

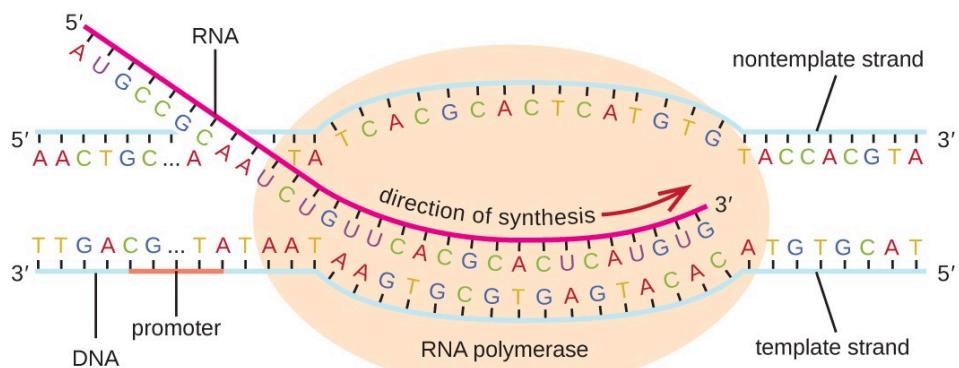
## Genes and Proteins

📌 What is a Gene? [https://www.youtube.com/watch?v=\\_Zyb8bpGMRO](https://www.youtube.com/watch?v=_Zyb8bpGMRO)

- Originally = **unit of heredity** (Mendel).  
Now = DNA sequence that can be replicated, transcribed, translated, mutated.  
Genes are arranged on chromosomes.

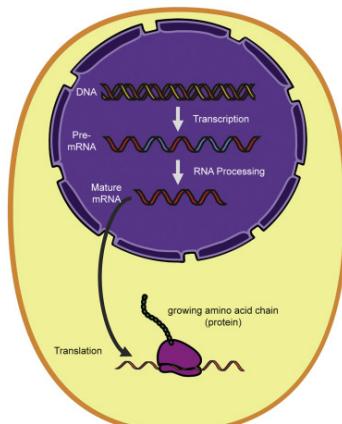
**Transcription:** the process by which a cell makes an RNA copy of a piece of DNA.

**RNA Polymerase:** RNA polymerases are DNA-dependent because they use a DNA template to synthesize RNA. Just like DNA polymerase uses a DNA strand to create a complementary strand, RNA polymerase uses the DNA template to create a complementary RNA strand. The RNA is synthesized in the  $5' \rightarrow 3'$  direction, with uracil (U) replacing thymine (T) in base pairing.

