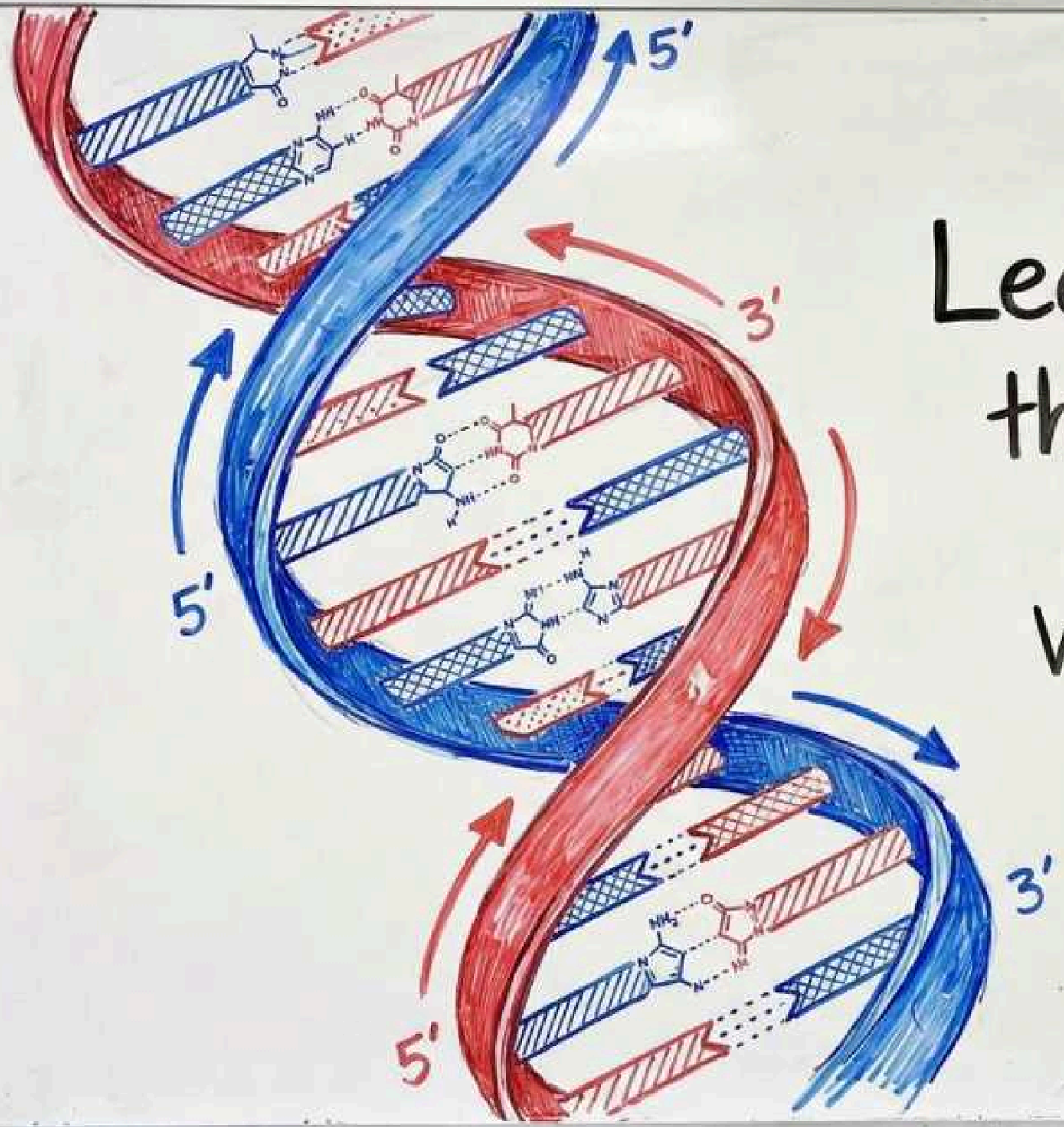
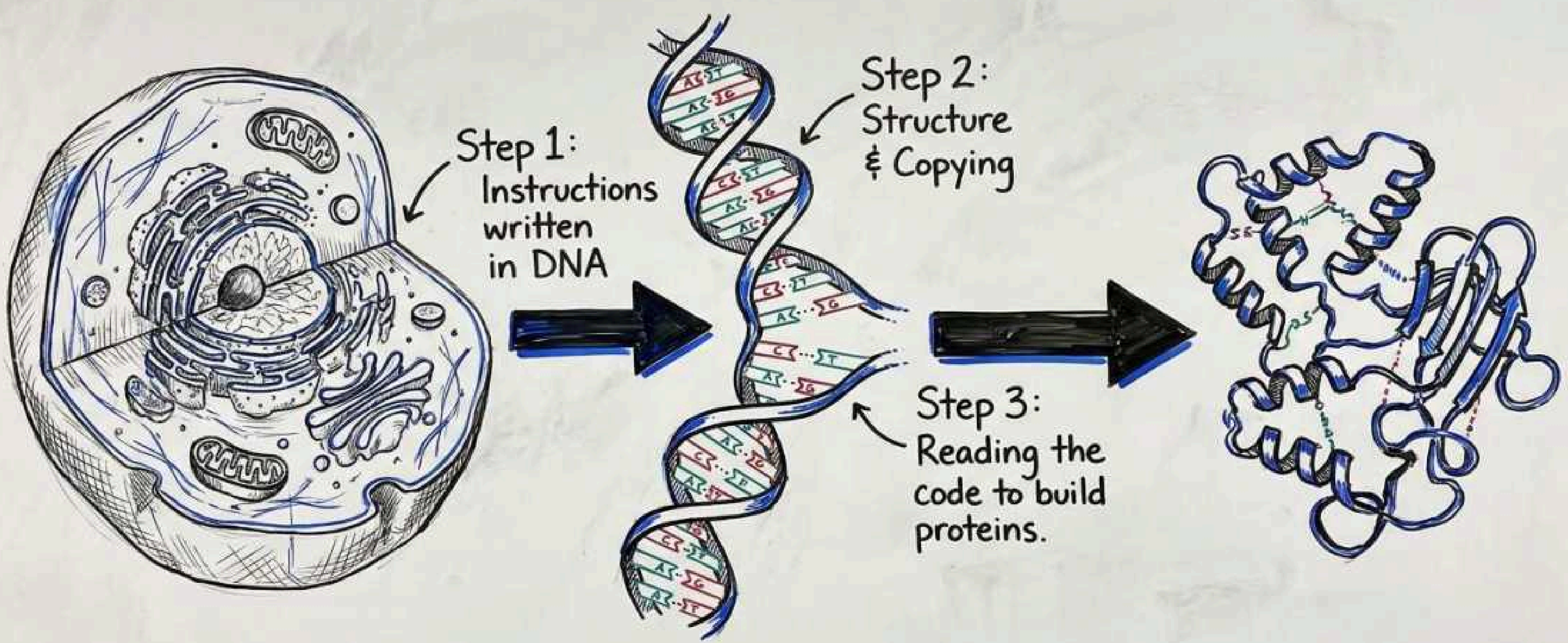
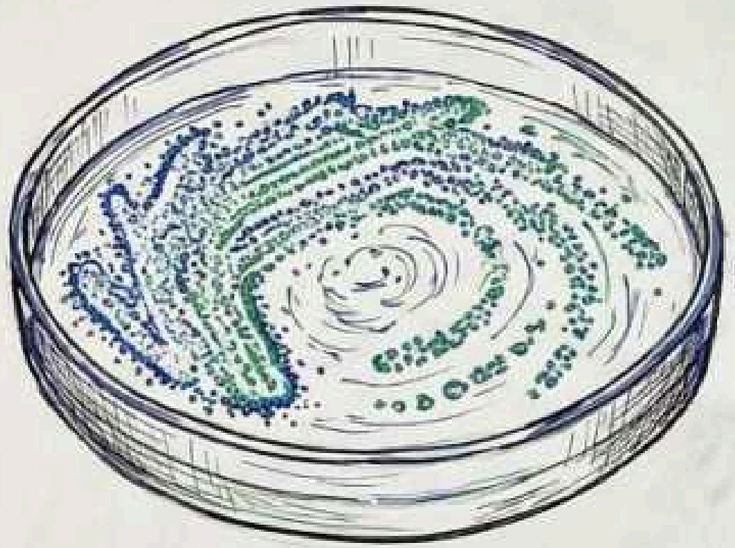


