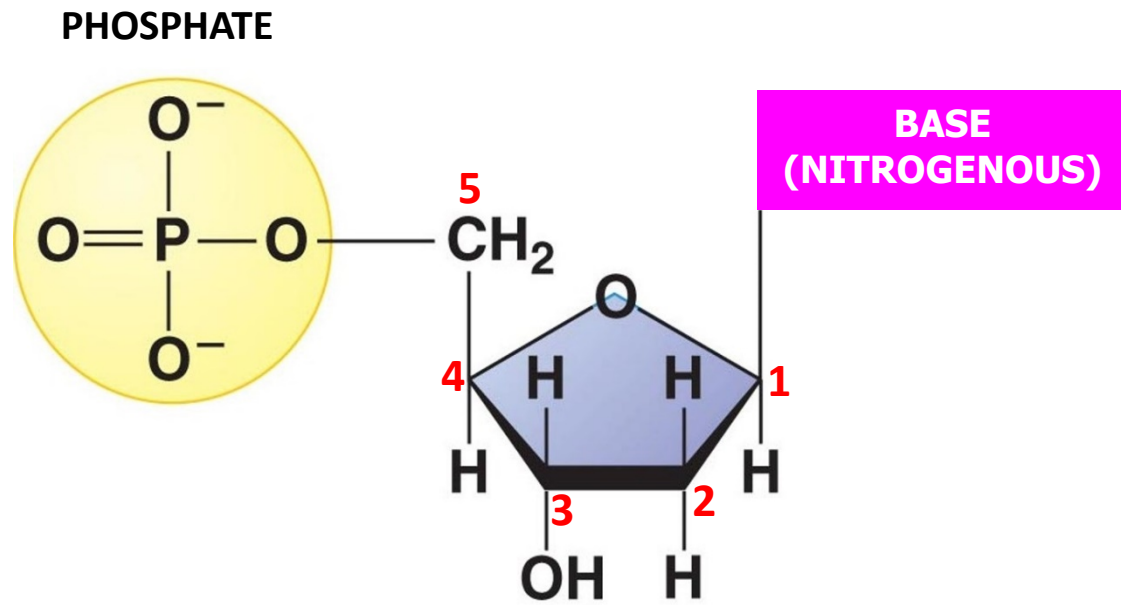


A. DNA STRUCTURE

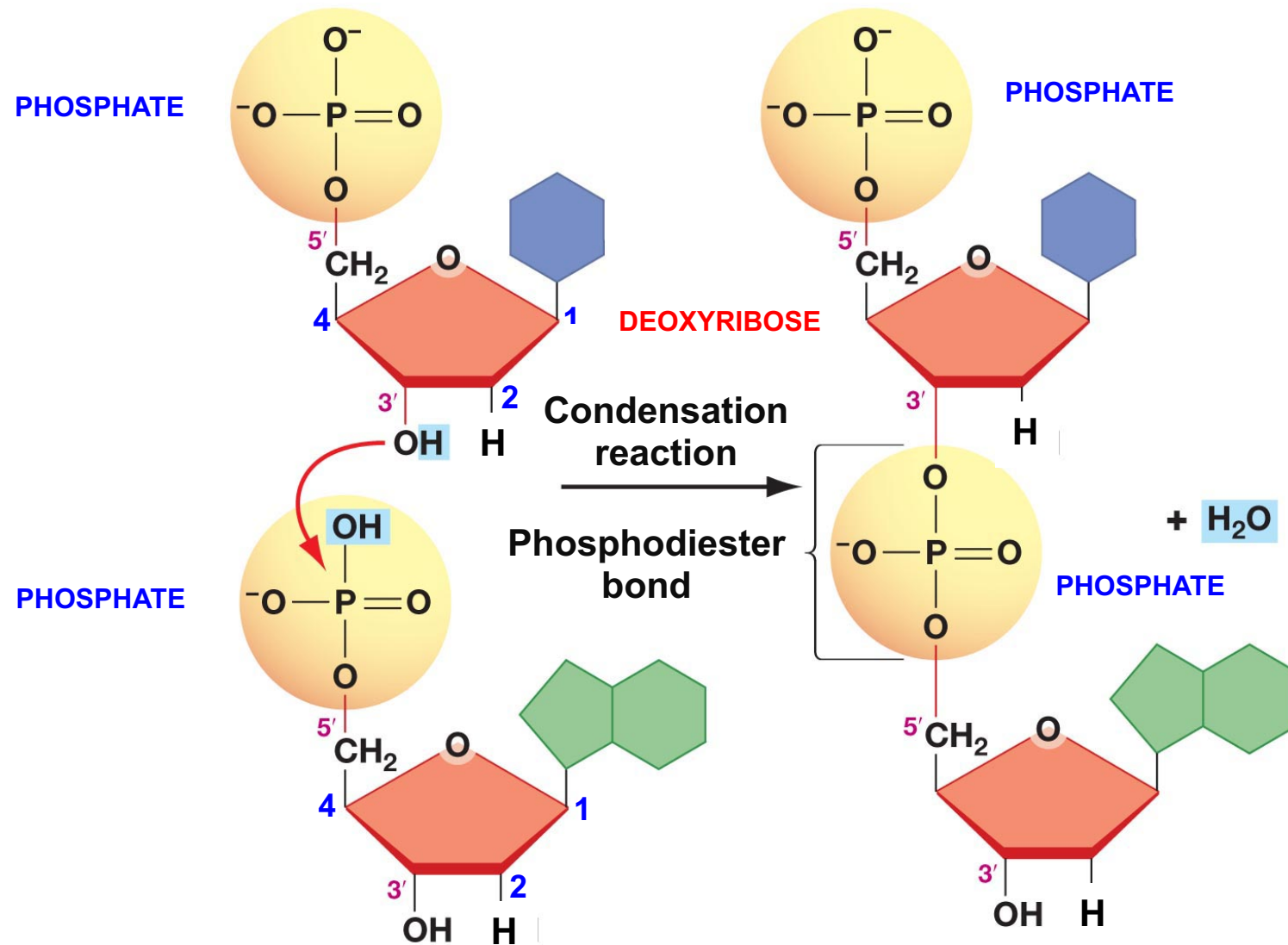
A nucleotide



DEOXYRIBOSE
has 5 carbon atoms and
the 5th is outside the ring

- The important **carbons** to remember here are 3' and 5'.

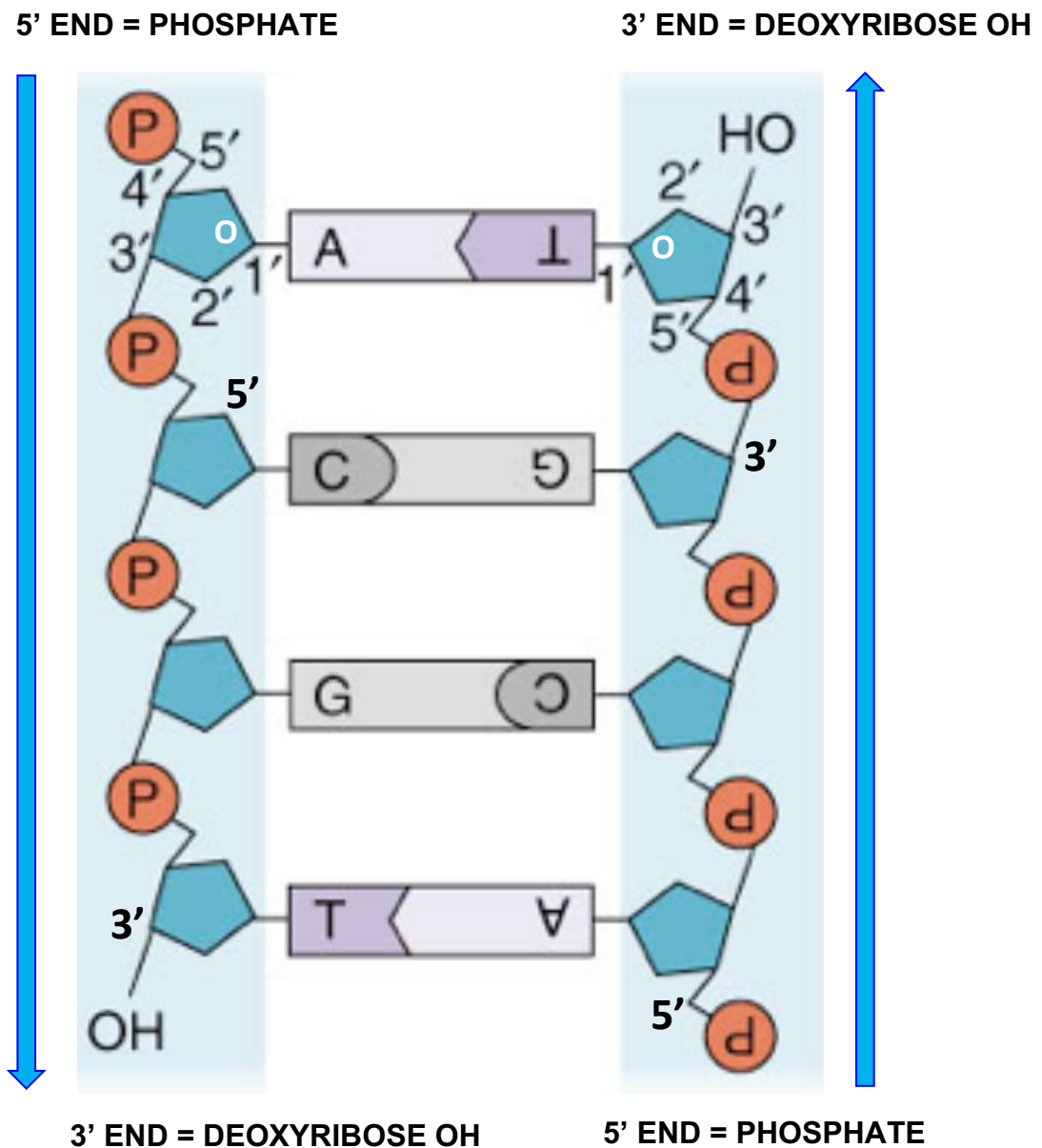
How nucleotides join together



- **New free nucleotides** are added to the **3'OH group** of the **previous deoxyribose** sugar.
- **Phosphates** are therefore **between** the **3'** and **5' carbons** of **two deoxyribose** sugars.
- The **3'OH** on **deoxyribose** reacts with the **OH** group on the **phosphate** in a **condensation reaction** to form a **phosphodiester bond**.

How the strands are labelled

- The two strands are **antiparallel** – they **run in opposite directions**.