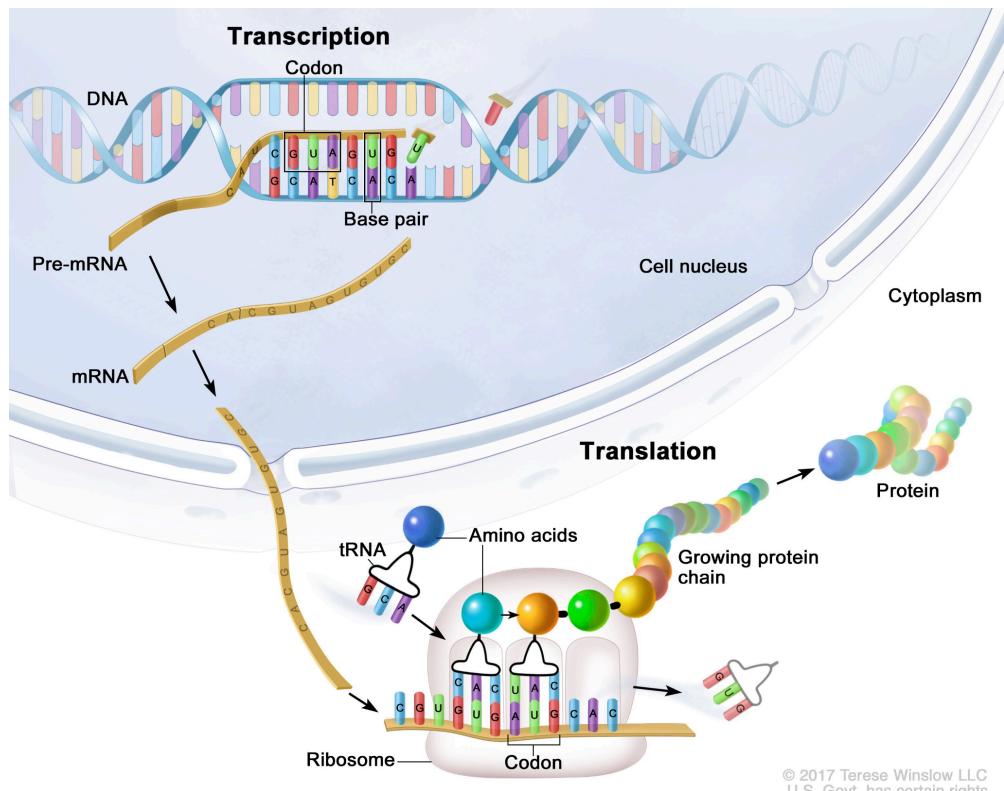
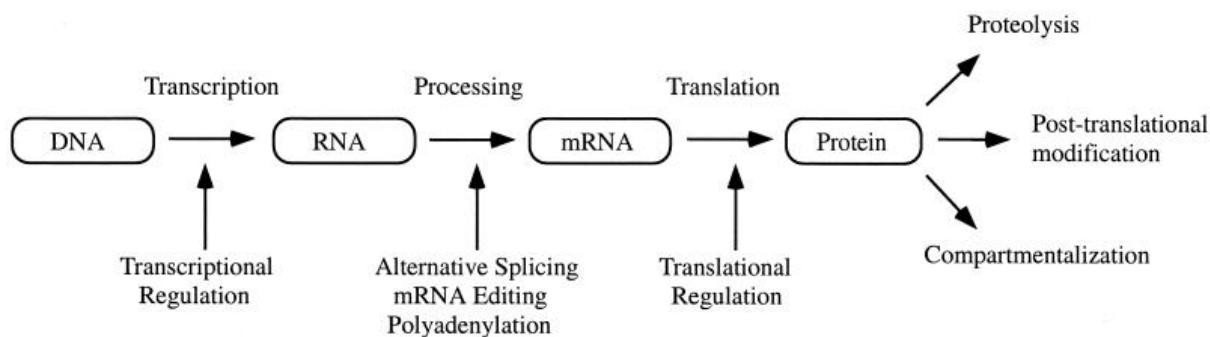


**Central Dogma is not this simple!**

The "central dogma" of molecular biology, first proposed by Francis Crick in 1957, explains how genetic information flows from DNA to RNA to proteins. In 1960, scientists discovered the first RNA polymerase activity in bacteria and rat liver cells. A year later, mRNA was identified as the link between DNA and protein, followed by the discovery of tRNA (adaptor molecule) and rRNA (ribosomal RNA).



