of X bases indicating number of Y bases.
- Know and explain two rules:
- Quantity A = quantity T
- Quantity G = quantity C
- Relative quantity of DNA varies from one sample to another one particularly in relative quantity of reasons ATGC



LIFE: THE SCIENCE OF BIOLOGY, Seventh Edition, **Figure 11.5 Chargaff's Rule**



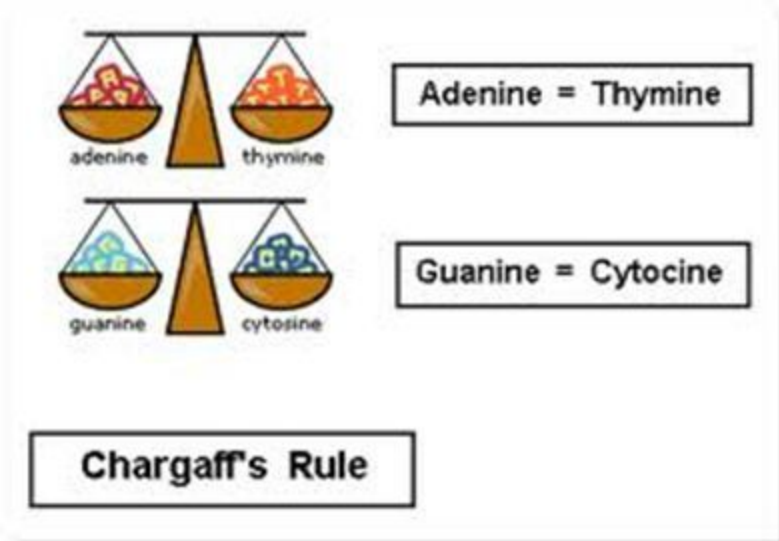
Erwin Chargaff

In 1947, an American scientist named Erwin Chargaff discovered that:
the amount of guanine and cytosine bases are equal in any sample of DNA.

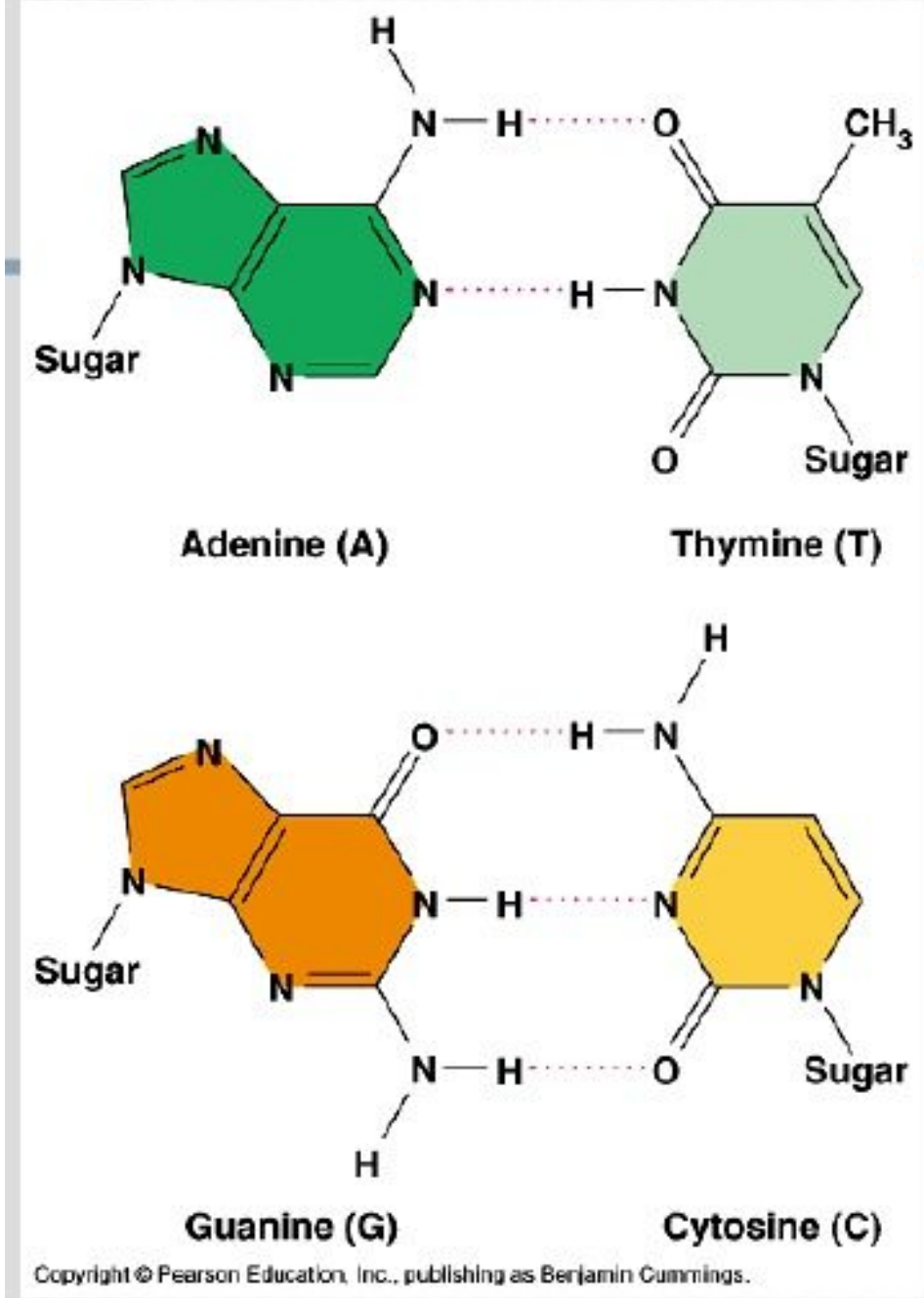
The same is true for the other two nitrogen bases:
The amount of adenine and thymine are equal in any sample of DNA.

The observation that A = T and that C = G became known as Chargaff's rules.

At the time this observation was made, it was not clear why this fact was so important.