Lecture 3: DNA and the Code of Life

Welcome to Lecture 3.

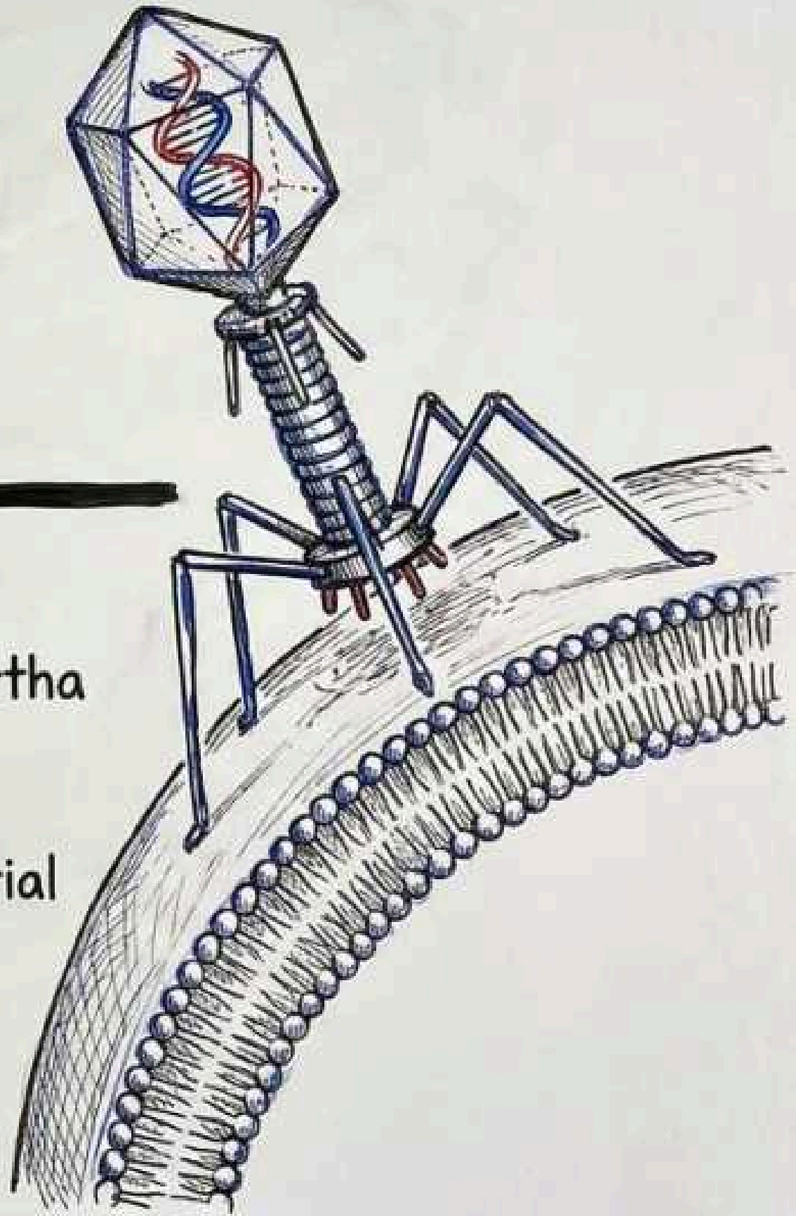


Step 4: Mutations & Gene Regulation



1944

1952

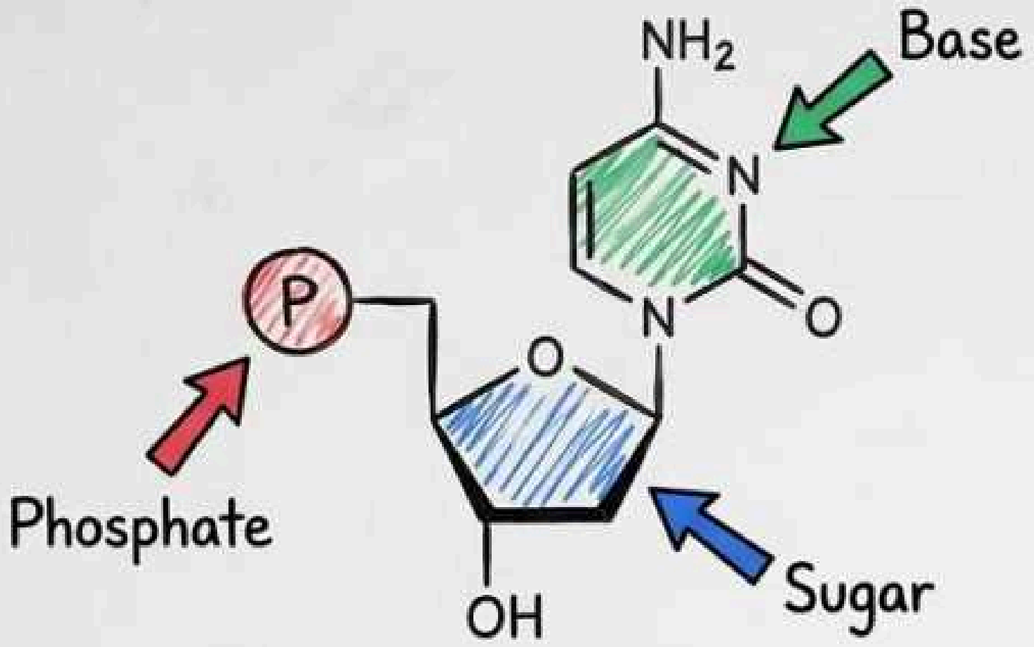


1944: Oswald Avery, Colin MacLeod, & Maclyn McCarty discover DNA transforms bacteria (suspicions previously pointed to proteins due to their variety).