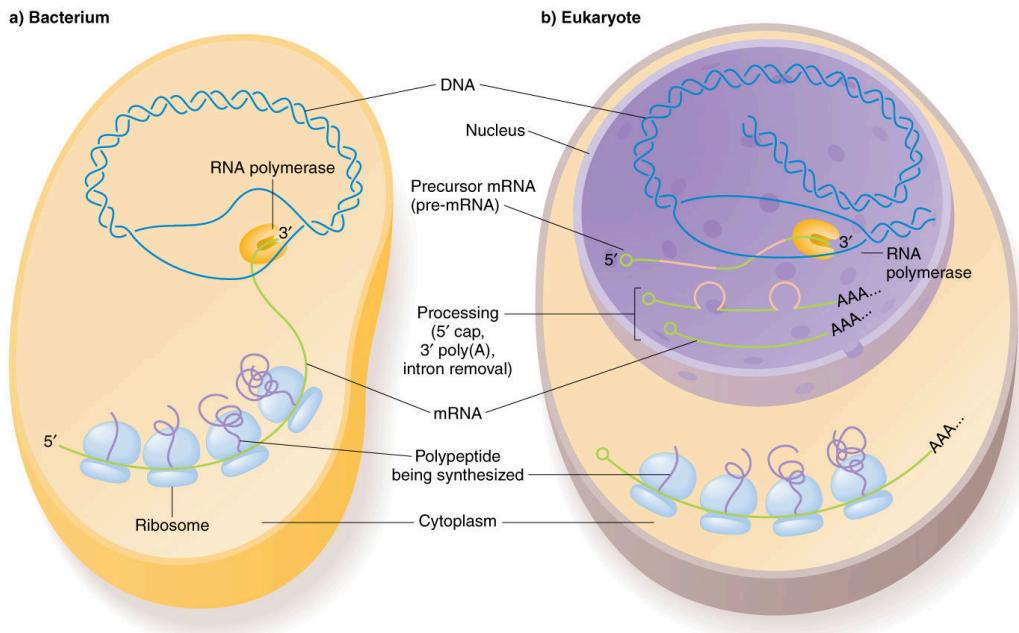
However, how RNA was made remained unclear until Robert Roeder's groundbreaking work in 1969, where he identified three distinct mammalian RNA polymerases. His research paved the way for understanding how different types of RNA are produced. +++++++



Transcription and translation are processes that turn DNA into proteins. DNA and RNA are made up of four building blocks (C, A, T/U, and G).

- **Transcription:** In the cell's nucleus, a gene in DNA is copied into mRNA.
- **Translation:** The mRNA moves to the cytoplasm, where ribosomes read the mRNA. tRNA brings amino acids to the ribosome, matching its sequence to the mRNA. The ribosome links the amino acids together to form a protein. Once all amino acids are joined, the protein is complete and released.

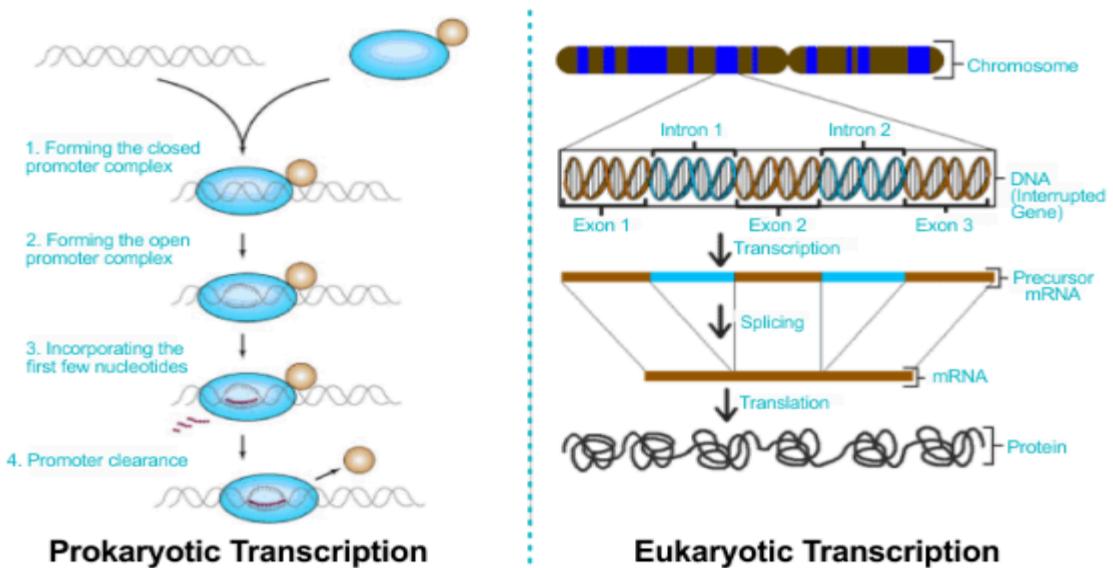
#### Transcription in Prokaryotes vs Eukaryotes