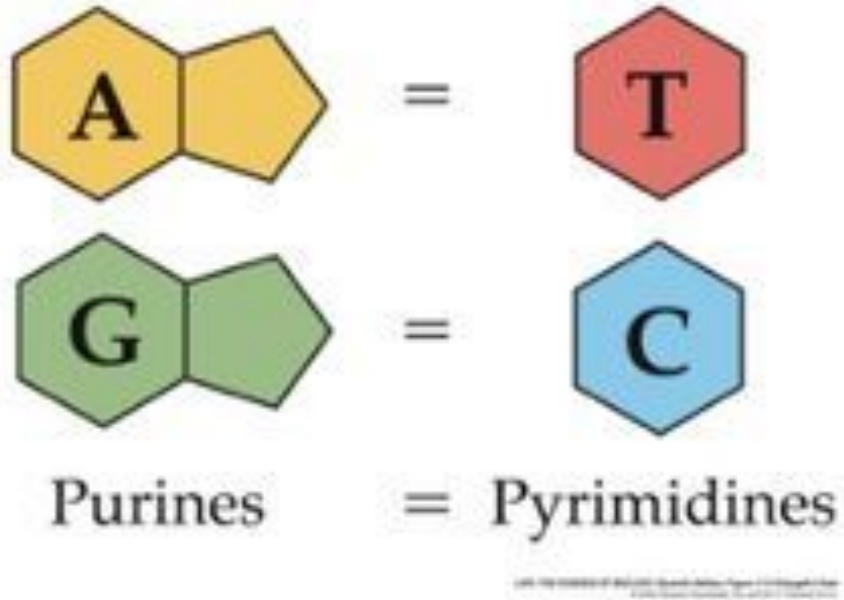


Confirms Erwin Chargaff's Rules

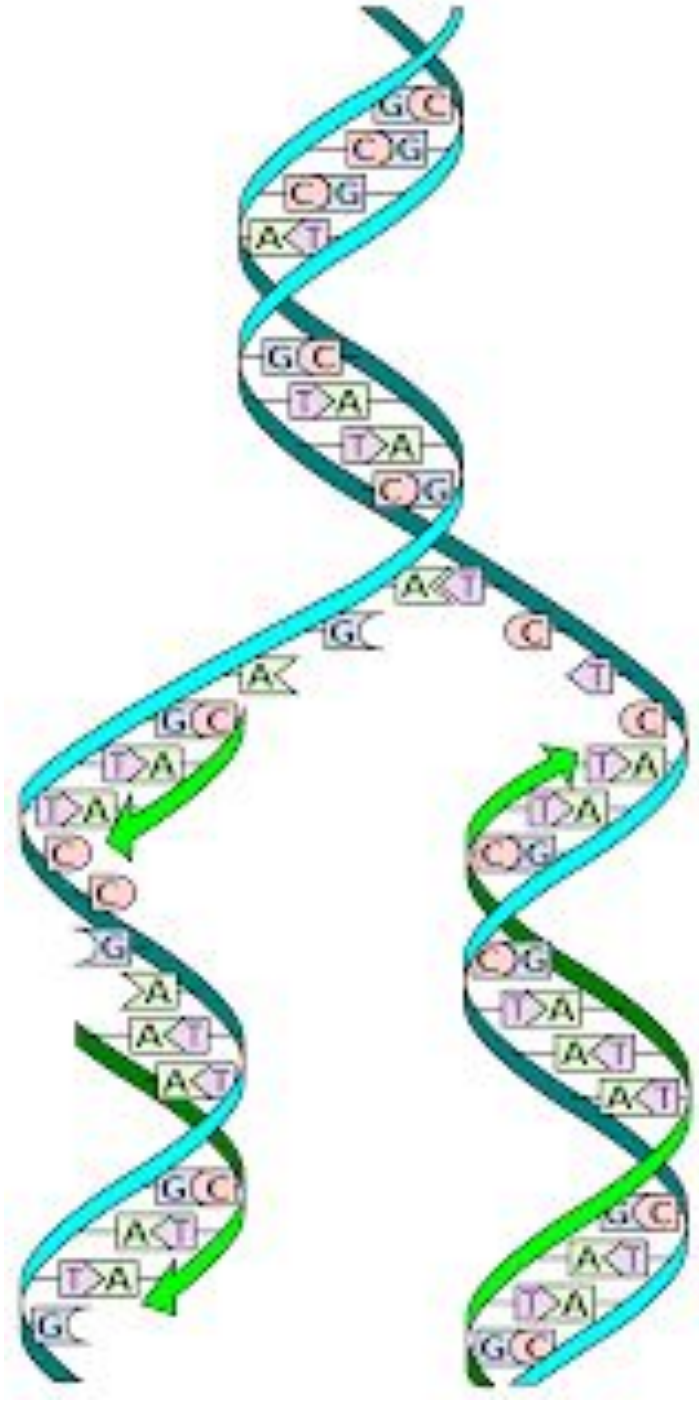


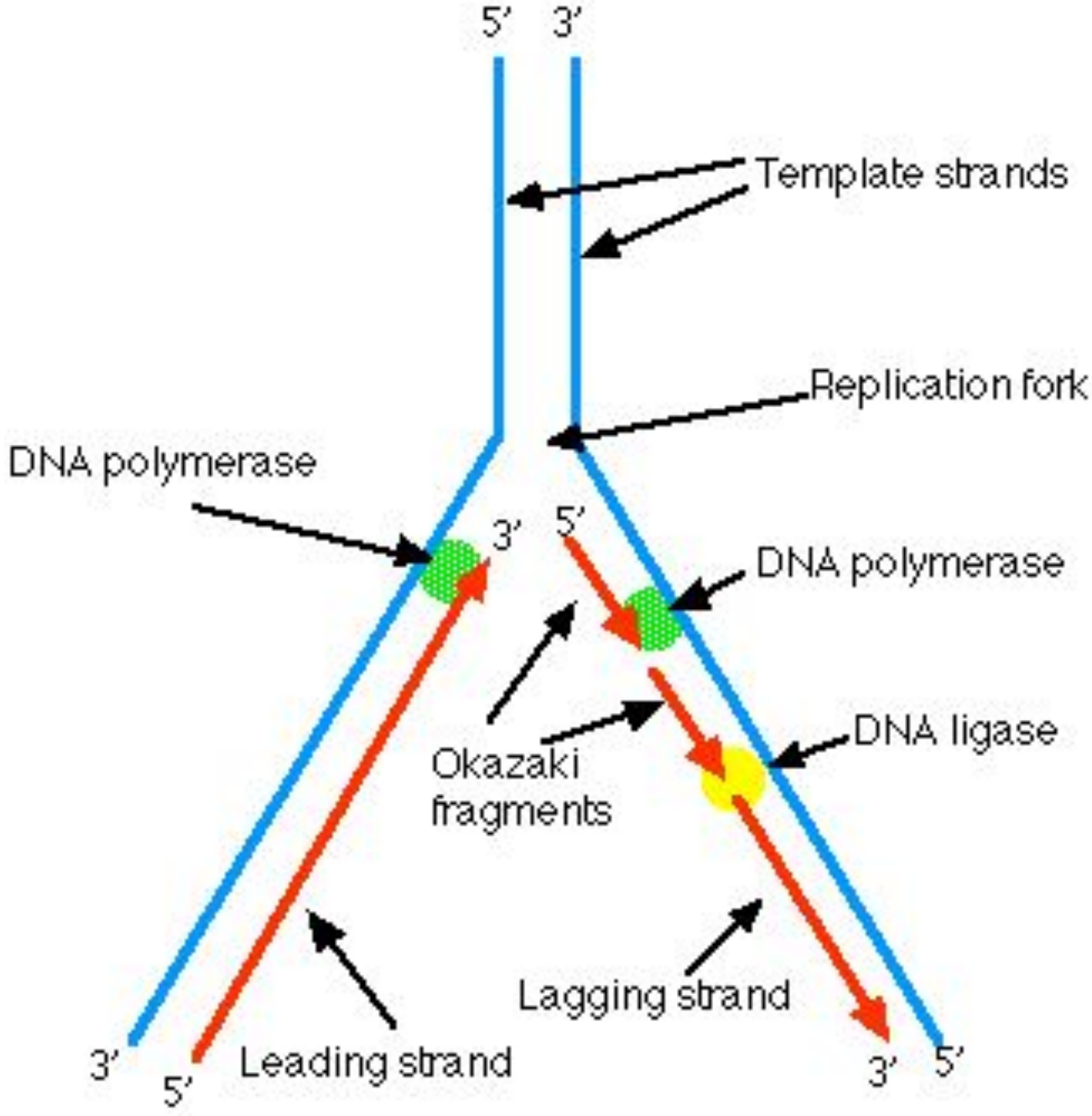
- # of Adenine = to # of thymine
- # of guanine equal to # of cytosine
- This dictates the combinations of N-bases that form steps/rungs
- Does not restrict the sequence of bases *along* each DNA strand

Chargaff's rule



- The amount of Adenine = the amount of Thymine.
- The amount of Guanine = the amount of Cytosine.
- He failed to make a connection to the structure of DNA.
- Indicated that DNA is symmetrical.




5′
3′
Template strands
Replication fork
DNA polymerase
3′
5′
DNA polymerase
Okazaki
fragments
DNA ligase
Lagging strand
3′
5′
Leading strand
3′
5′