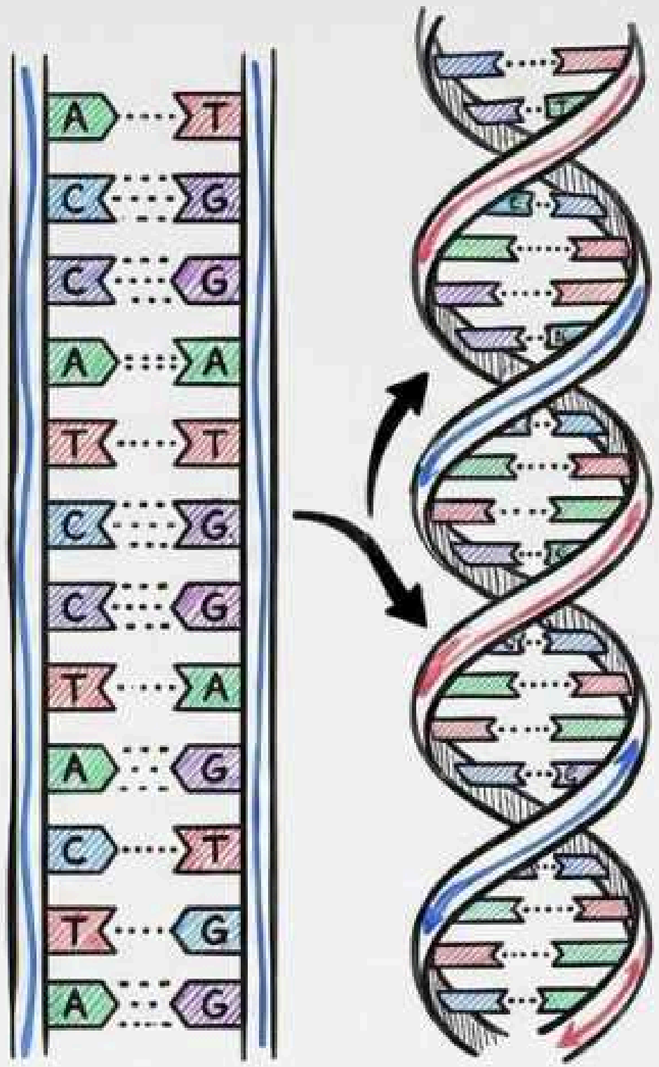
1952: Alfred Hershey & Martha Chase confirm DNA is the heredity material using viruses.

Deoxyribonucleic acid (DNA)