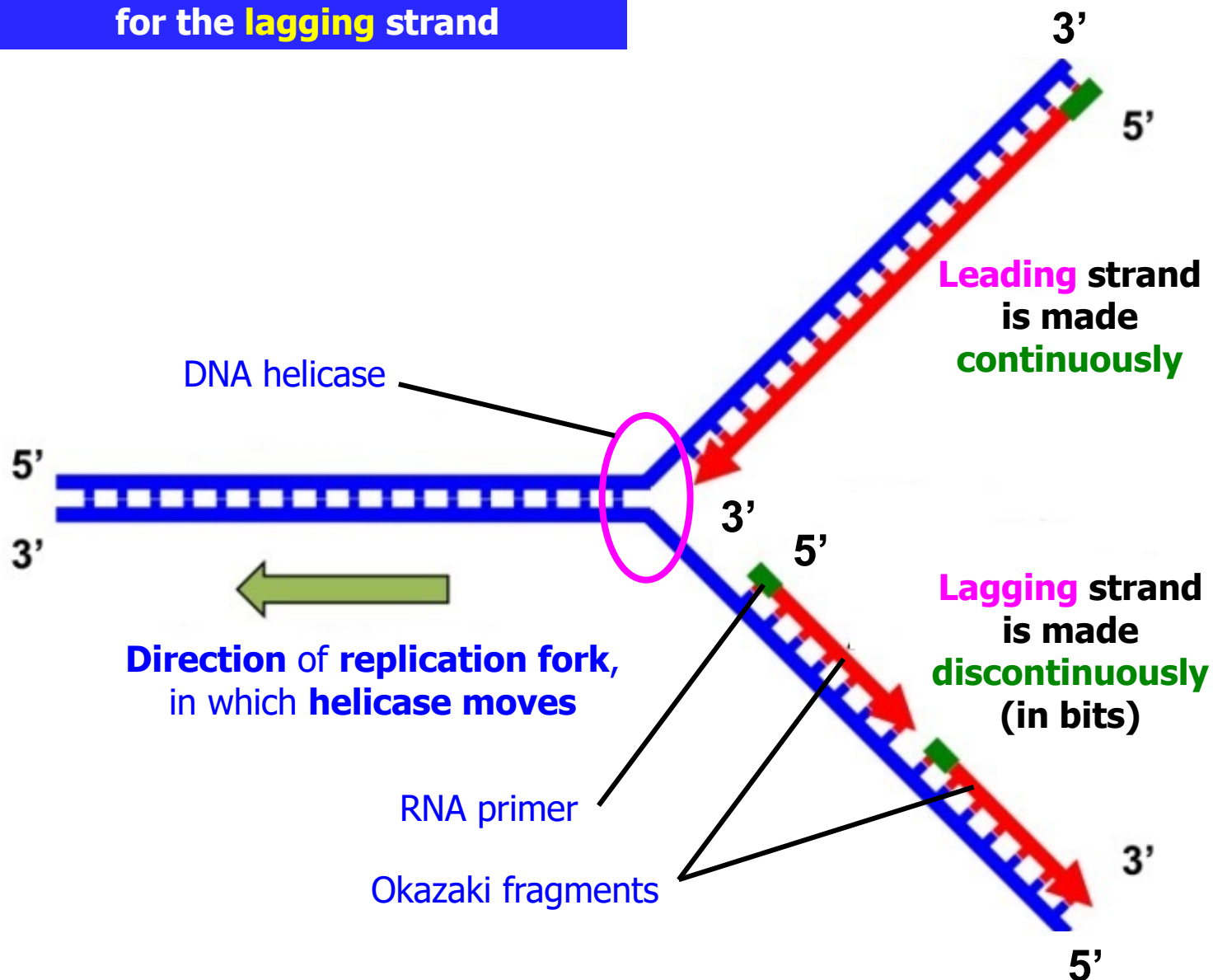
- DNA strands** can only be made in a **5' → 3'** direction.
- Remember that **new nucleotides** react with the **3'OH** group on the **previous deoxyribose** sugar.