DNA replication

Learning objectives

11.4.1.11 describe the process of DNA replication based on Chargaff rules

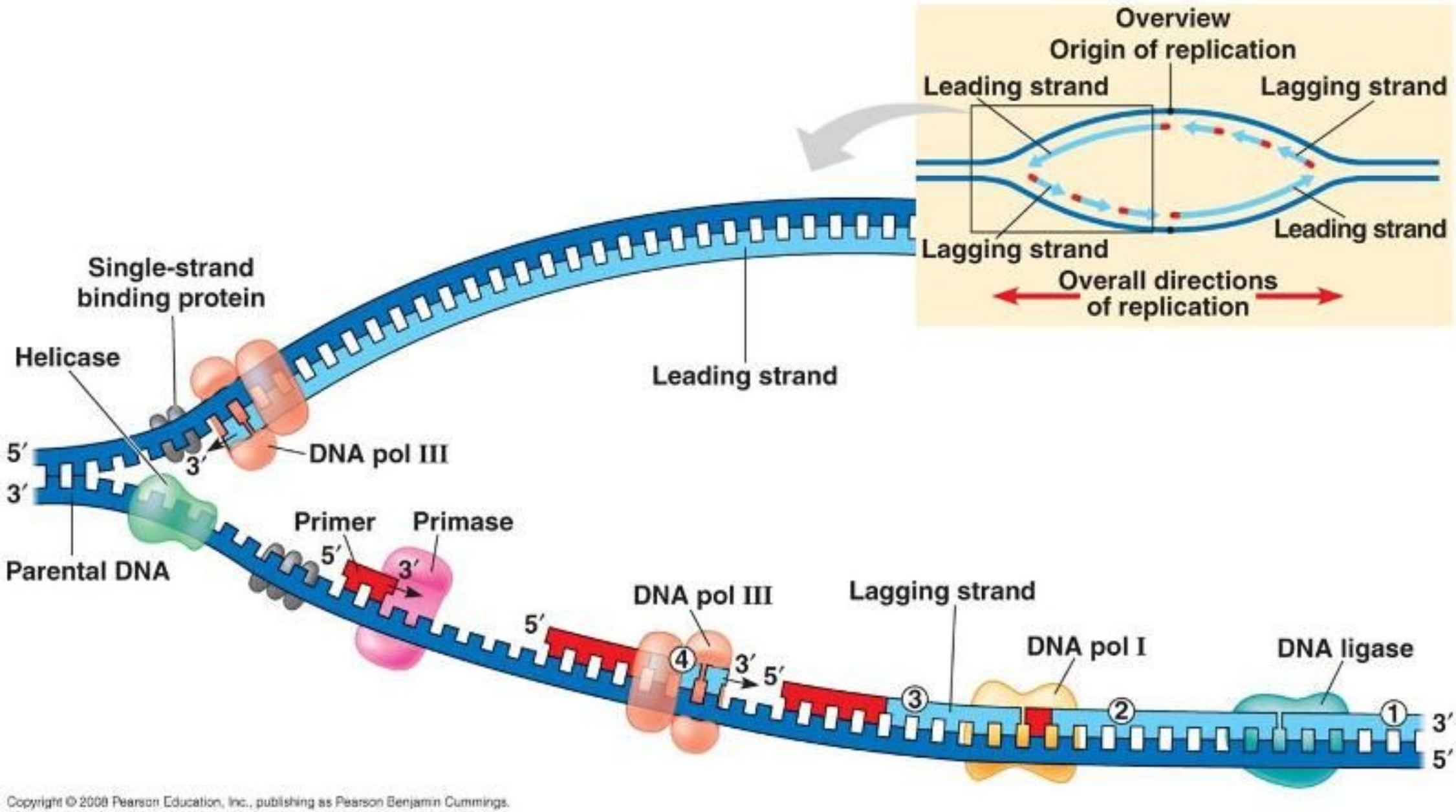
Success criteria

- Know and understand the process of DNA replication.
- Apply knowledge in completing diagram.
- Use correctly and explain terms.

Terminology

- DNA replication, 5' and 3' end,
- Primer Binding,
- Elongation, Termination,
- Enzymes: DNA helicase, DNA primase, DNA polymerases, Topoisomerase or DNA Gyrase, Exonucleases, DNA ligase,
- original strands

DNA replication



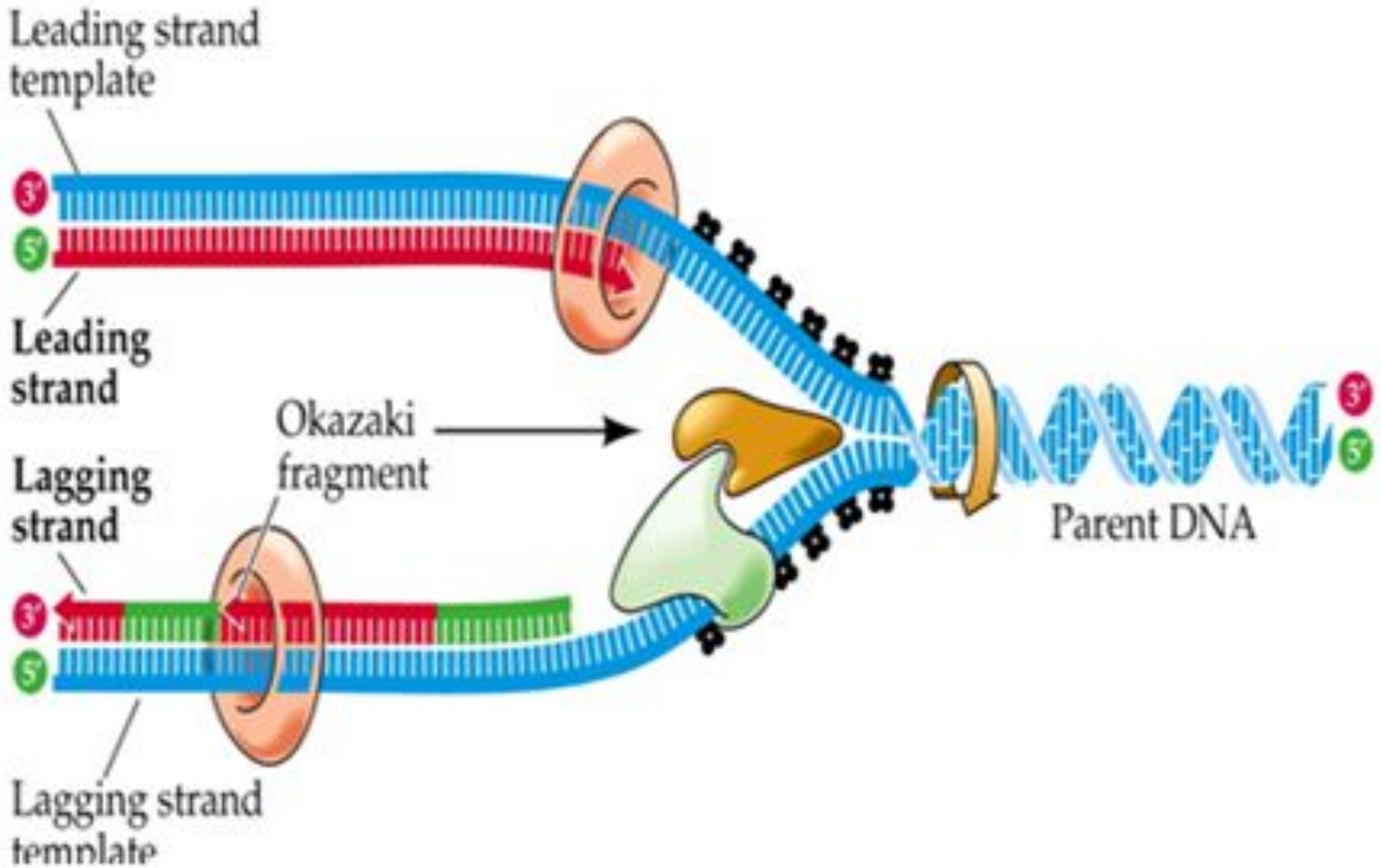
DNA replication

As essential feature of DNA is that it must be able to replicate itself accurately, so that when a cell divides, the genetic code it carries can be passed on to the daughter cells.

DNA replication copies DNA precisely so that new molecules are produced with exactly the same sequence of bases as the original strands.