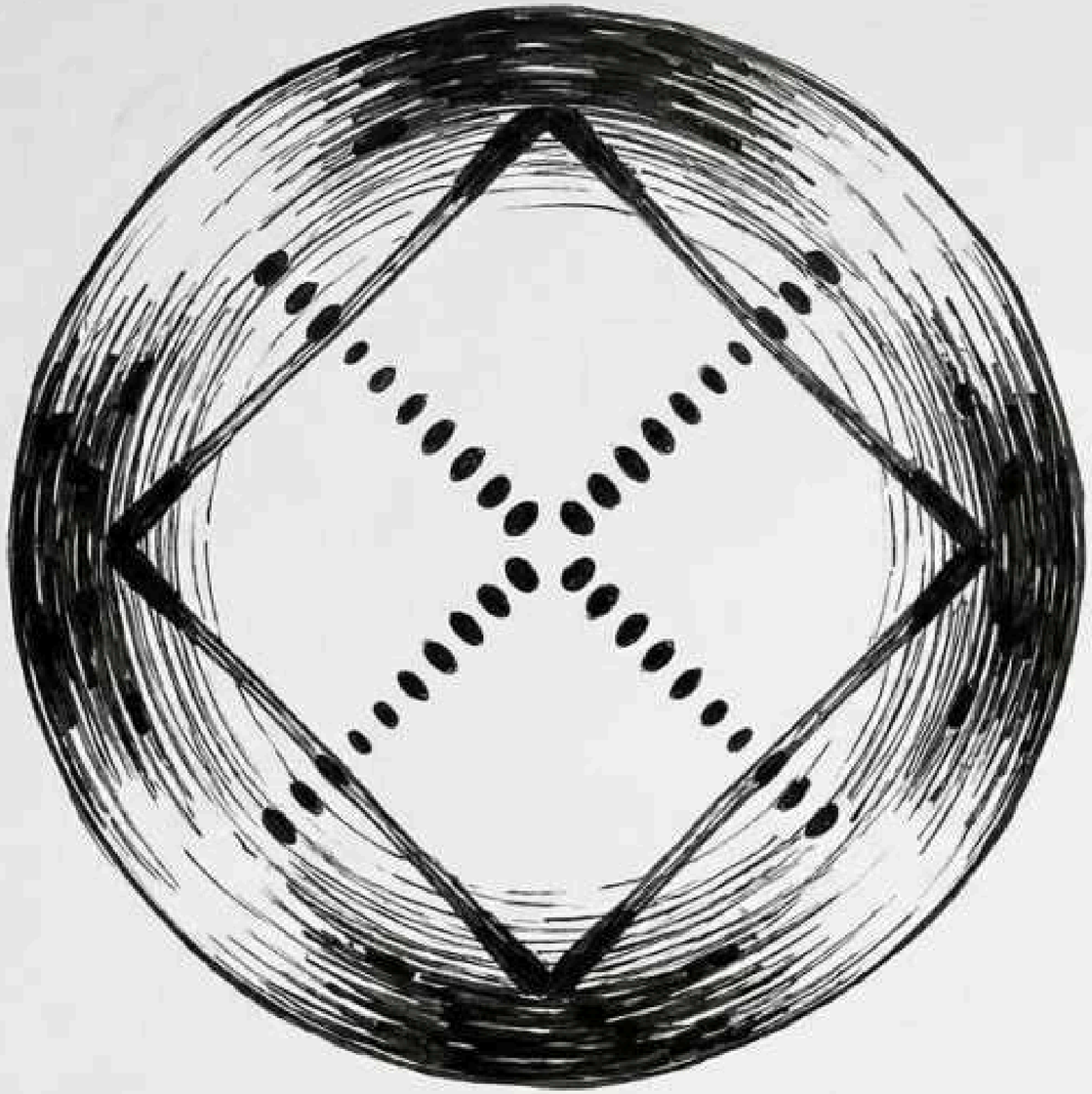
¶ 3.4



Nucleotide = Sugar + Phosphate + Base



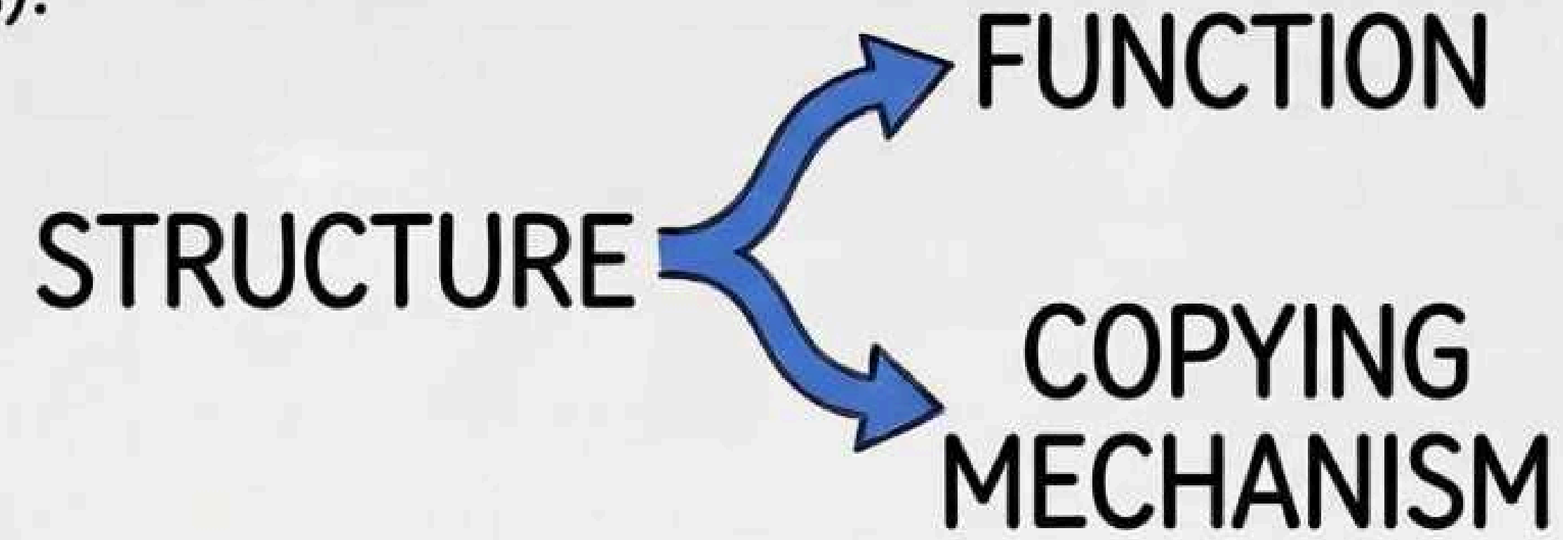
Base Pairing:
Adenine (A) always pairs with Thymine (T); Cytosine (C) always pairs with Guanine (G).



- 1953 Structure Discovery: James Watson & Francis Crick built the model.
- Critical Data Contributors: Rosalind Franklin (with Raymond Gosling) captured the defining X-ray image; Maurice Wilkins also contributed.
- Historical Note: Franklin died in 1958; historians widely agree her vital credit was long understated.

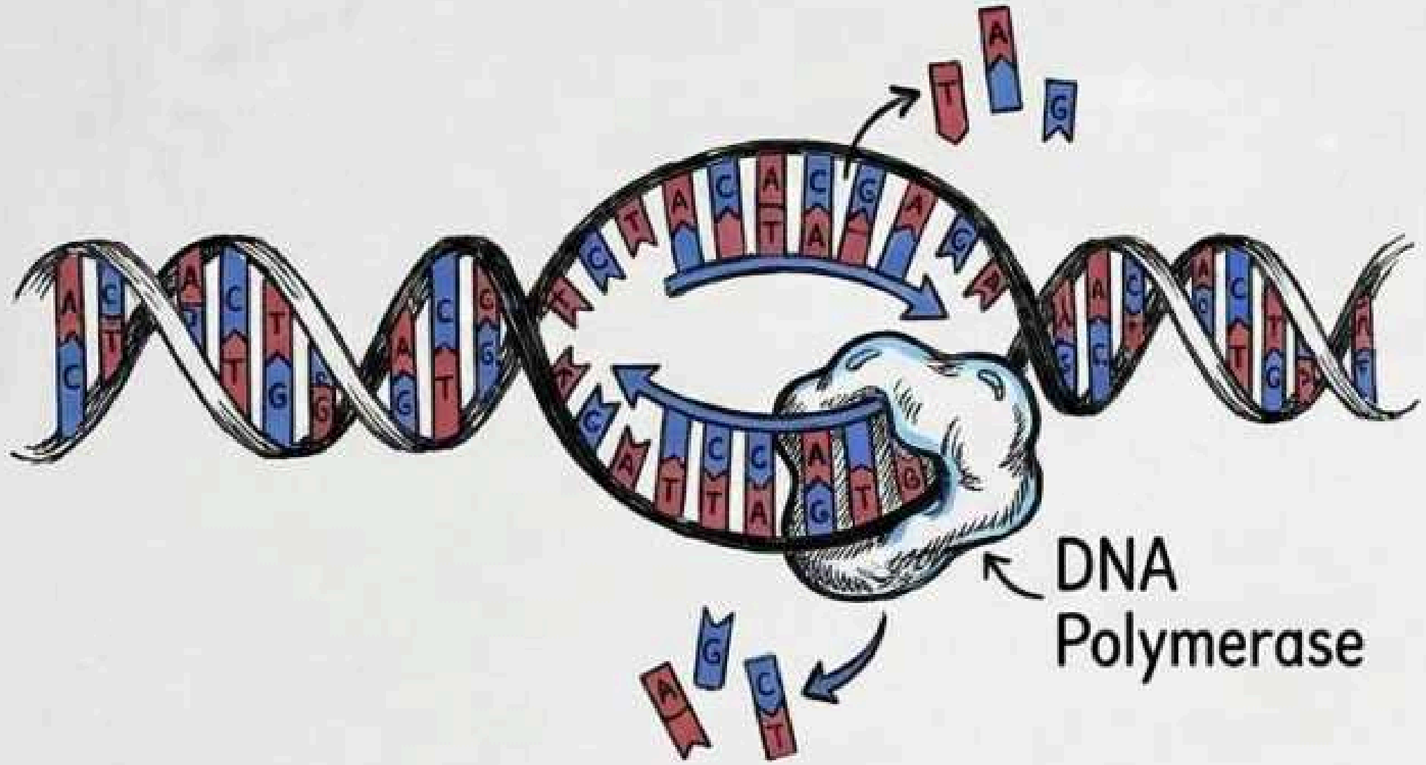
Erwin Chargaff's Rules
(consistent across species):

[A] = [T]
[C] = [G]



The Breakthrough: The double helix structure explained why the amounts matched. As Watson and Crick noted, this specific pairing immediately suggested how genetic material is copied.

Semiconservative Replication:

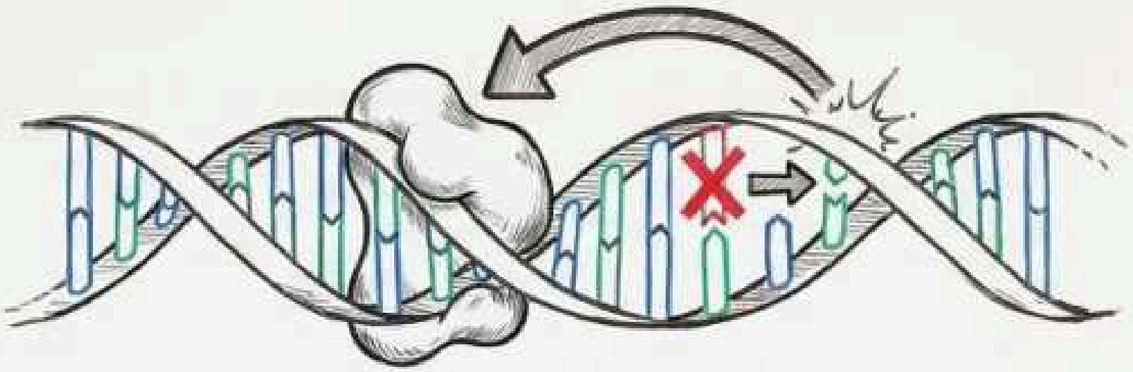


1. The two strands unzip to act as templates.

2. An enzyme (DNA polymerase) adds matching bases.

3. Result: Each new double helix holds one old strand and one new strand.

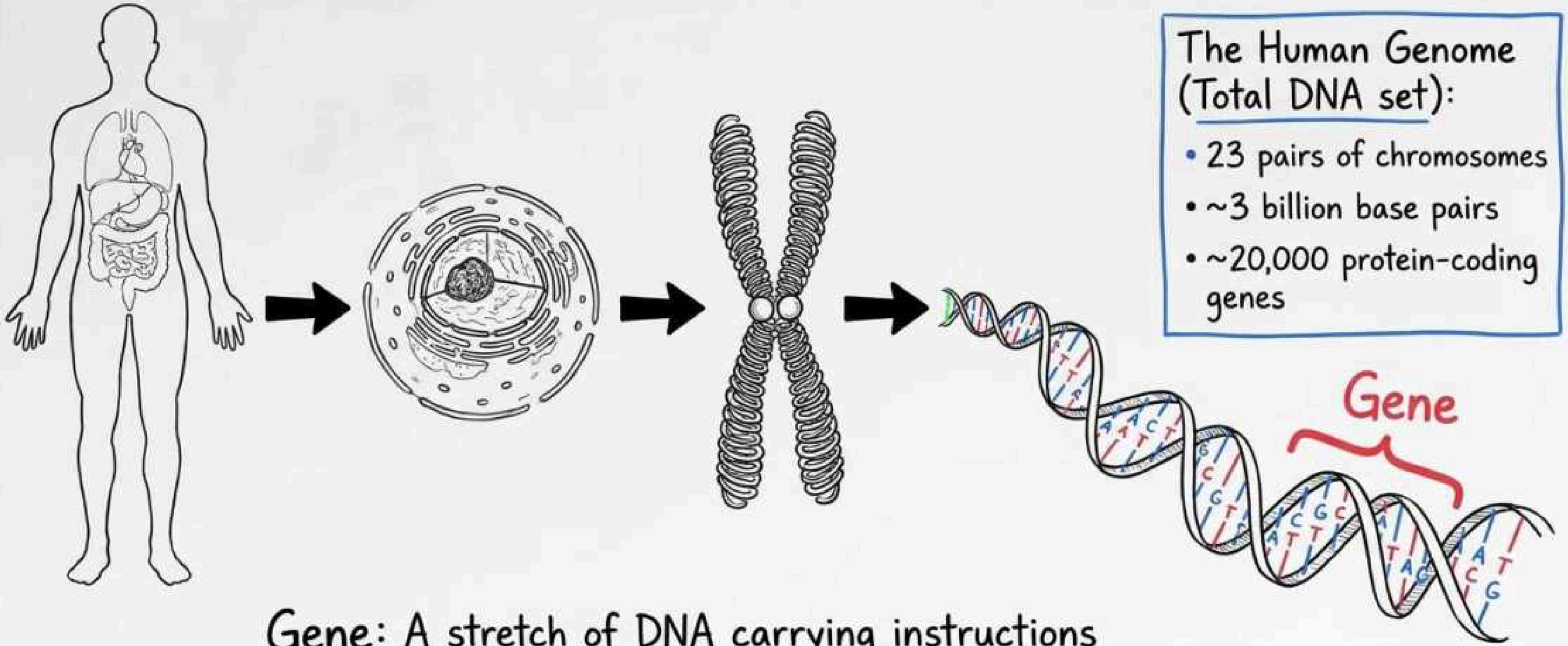
$$\frac{1}{1{,}000{,}000{,}000}$$



Quality Control: Copying errors can harm the cell. DNA polymerase proofreads as it goes, and separate repair systems fix missed mismatches.

Final Error Rate: ≈ 1 in a billion bases copied.

Consequence: The few errors that remain become the raw material of mutation.



The Human Genome (Total DNA set):

- 23 pairs of chromosomes
- ~3 billion base pairs
- ~20,000 protein-coding genes

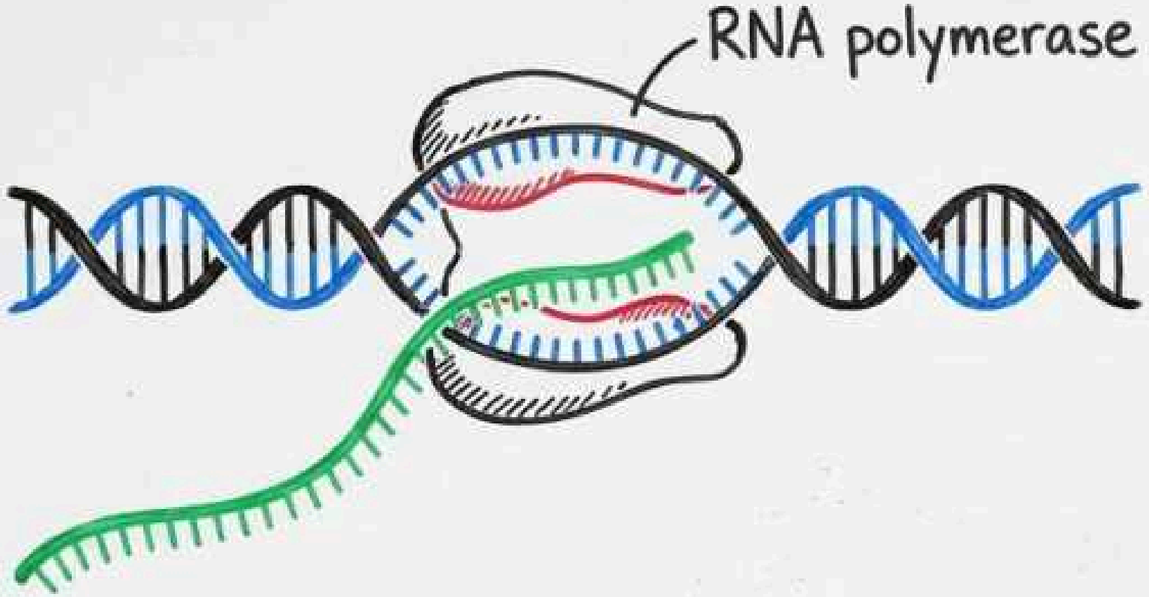
Gene: A stretch of DNA carrying instructions for a protein or functional RNA.

The Central Dogma (Coined by Francis Crick):

The Exception: Retroviruses can copy RNA back into DNA, but the main flow holds for most genes.