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Feature	Prokaryotes	Eukaryotes
Location	Cytoplasm	Nucleus
Main Enzyme	One RNA polymerase	RNA polymerase II
Promoter Recognition	-35 and -10 regions	TATA box
Helpers	$\sigma$ -factor	Multiple transcription factors (TFIIA, B, D, E, F, H)
Termination	Rho-dependent or independent	CPSF/CSTF recognize poly-A signal
RNA Product	mRNA (ready for translation)	pre-mRNA $\rightarrow$ processed into mature mRNA

## PROKARYOTIC TRANSCRIPTION VS. EUKARYOTIC TRANSCRIPTION



### Transcription in Prokaryotes:

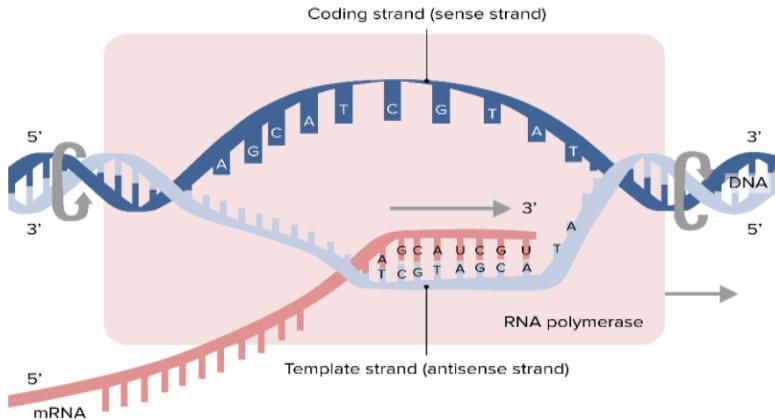
#### 1. Initiation: Transcription Bubble

- Topoisomerase relaxes both positive (before replication bubble) and negative supercoiling (after) of DNA. RNA polymerase follows the template strand around the duplex, so that it can avoid any supercoiling of DNA
- RNA Polymerase binds to the promoter region on the DNA (in E. coli, it recognizes -35 and -10 regions).
- The RNA polymerase unwinds the DNA to form an "open complex."
- It starts making a short RNA. If it makes more than 10 nucleotides, it leaves the initiation phase and continues.



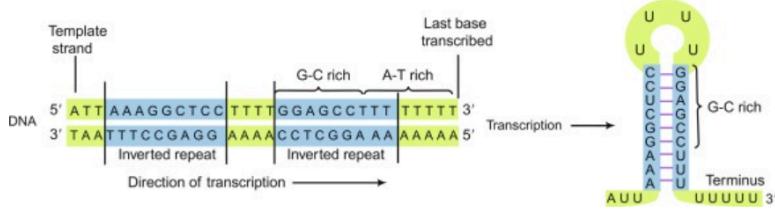
#### 2. Elongation:

- After the RNA is long enough, the σ-factor is released, and RNA polymerase moves along the DNA to make the RNA in the 5' to 3' direction.
- The RNA exits the polymerase.

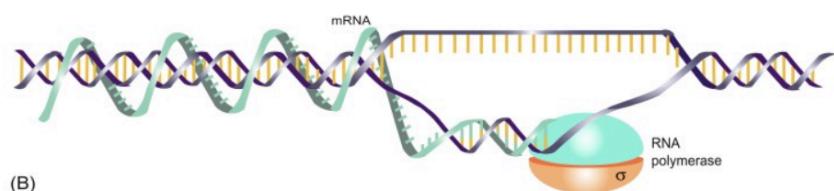
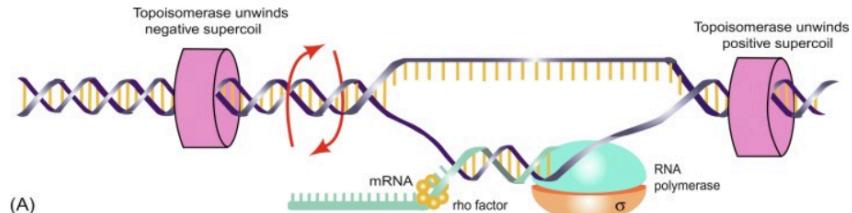