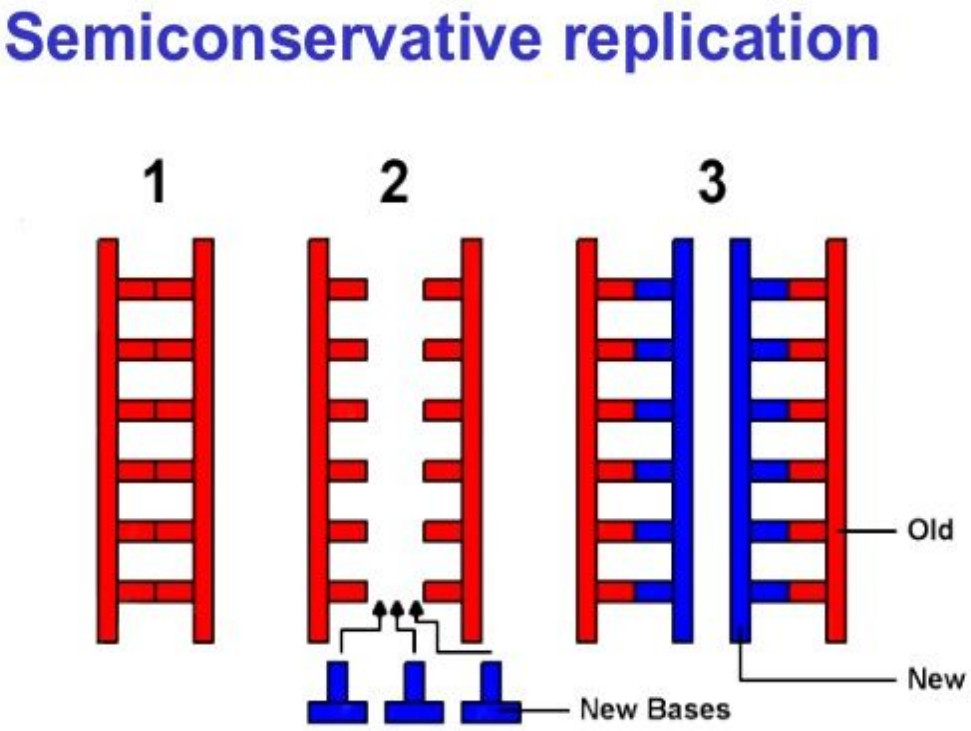
DNA replication

- Place: Nucleus
- Phase: interphase of the cell cycle



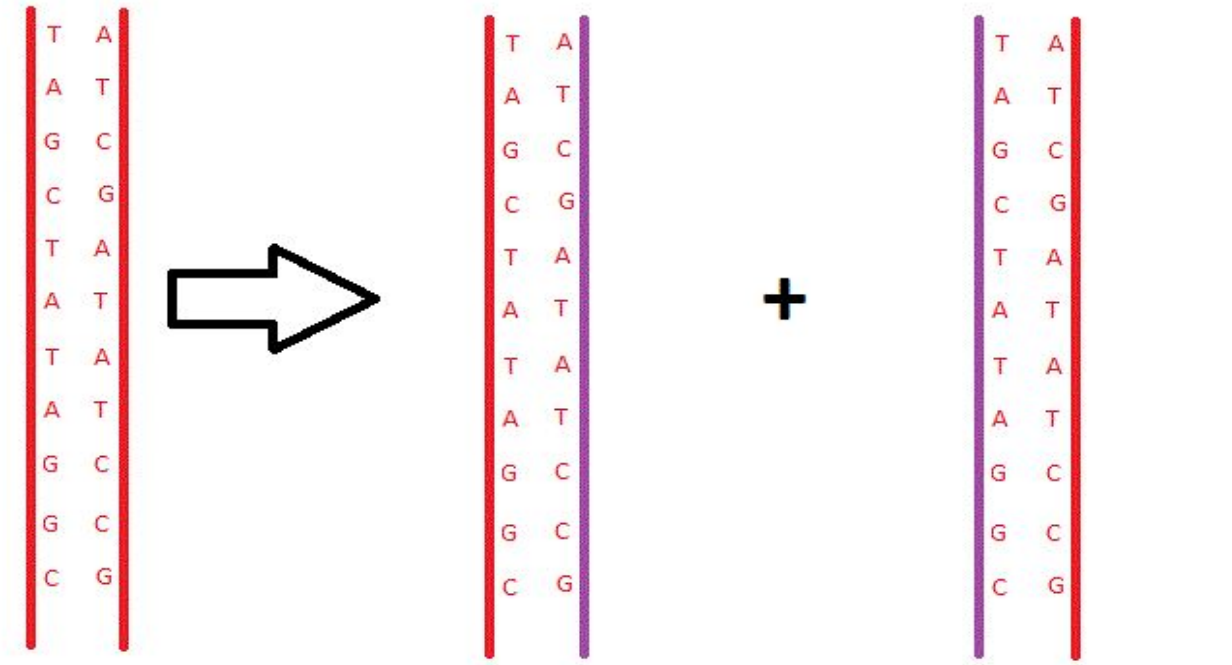
Semi-conservative replication

New nucleotides could then line up along each strand, opposite their appropriate partners, and join up to form complementary strands along each half of the original molecule. The **new DNA molecules would be just like the old ones, because each base would only pair with its complementary one.** Each pair of strands could then wind up again into a double helix, exactly like the original one.



Semi-conservative replication

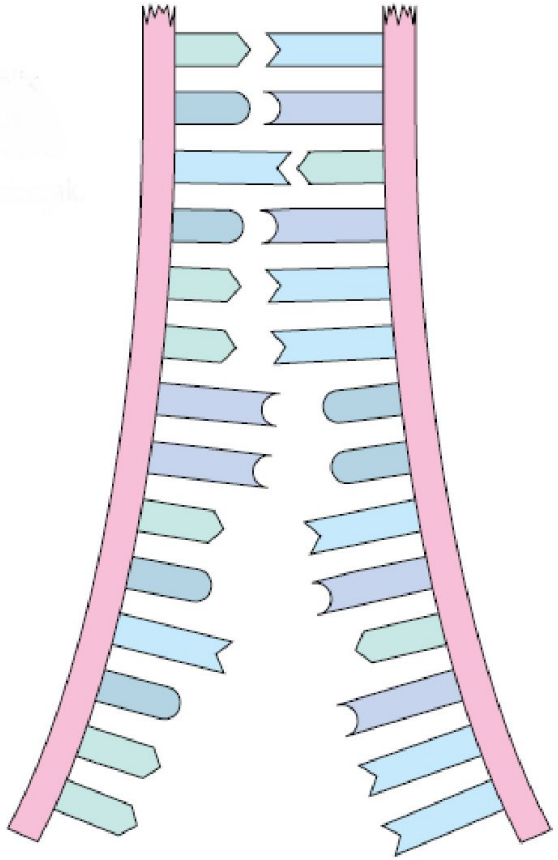
This method of copying is called **semi-conservative replication**, because half of the original molecule is kept (conserved) in each of the new molecules.



DNA replication: step by step

- First:

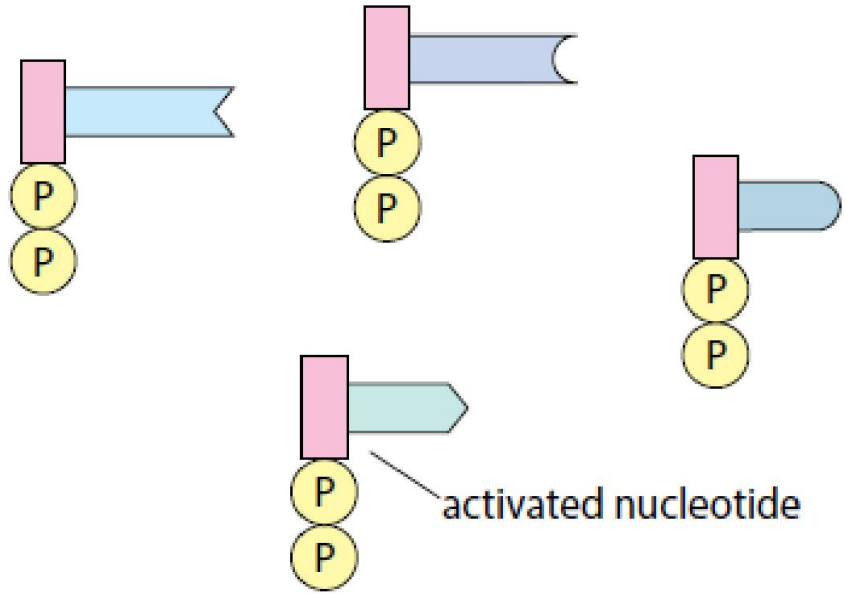
The DNA double helix unwinds and ‘unzips’ as the hydrogen bonds between the bases break.