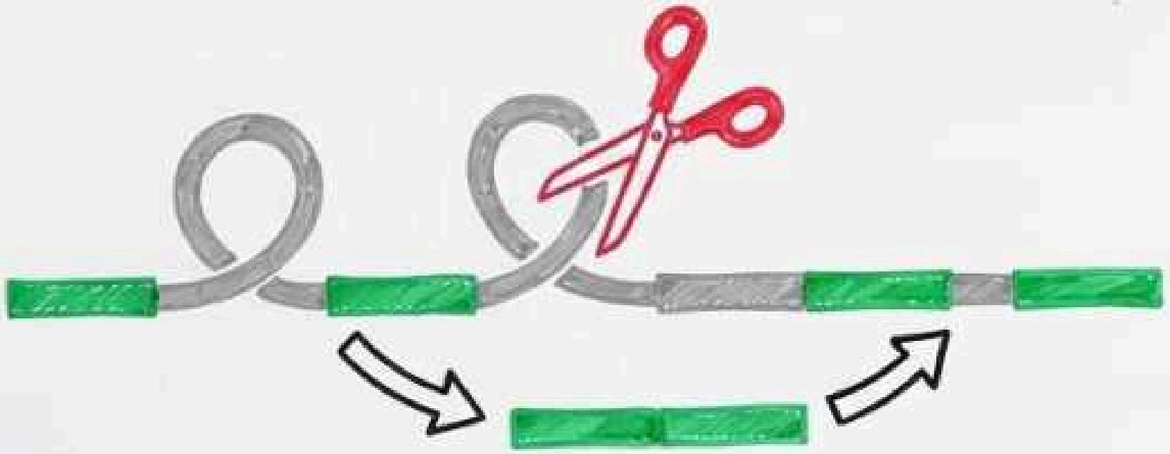


Information flows in a particular direction inside the cell.



Step 1: Transcription
(Reading genes to build mRNA)

Chemical Shift: RNA uses Uracil (U) in place of Thymine (T).



Splicing (in Eukaryotes):
Non-coding stretches (introns) are cut out; coding pieces (exons) are joined.

A-U-G-C-C-A

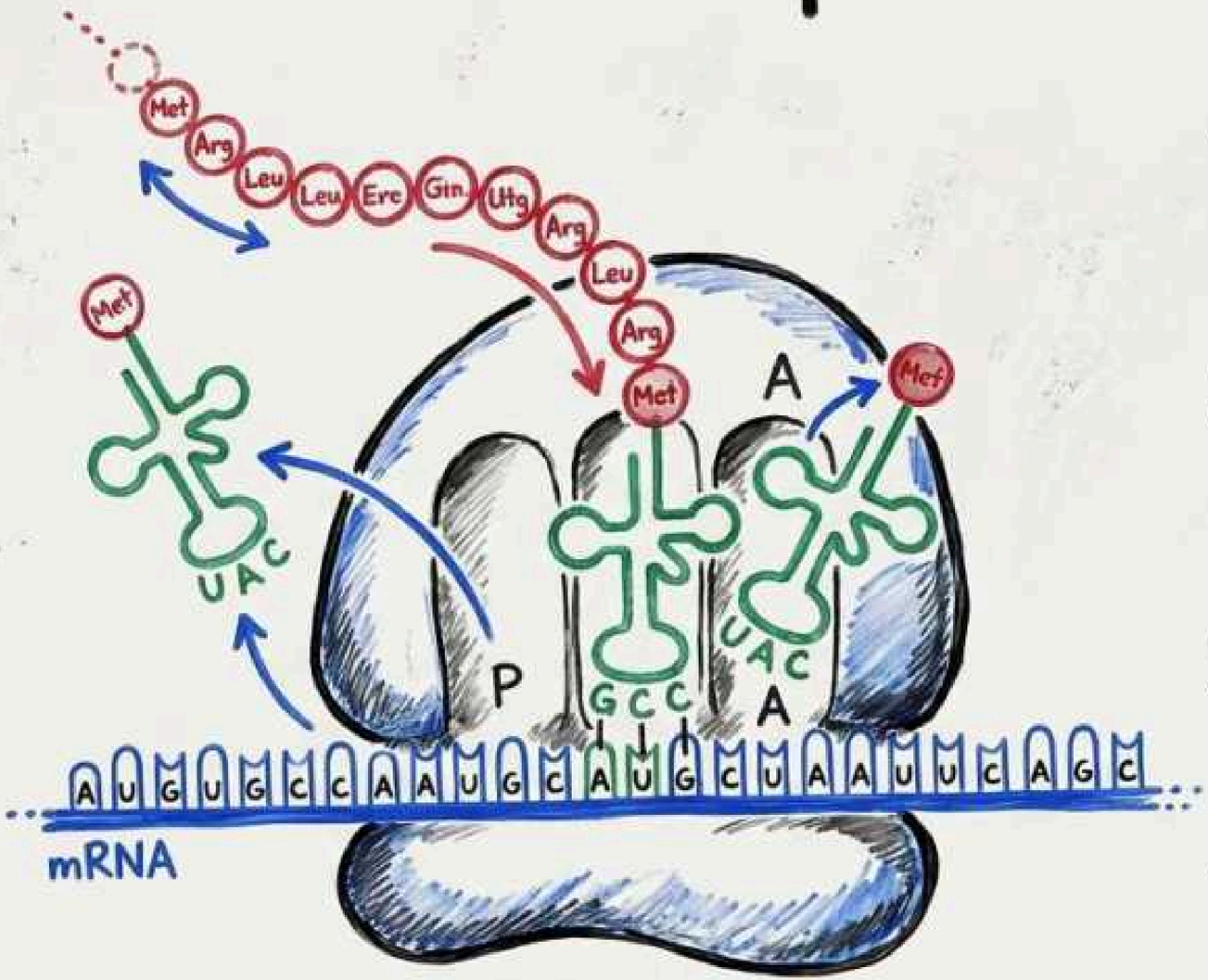
Codons

$4 \text{ bases}^3 = 64$ possible codons.

- Codons: The mRNA is read in groups of 3 bases.
- Because there are only 20 amino acids, most have more than one codon.
- Signals: 1 Start Codon (AUG), 3 Stop Codons.
- Universal: This exact code is shared by nearly all life on Earth.