B. DNA REPLICATION

The leading and lagging strands

DNA polymerase can only add nucleotides in a **5' → 3' direction**

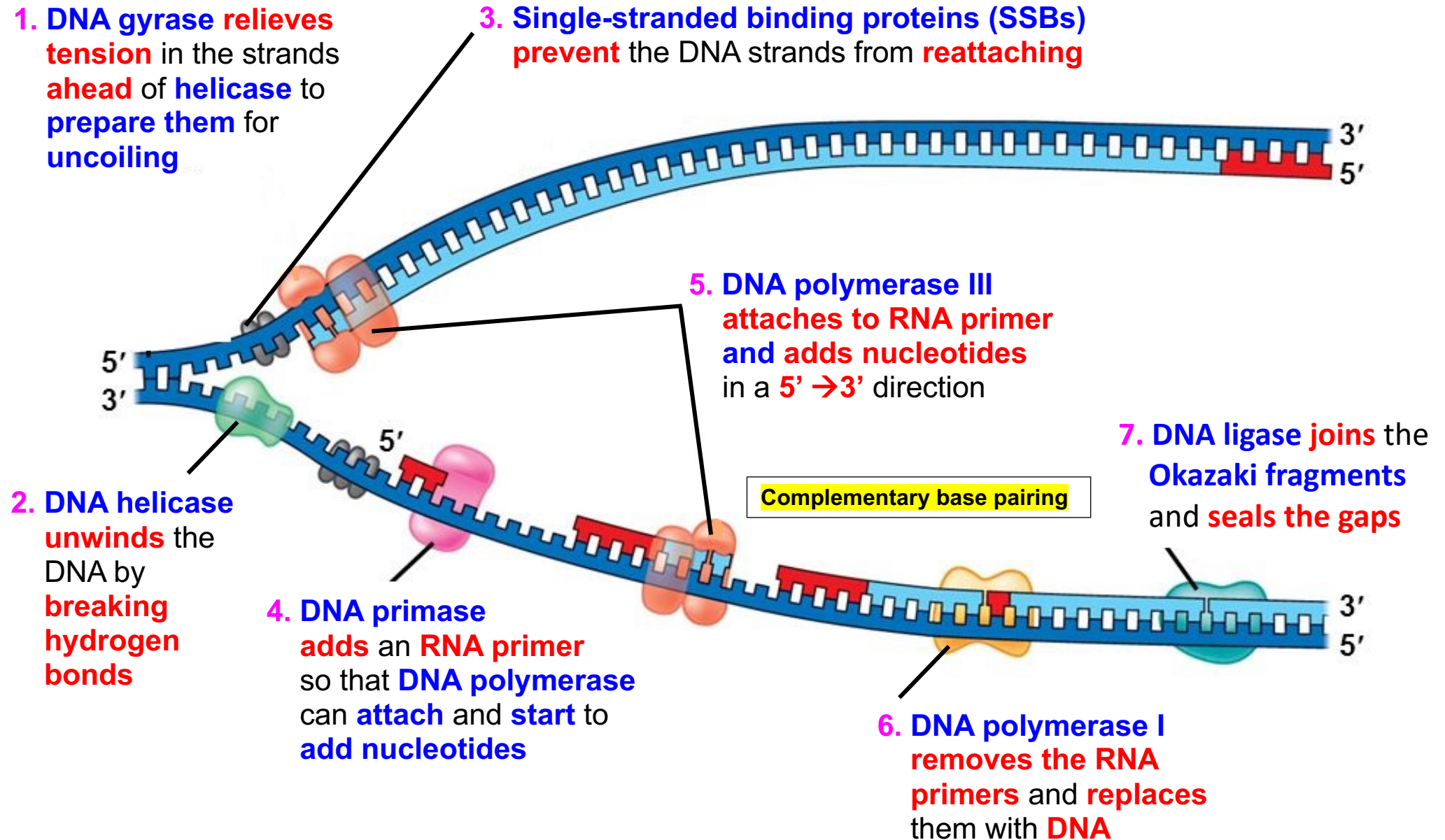
This is in the **opposite direction** to **helicase** and the **replication fork** for the **lagging** strand



- **Okazaki fragments** are the **short fragments** of **DNA** made on the **lagging strand** that are eventually **joined** together.
- **RNA primers** are **short fragments** of **RNA**, which are needed to allow **DNA polymerase III** to **attach** and **start replication**.

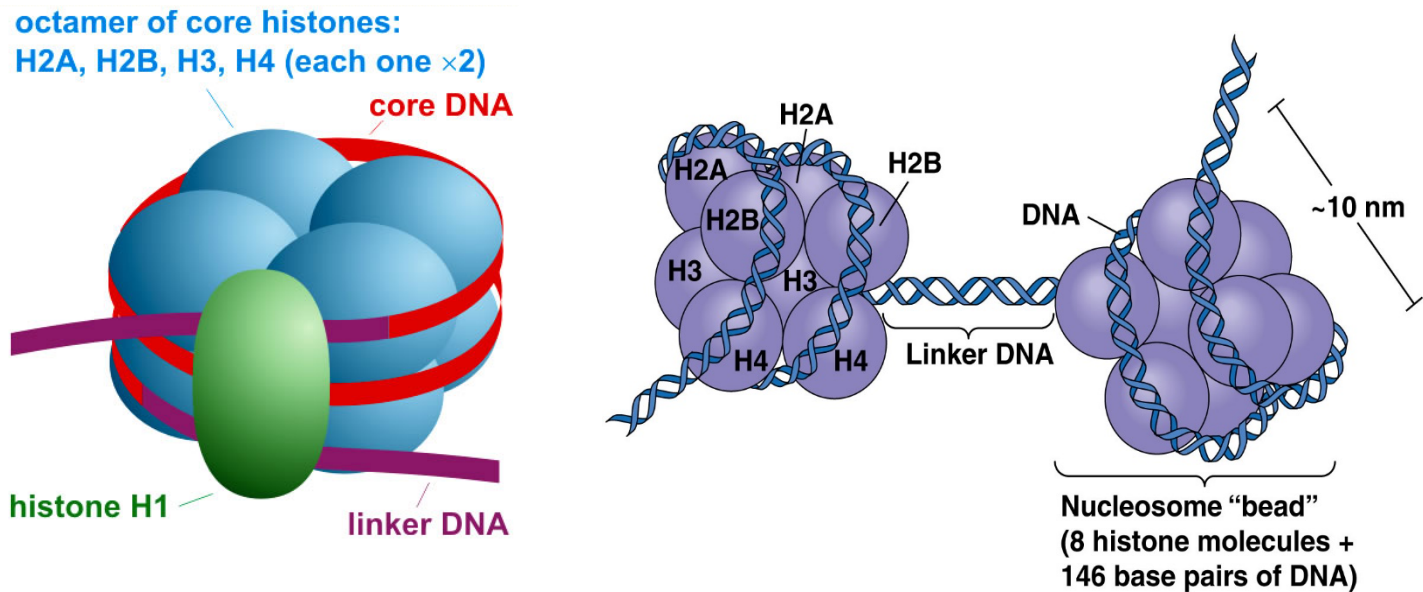
Enzymes involved in DNA replication

The **leading strand** is built up **continuously** and the **lagging strand** is built up in **short pieces** called **Okazaki fragments**.