DNA replication: step by step

- Second:

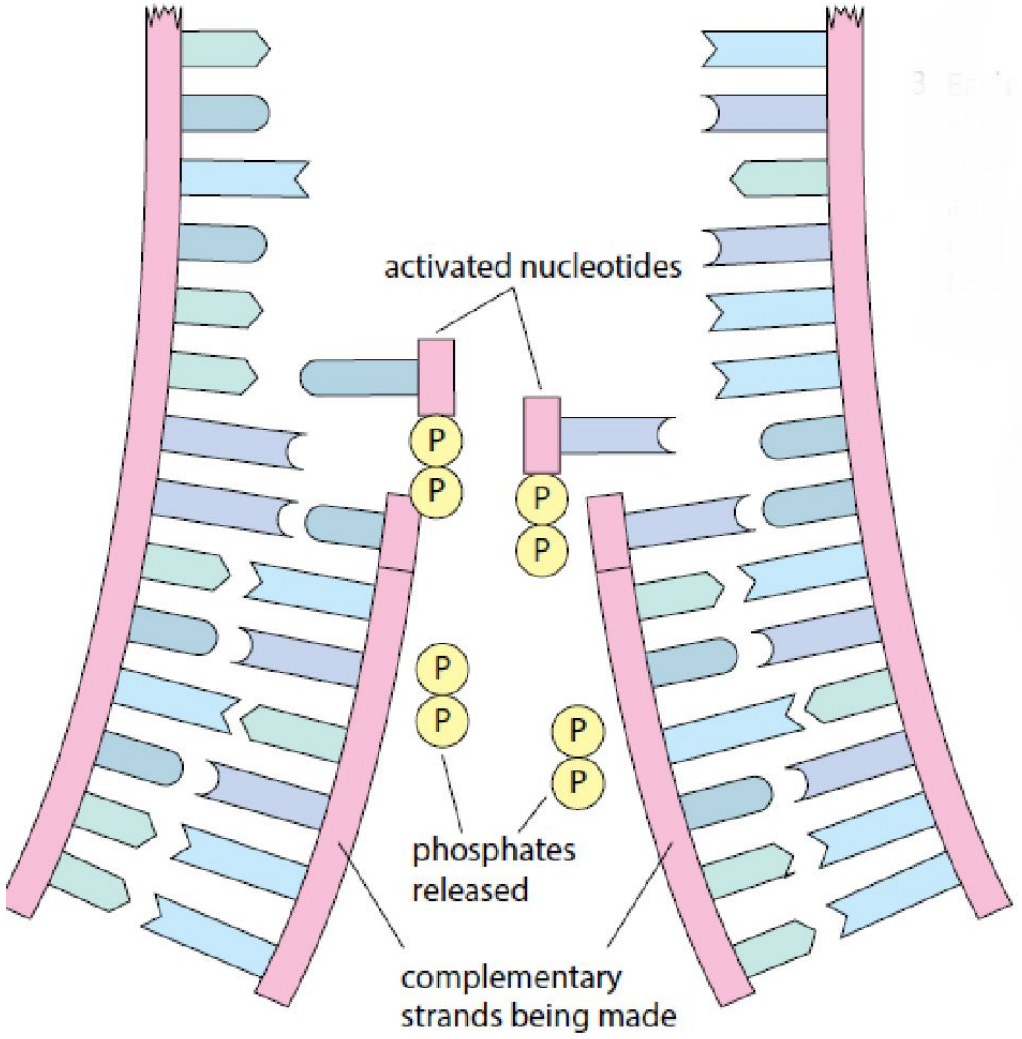
In the nucleus, there are nucleotides to which two extra phosphates have been added. The extra phosphates activate the nucleotides, enabling them to take part in the following reactions.



DNA replication: step by step

- Third:

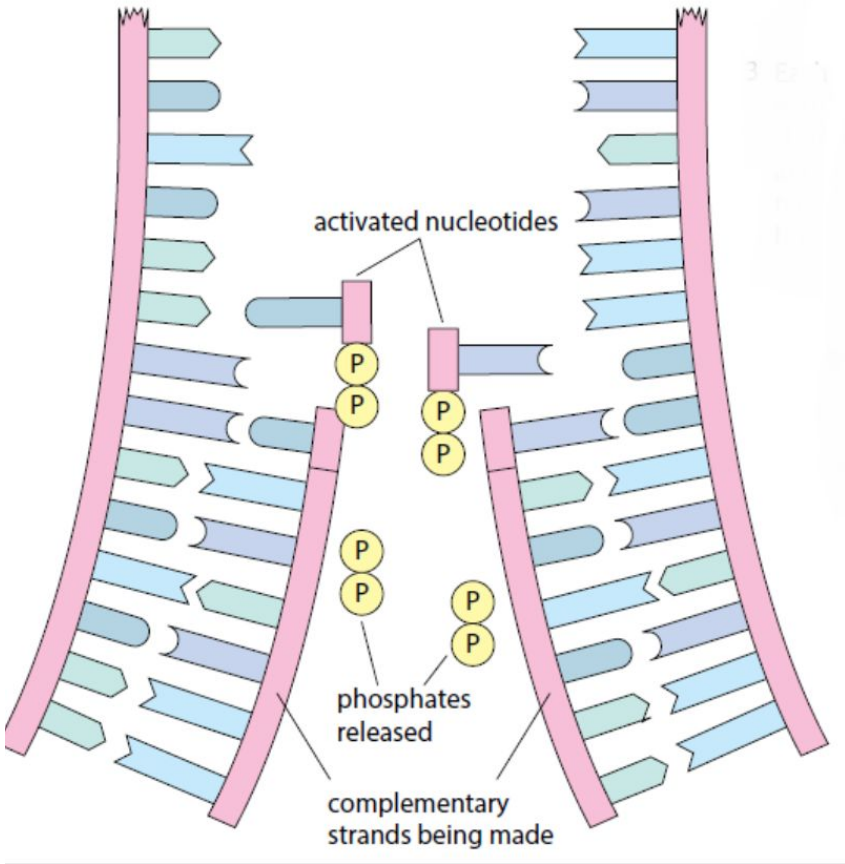
Each of the bases of the activated nucleotides pairs up with its complementary base on each of the old DNA strands. An enzyme, DNA polymerase, links the sugar and innermost phosphate groups of next-door nucleotides together. The two extra phosphates are broken off and released into the nucleus.



DNA replication: step by step

- Fourth:

DNA polymerase will only link an incoming nucleotide to the growing new chain if it is complementary to the base on the old strand. Thus very few mistakes are made, perhaps around one in every 10*8* base pairs.



Preparation For Replication

- ***Step 1: Replication Fork Formation***

DNA helicase disrupts the hydrogen bonding between base pairs to separate the strands into a Y shape known as the replication fork.

Replication Begins

- ***Step 2: Primer Binding***

Once the DNA strands have been separated, a short piece of RNA called a primer binds to the 3' end of the strand. The primer always binds as the starting point for replication. Primers are generated by the enzyme DNA primase.

Replication

- ***Step 3: Elongation***

DNA polymerases are responsible creating the new strand by a process called elongation.

DNA polymerase then adds pieces of DNA, called Okazaki fragments, to the strand between primers. This process of replication is discontinuous as the newly created fragments are disjointed.

Replication

•*Step 4: Termination*

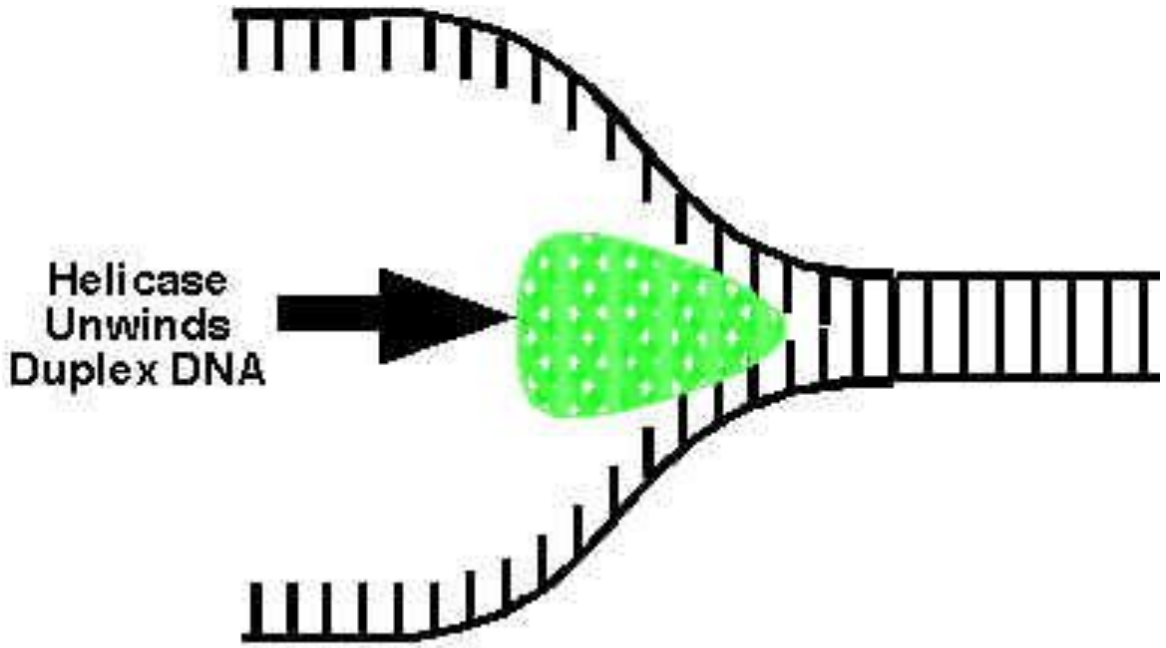
Once both the continuous and discontinuous strands are formed, an enzyme called exonuclease removes all RNA primers from the original strands.