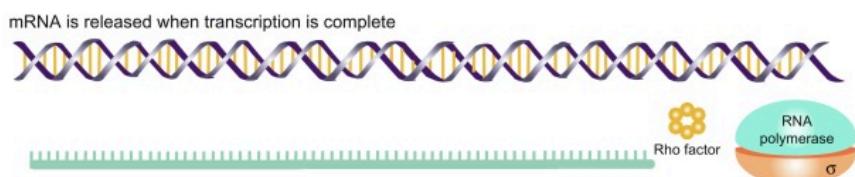
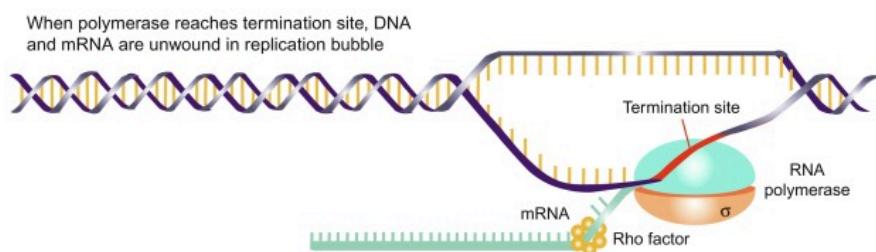
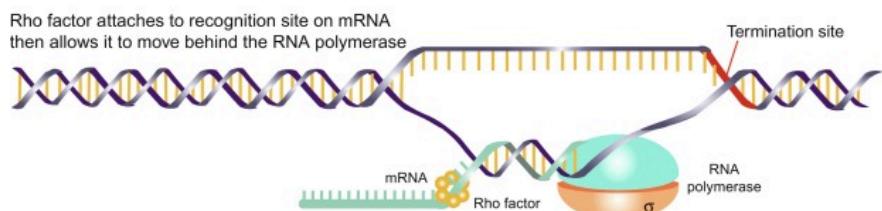
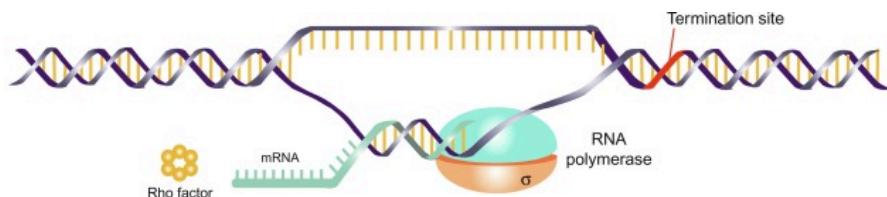
### 3. Termination:

- **Rho-Independent:** The RNA forms a hairpin structure due to a GC-rich sequence, causing it to detach from the DNA and stop transcription.



- **Rho-Dependent:** The Rho protein moves up the RNA, reaches the RNA polymerase, and causes it to release the RNA, stopping transcription.





### Transcription in Eukaryotes:

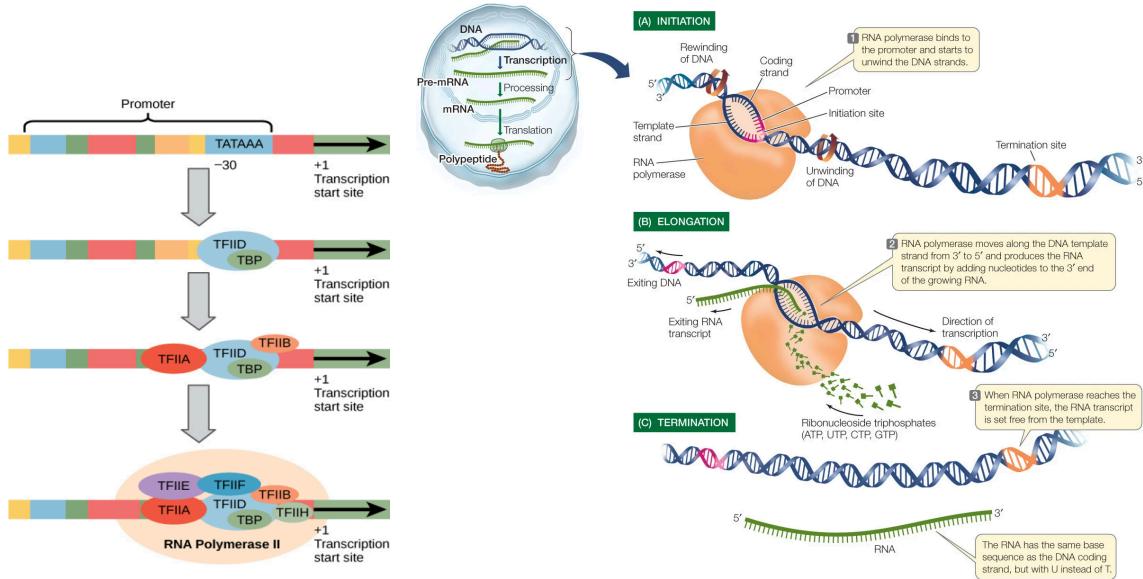
#### 1. Steps of Transcription: **Initiation:**