C. NUCLEOSOMES

- In **eukaryotes**, DNA is **packaged** with **histone** proteins to create a **compact** structure called a **nucleosome**.



- found in **eukaryotes**
- made up of **DNA wrapped around histones (proteins)**
- histones** are in an **octamer/group of eight**
- are **held together** by another histone/H1
- in **linker region**
- (function is to) help to **supercoil chromosomes/** help in **DNA packing/supercoiling**
- (function is to) **control transcription/gene expression**

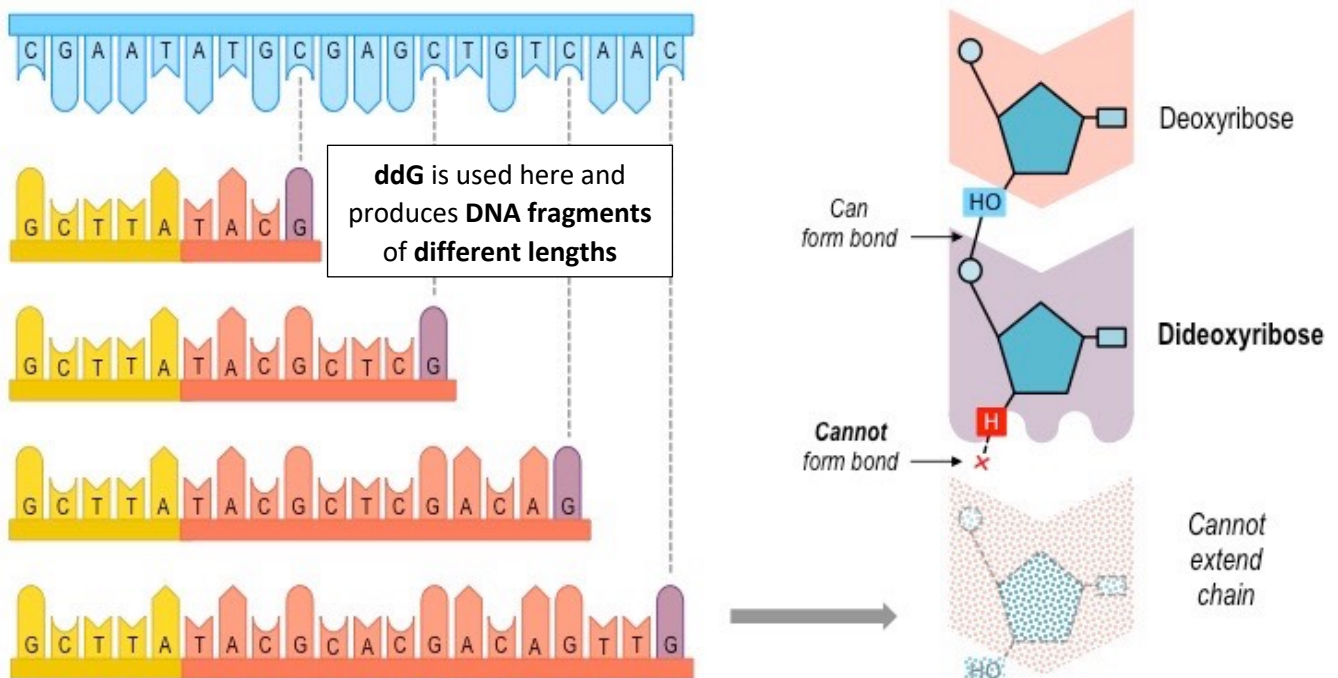
D. FUNCTIONS OF DNA BASE SEQUENCES THAT DO NOT CODE FOR PROTEINS

- Non-coding** DNA base sequences can have **four** main roles:
 - Introns** – involved in **processing mRNA**
 - Coding for tRNA and rRNA** – these are involved in **translation**
 - Controlling transcription/gene expression** – **binding sites** for **proteins** that can **allow** or **prevent** transcription.
 - Telomeres** – **repetitive base sequences** at the **ends** of **chromosomes**, which **prevent** parts of genes here from being **lost** each time the **DNA is replicated**.