Once completed, the parent strand and its complementary DNA strand coils into the familiar double helix shape. In the end, replication produces two DNA molecules, each with one strand from the parent molecule and one new strand.

Enzymes in DNA replication

- ***DNA helicase***

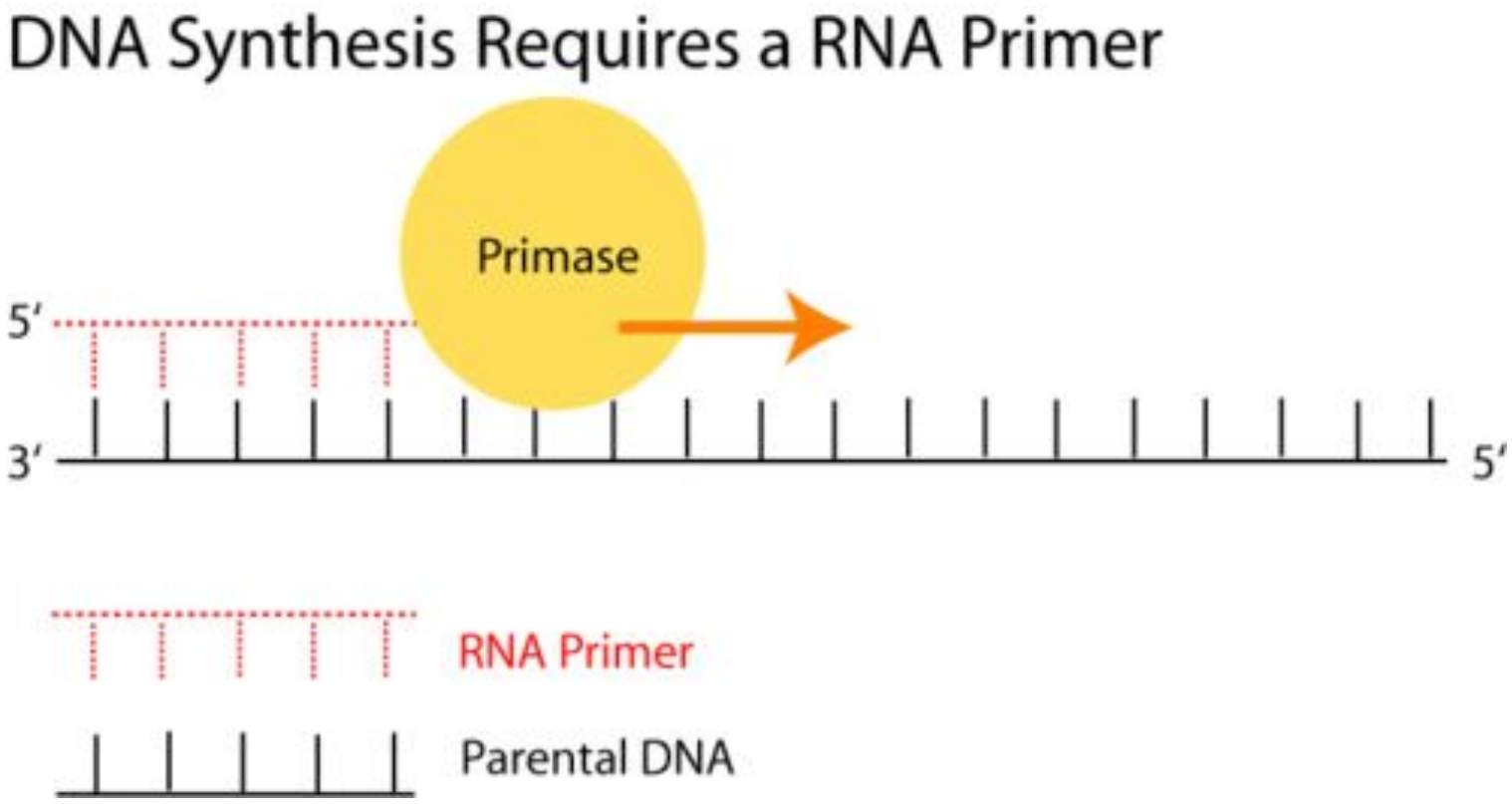
It forms the replication fork by breaking hydrogen bonds between nucleotide pairs in DNA.



Enzymes in DNA replication

- ***DNA primase***

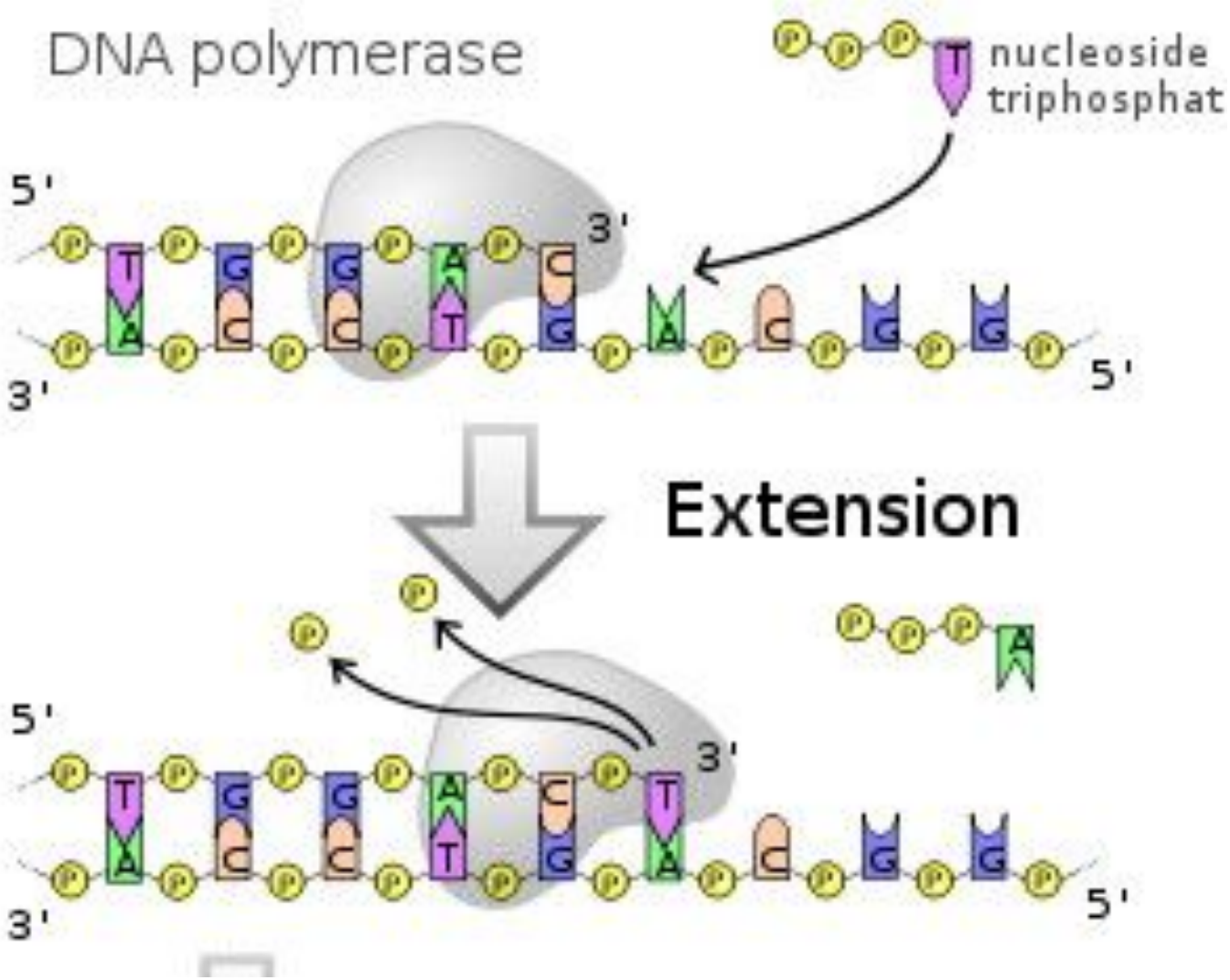
Primers are short RNA molecules that act as templates for the starting point of DNA replication.