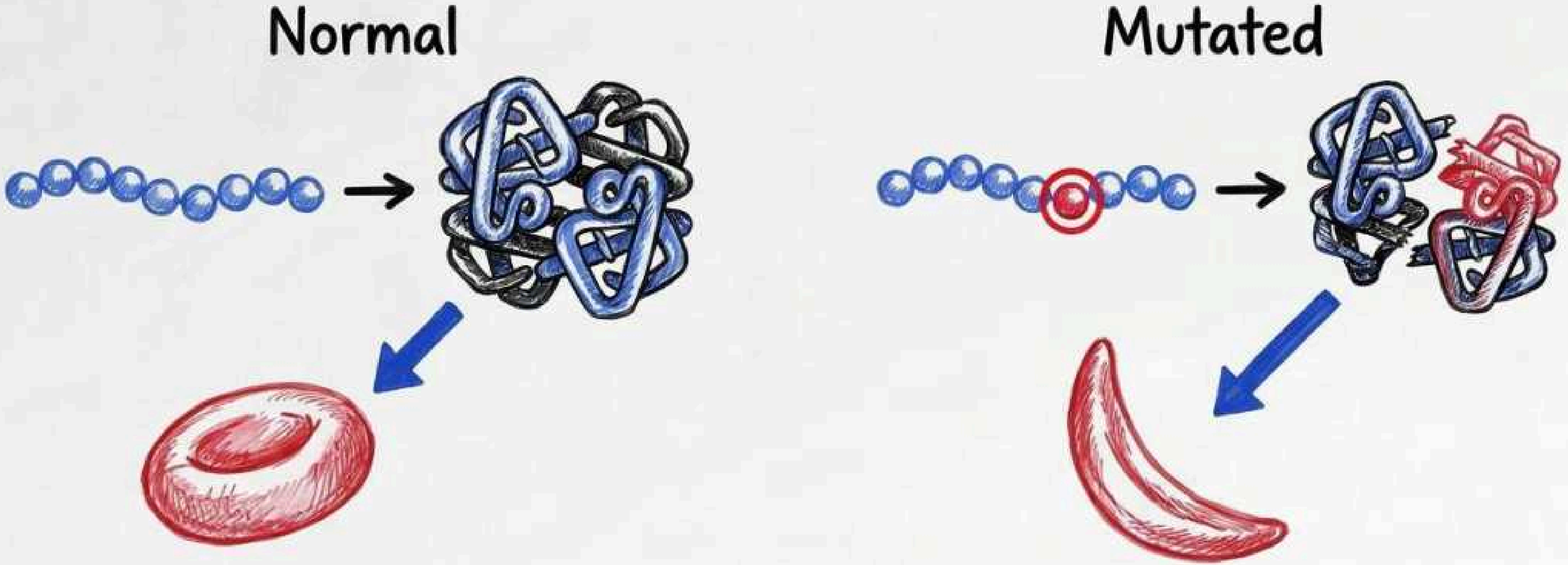
Step 2: Translation

¶ 3.13



1. The ribosome moves along mRNA, reading one codon at a time.
2. Transfer RNA (tRNA) molecules bring the matching amino acids.
3. The ribosome links them into a growing chain.
4. The finished chain releases upon reaching a stop codon.

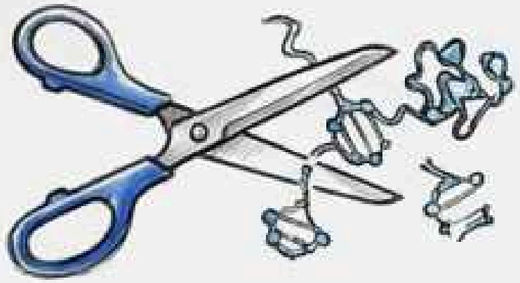
A chain of amino acids folds into a 3D shape; shape determines protein function.



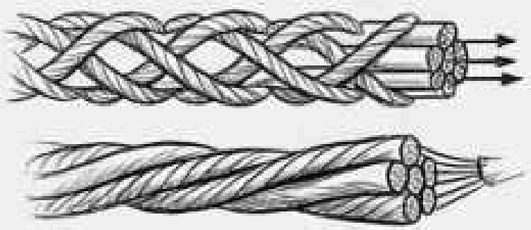
Sickle Cell Disease: A single base change alters just one amino acid in haemoglobin.

Result: The altered shape causes red blood cells to bend into a sickle.

Proteins do most of the work in a cell.
A human cell can make thousands of them.

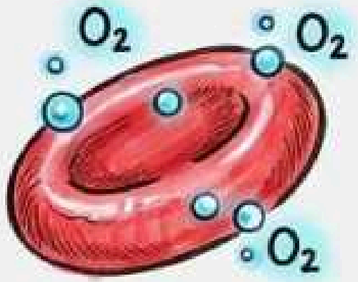


• Enzymes

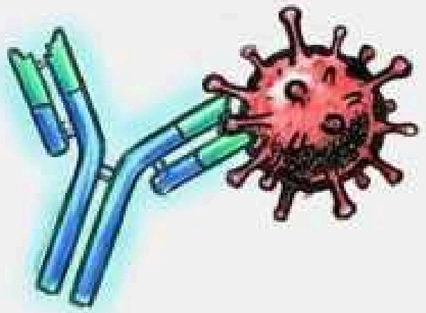


• Structural building blocks
(Collagen in skin)

PROTEINS



• Transporters (Haemoglobin)



• Hormones & Antibodies

The Core Rule: Change the gene → Change the protein → Change the cell, the body, and sometimes the next generation.

Mutations: A change in the DNA sequence.

¶ 3.16

Original Sequence

C-A-T-G-G-A

Substitution: Swaps one base for another.

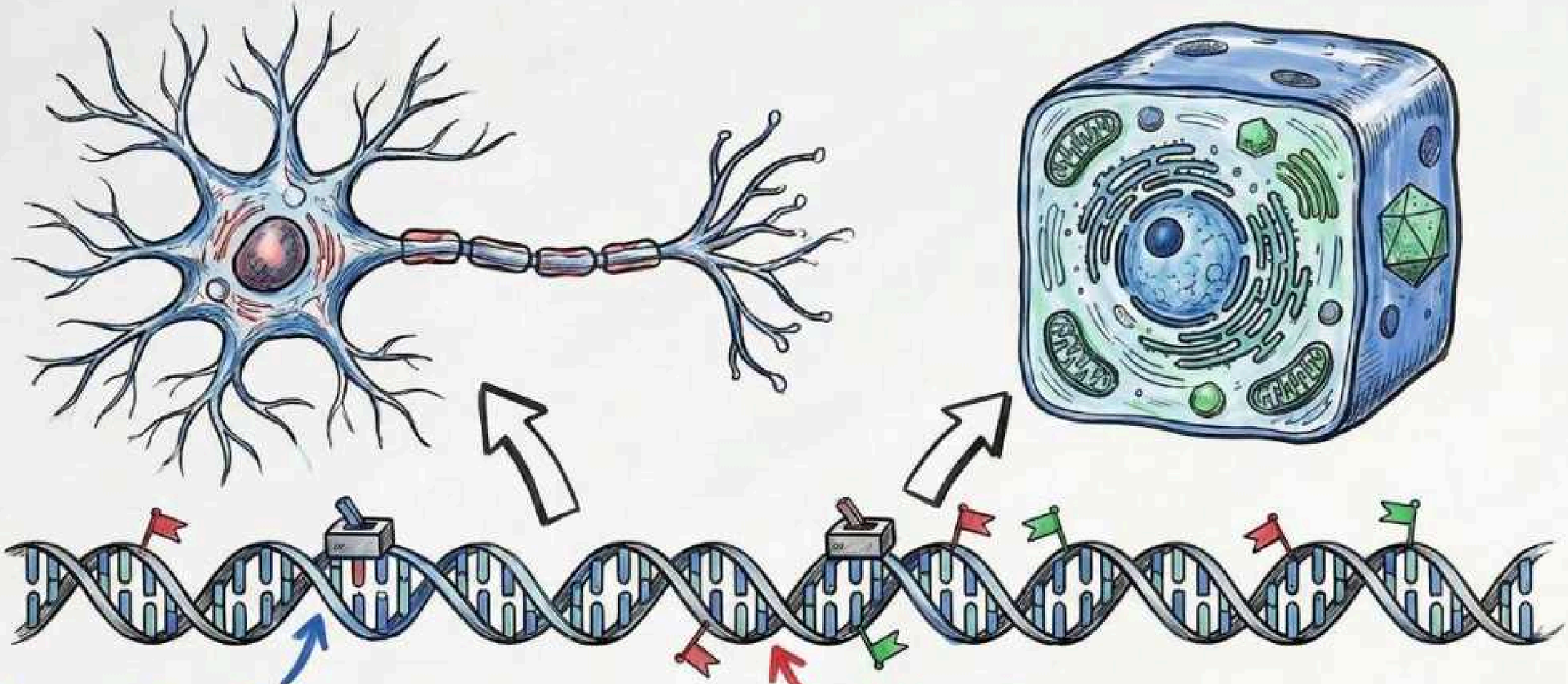
C-A-A-G-G-A

Insertion / Deletion: Adds or removes bases, shifting the whole reading frame.