E. DNA SEQUENCING BY THE SANGER METHOD

Chain Terminators

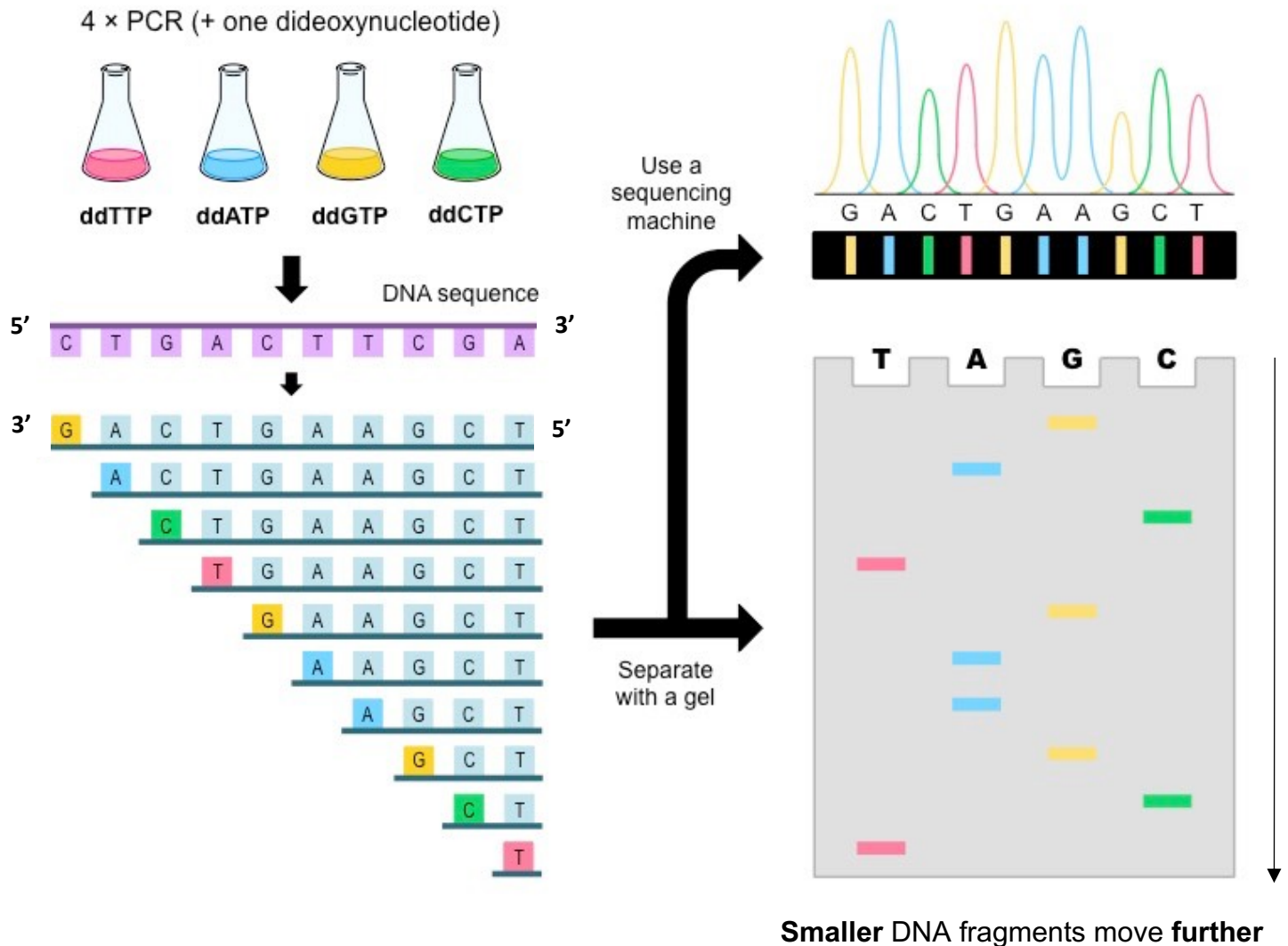
- The Sanger method is used to determine the **DNA base sequence** of a gene.
- Special DNA nucleotides called **dideoxynucleotides (ddNTPs)** are used that act as **chain terminators**.
- **ddNTPs** contain the sugar **dideoxyribose**, instead of the usual sugar of deoxyribose.
- There are **four** types of **ddNTP**: ddA, ddT, ddC or ddG.
- When **ddNTPs** attach to the growing DNA chain, they **stop it from growing**.



Mixing

- Four separate mixes are set up, each containing **normal nucleotides** plus **one** type of **dideoxynucleotide** (ddA, ddT, ddC or ddG).
- The DNA fragments produced will **vary in length**, depending on **how far replication got to** before a **dideoxynucleotide** was **added** to the end of a chain.
- A typical PCR will generate over 1 billion DNA molecules, so each PCR mix should generate **all the possible terminating fragments** for that **specific base**.

Separating the DNA fragments by gel electrophoresis



The **newly** made DNA strand is made from **5' → 3'**

But this is **complementary** to the **original** DNA strand

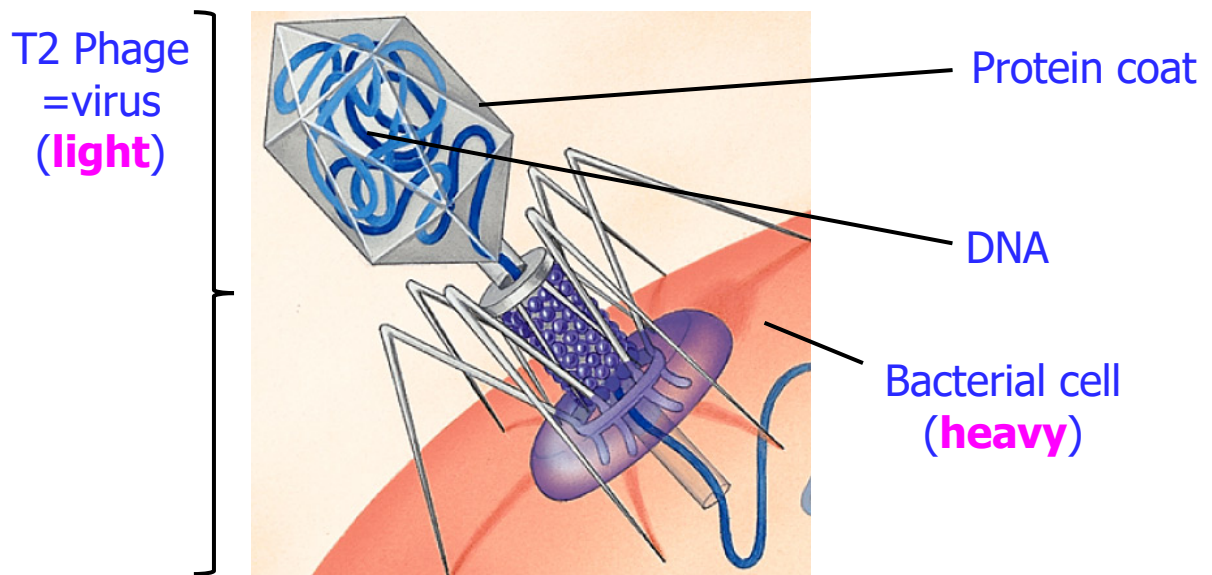
The **first** base of the **new complementary** strand must be the **smallest** DNA fragment