Enzymes in DNA replication

- ***DNA polymerases***

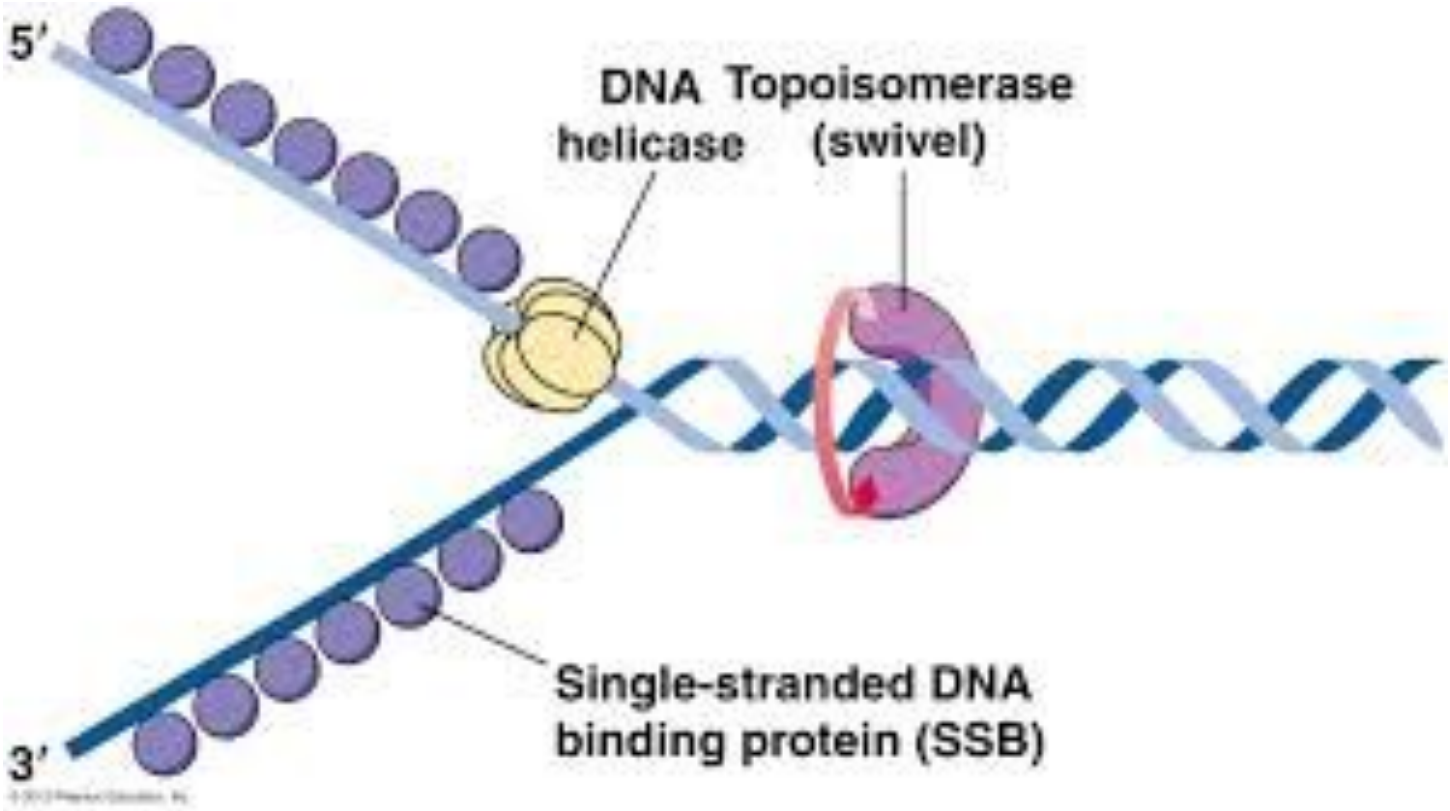
Synthesize new DNA molecules by adding nucleotides to leading and lagging DNA strands.



Enzymes in DNA replication

- ***Topoisomerase or DNA Gyrase***

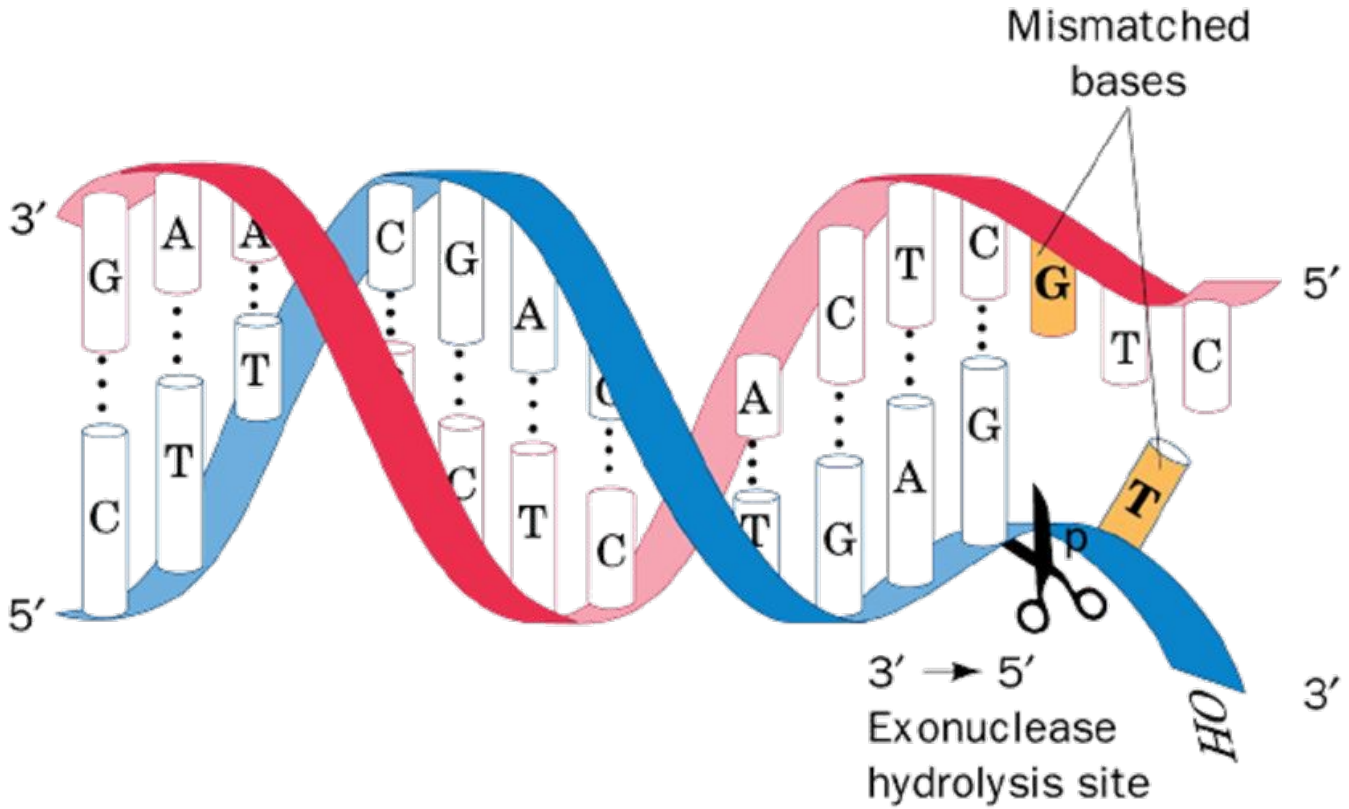
Unwinds and rewinds DNA strands to prevent the DNA from becoming tangled or supercoiled.