The TATA-binding protein (TBP) binds to the TATA element in the promoter region of the gene.

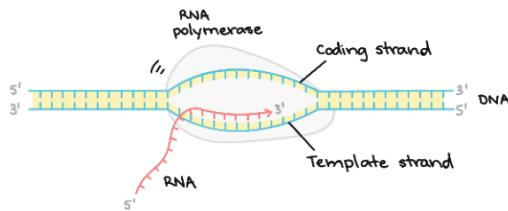
Transcription factors (TFs) bind sequentially to the promoter and form the pre-initiation complex: TFIID binds first, followed by other factors:

- TFIID stabilizes TFIID binding,
- TFIIB recruits TFIIE,
- TFIIE recruits TFIIF,
- TFIIF acts as a helicase, unwinding the DNA.
- TFIIF helps recruit RNA polymerase II to the promoter.

In eukaryotes, promoter regions are located upstream (towards the 5' end) of a gene and consist of a core promoter, a proximal promoter, and can include distal promoter elements. The core promoter contains the **transcription start site (TSS)** and binding sites for RNA polymerase and general transcription factors, with the **TATA box** typically positioned around 25–35 base pairs upstream of the TSS.

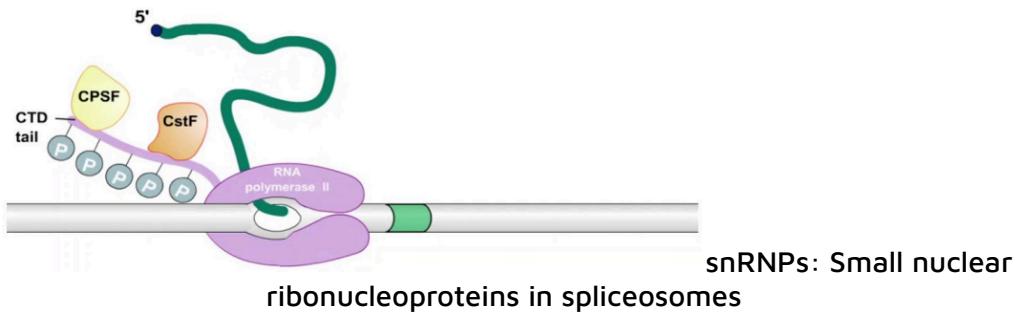


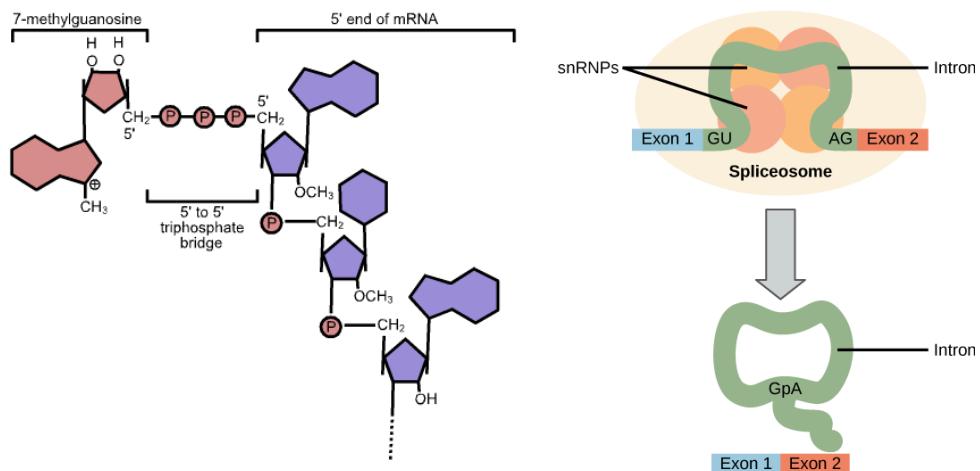
- **Elongation:** After initiation, RNA polymerase is released from transcription factors. The pre-mRNA is synthesized in the 5' to 3' direction.