- The gel is read from **bottom** to **top**.
- (So) base sequence of **new complementary** DNA strand is **5' T C G A A G T C A G 3'**
- The two DNA strands are **antiparallel**.
- (So) base sequence of **original** strand must be **5' C T G A C T T C G A 3'**

F. HERSHEY & CHASE EXPERIMENT

Background

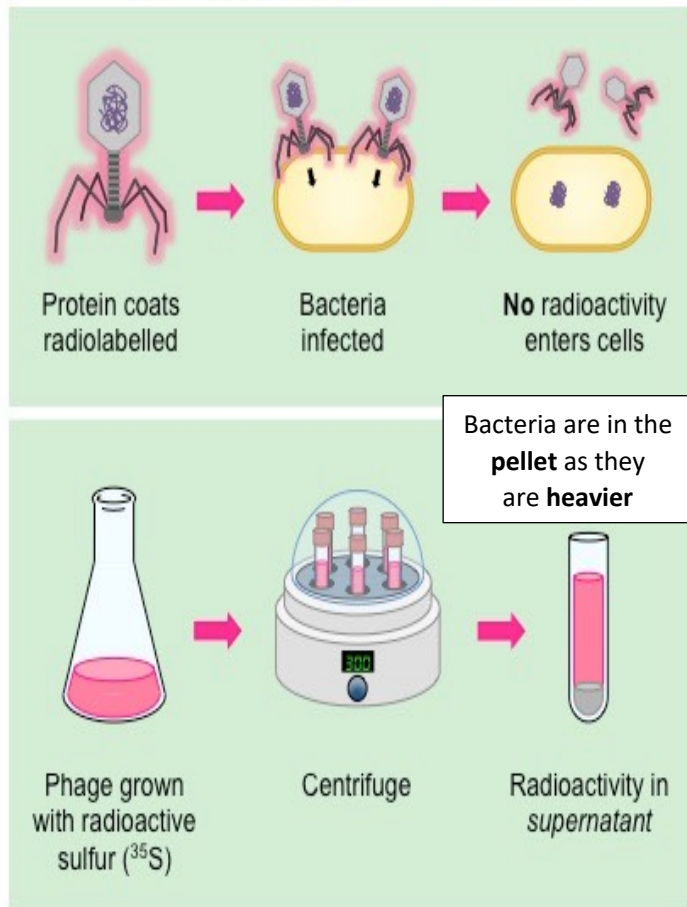
- Showed that **DNA**, rather than protein, is the **genetic material**.
- Used a **virus** (T2 phage) that infects bacteria.
- This virus contains **DNA** inside a **protein coat**.



- This virus **injects** its **genetic material** into bacteria and this is used to make **more copies of the virus**.
- They used two **radioactive** isotopes, which can be **detected**:
 - ^{35}S (found in **protein** but not in DNA)
 - ^{32}P (found in **DNA** but not in protein).
- **Bacteria** are **heavier** than viruses.