C-A-T-_-G-A

- **Outcomes:** Many are neutral, some harmful, a few helpful.
- **Causes:** Copying errors, radiation, and chemicals.

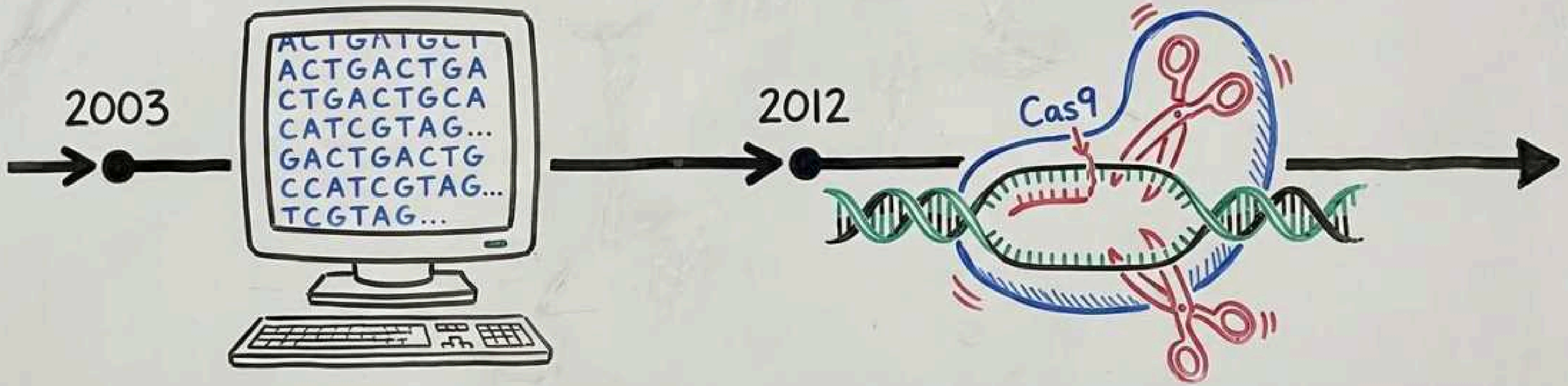
Almost every cell in your body carries the exact same DNA. ¶ 3.17
They look and act completely different because of Gene Regulation.



Transcription Factors: Proteins that physically switch genes on and off.

Epigenetics: Chemical marks directly on the DNA that affect which genes are read.

Our tools for reading and editing DNA have grown incredibly fast.



2003: The Human Genome Project finishes a first reference sequence. Modern sequencing is now cheap and quick.

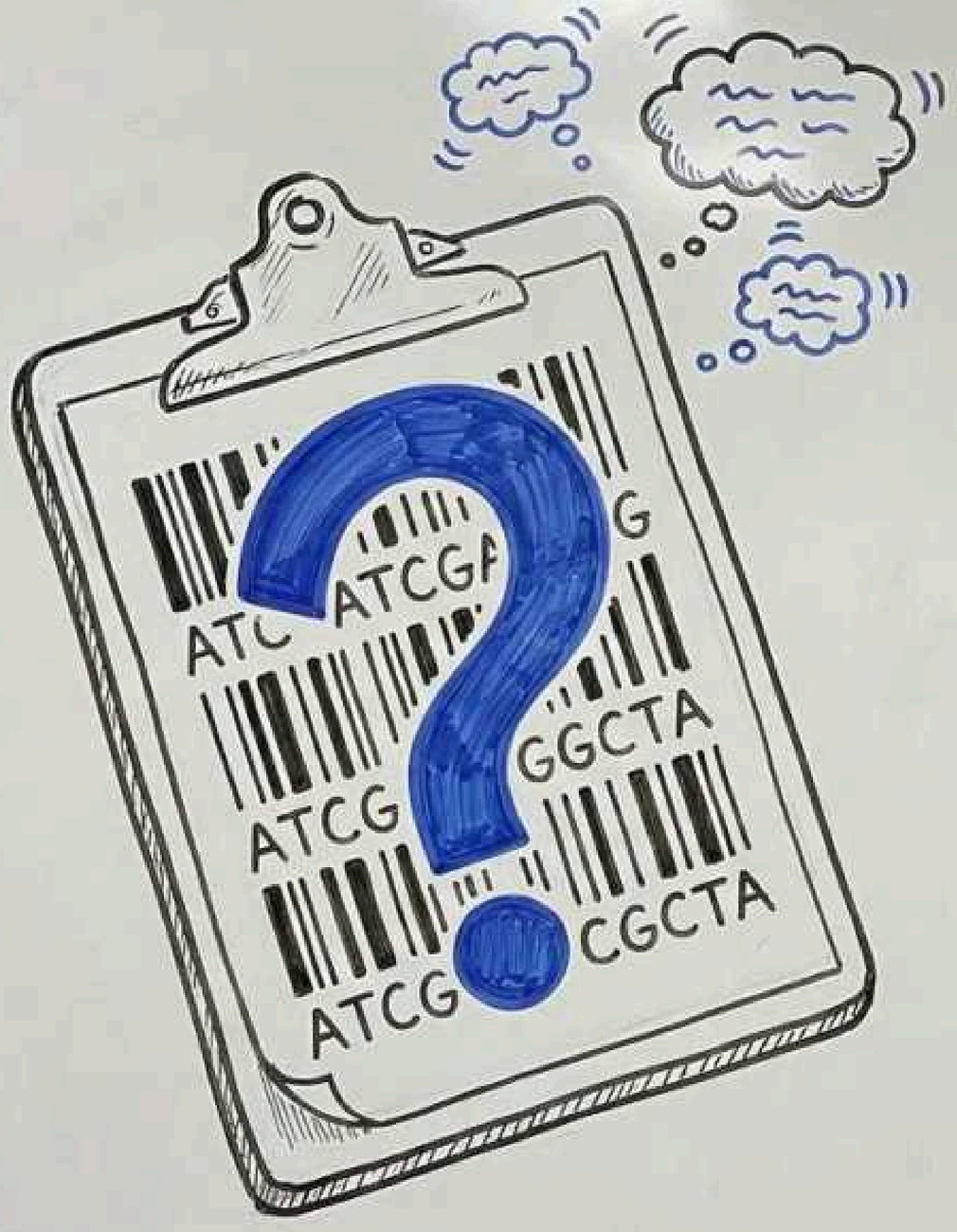
2012: Jennifer Doudna and Emmanuelle Charpentier describe the gene-editing tool CRISPR (work that won the Nobel Prize in 2020).

- Genes ≠ Destiny.

Many Genes + Diet + Upbringing + Chance = Complex Traits



- While a few conditions follow directly from a single gene, a gene usually just raises the odds without guaranteeing an outcome.
- Most complex behaviours and traits arise from multiple factors working together. Be wary of reductionist headlines.



The Takeaway Question:

Imagine a test could read your genome and list your risks for diseases:

1. What would you **want to know**?
2. **Who** should be allowed to see the results?
3. **How** would you decide?

(There is no single right answer).



Coming up in Lecture 4:

Following **genes** from **parents** to **children**, starting with a monk and his pea plants.