Enzymes in DNA replication

- ***Exonucleases***

Group of enzymes that remove nucleotide bases from the end of a DNA chain.

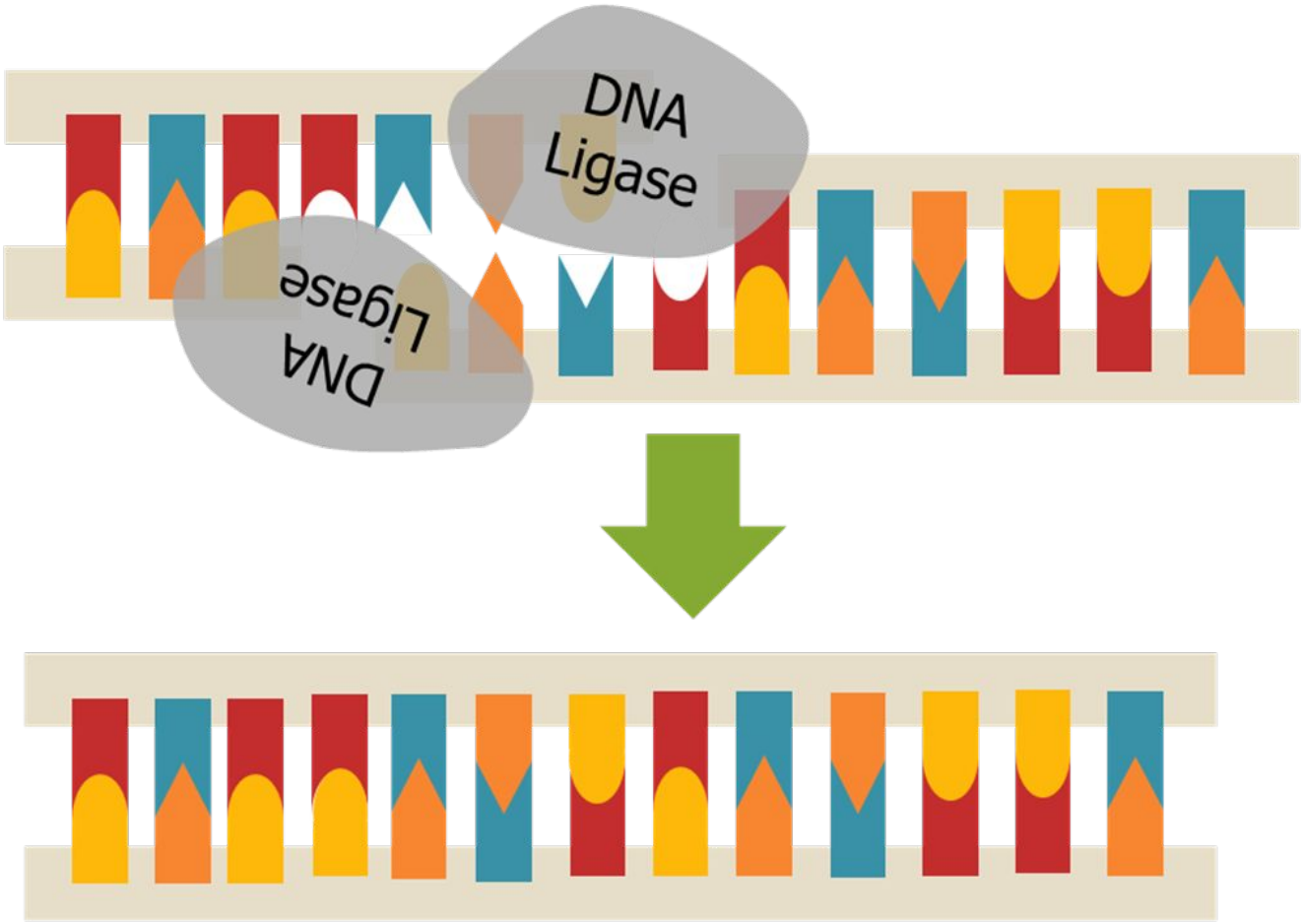


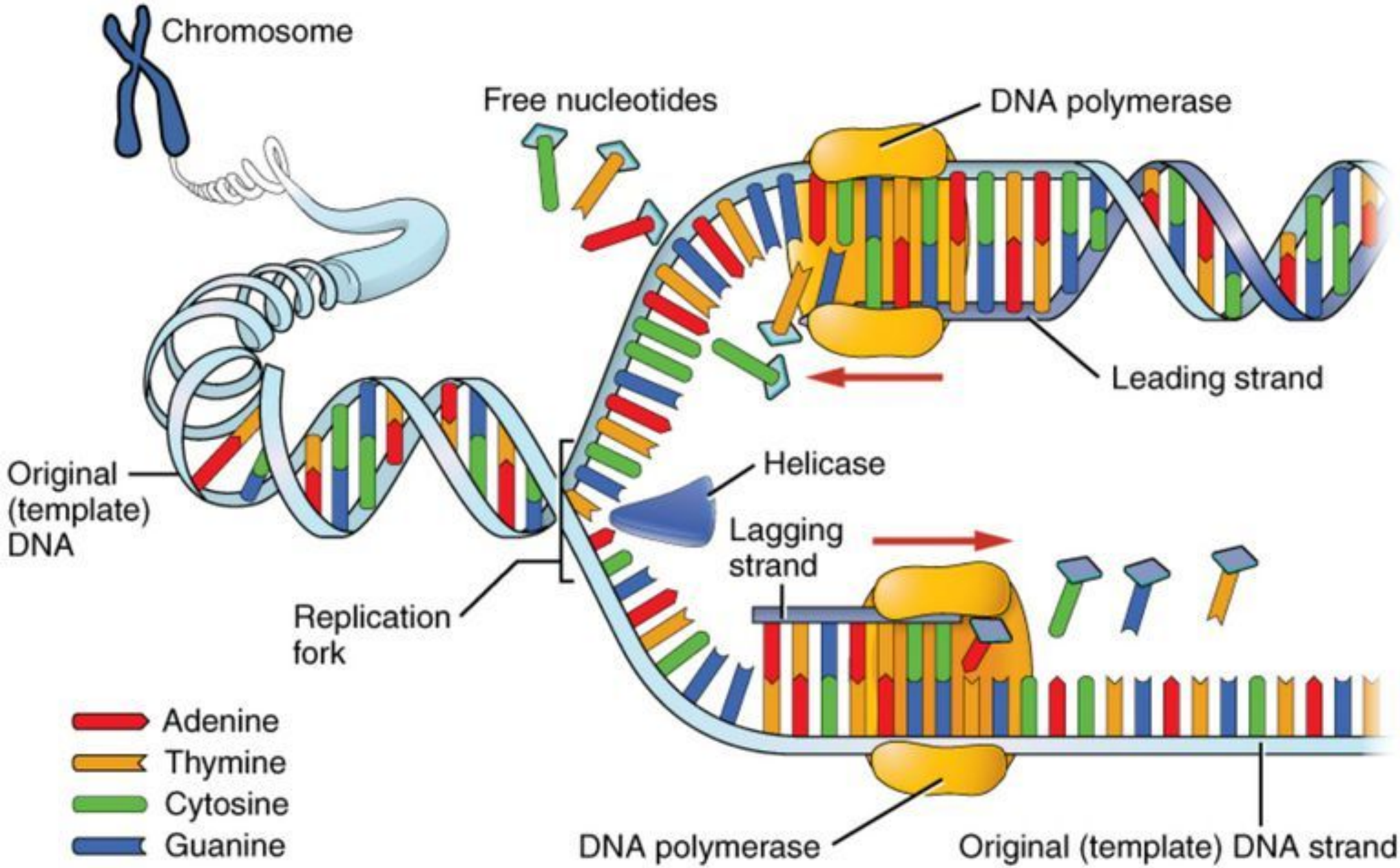
The 3′ →5′ exonuclease function of DNA polymerase I and DNA polymerase III

Enzymes in DNA replication

- ***DNA ligase***

Joins DNA fragments together by forming phosphodiester bonds between nucleotides.




Chromosome
Free nucleotides
DNA polymerase
Leading strand
Original (template) DNA
Helicase
Lagging strand
Replication fork
Adenine
Thymine
Cytosine
Guanine
DNA polymerase
Original (template) DNA strand