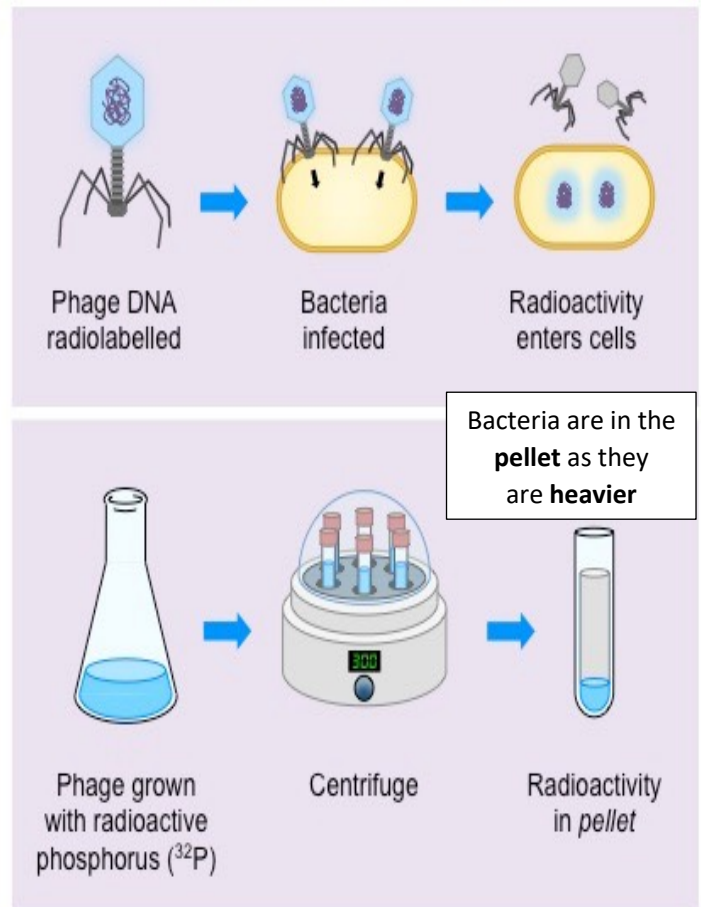
What They Did & Found Out

Experiment 1: Testing Proteins



Conclusion: Proteins are **not** genetic material

Experiment 2: Testing DNA



Conclusion: DNA is the genetic material

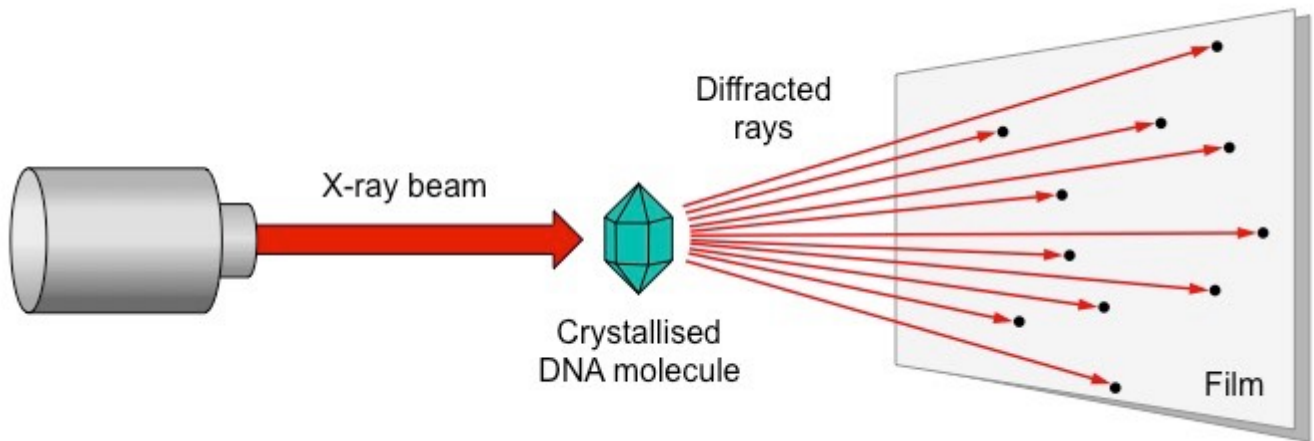
- Virus **protein coats** were labelled with **radioactive ^{35}S**
- **Infected** the bacteria with virus to allow **genetic material** to be **transferred**
- Centrifugation then used to **break attachment, separating** the virus and bacteria
- **Radioactivity detected** in the **virus** (supernatant = fluid above = lighter)
- (So) **protein** had **not** been **transferred** to the bacteria
- (So) **protein** is **not** the **genetic material**

- Virus **DNA** was labelled with **radioactive ^{32}P**
- **Infected** the bacteria with virus to allow **genetic material** to be **transferred**
- Centrifugation then used to **break attachment, separating** the virus and bacteria
- **Radioactivity detected** in the **bacteria** (pellet = pellet at bottom = heavier)
- (So) **DNA** had been **transferred** to the bacteria
- (So) **DNA** is the **genetic material**

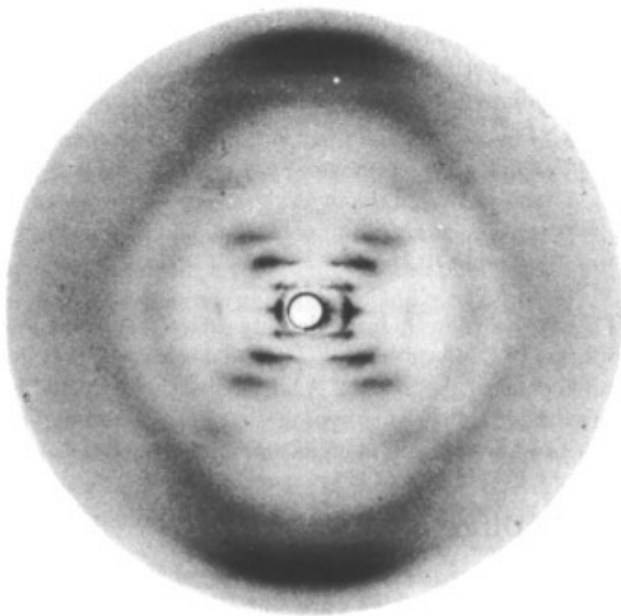
G. X-RAY DIFFRACTION

- Rosalind Franklin and Maurice Wilkins used a method of **X-ray diffraction** to investigate the structure of DNA.

The technique



- From the **scattering pattern** produced by a **DNA molecule**, certain inferences could be made about its structure



1. It is a **double stranded** molecule
2. **Bases** are packed closely together on the **inside** and **phosphates** form an **outer** backbone
3. The molecule **twists** at **regular intervals** (every 34 Angstroms) to form a **helix**
4. There are **10 bases per twist**