- **Termination:**

- As RNA polymerase II reaches the end of the gene, two protein complexes (CPSF and CSTF) attached to the C-terminal domain (CTD) recognize the poly-A signal in the RNA.
- CPSF and CSTF help recruit other proteins to cut the RNA and end transcription.





Enzyme	Transcription Product	Minimum Required Initiation Factors
RNA Pol I (14 subunits)	rRNA 45S	SL1*/TIF1B/core factor TIF1A/RRN3 UBF/UAF
RNA Pol II (12 subunits)	mRNA snRNA miRNA	TFIIA TFIIB TFIID* TFIIE TFIIF TFIIH
RNA Pol III (17 subunits)	tRNA rRNA 5S small RNAs	TFIIC TFIIB*

## RNA Transcription and Processing

### 1 RNA Synthesis (Transcription)

- Only one DNA strand (the *template strand*) is copied by RNA polymerase.  
The result is a single-stranded RNA molecule.  
Transcription stops when RNA polymerase reaches a stop signal at the end of the gene.  
The first RNA made is called pre-mRNA (or hnRNA).

### 2 Error Rate

- RNA polymerase makes more mistakes than DNA polymerase.  
**Error rate: about 1 mistake per 100,000 bases transcribed.**

### 3 Post-Transcriptional Modifications

After transcription, pre-mRNA is modified in the nucleus to form mature mRNA that can be used in translation.

#### a. 5' Cap

- A methylated guanine (7-methylguanosine) is added to the 5' end.  
Purpose: Protects mRNA from breakdown and helps it attach to the ribosome.

#### b. 3' Poly-A Tail

- A chain of 50–250 adenine (A) bases is added to the 3' end.  
Purpose: Increases stability and helps mRNA move out of the nucleus.

#### c. RNA Splicing

- Introns (non-coding regions) are removed.  
Exons (coding regions) are joined together.  
The result is a continuous coding sequence — the mature mRNA.

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### 4 Alternative Splicing

- Different combinations of exons can be joined.  
This allows one gene to make different mRNAs and proteins.  
Seen in many organisms — even viruses like HIV use it.

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### 5 Role of Introns

Introns are not just “junk DNA” — they have important functions:

Function	Description
Gene Regulation	Help control how often and how much a gene is expressed.
mRNA Stability	Affect how stable and long-lasting an mRNA molecule is.
Alternative Splicing	Allow one gene to create many versions of mRNA (and proteins).
Genome Organization	Help organize genes and regulate transcription.
Stress Response	May slow down or control splicing during stress to help cells survive.
Evolutionary Role	May have helped in the evolution of complex organisms and traits.

- [https://bio.libretexts.org/Bookshelves/Introductory\\_and\\_General\\_Biology/General\\_Biology\\_\(Boundless\)/15%3A\\_Genes\\_and\\_Proteins/15.02%3A\\_The\\_Genetic\\_Code\\_-\\_The\\_Central\\_Dogma-\\_DNA\\_Encodes\\_RNA\\_and\\_RNA\\_Encodes\\_Protein](https://bio.libretexts.org/Bookshelves/Introductory_and_General_Biology/General_Biology_(Boundless)/15%3A_Genes_and_Proteins/15.02%3A_The_Genetic_Code_-_The_Central_Dogma-_DNA_Encodes_RNA_and_RNA_Encodes_Protein)



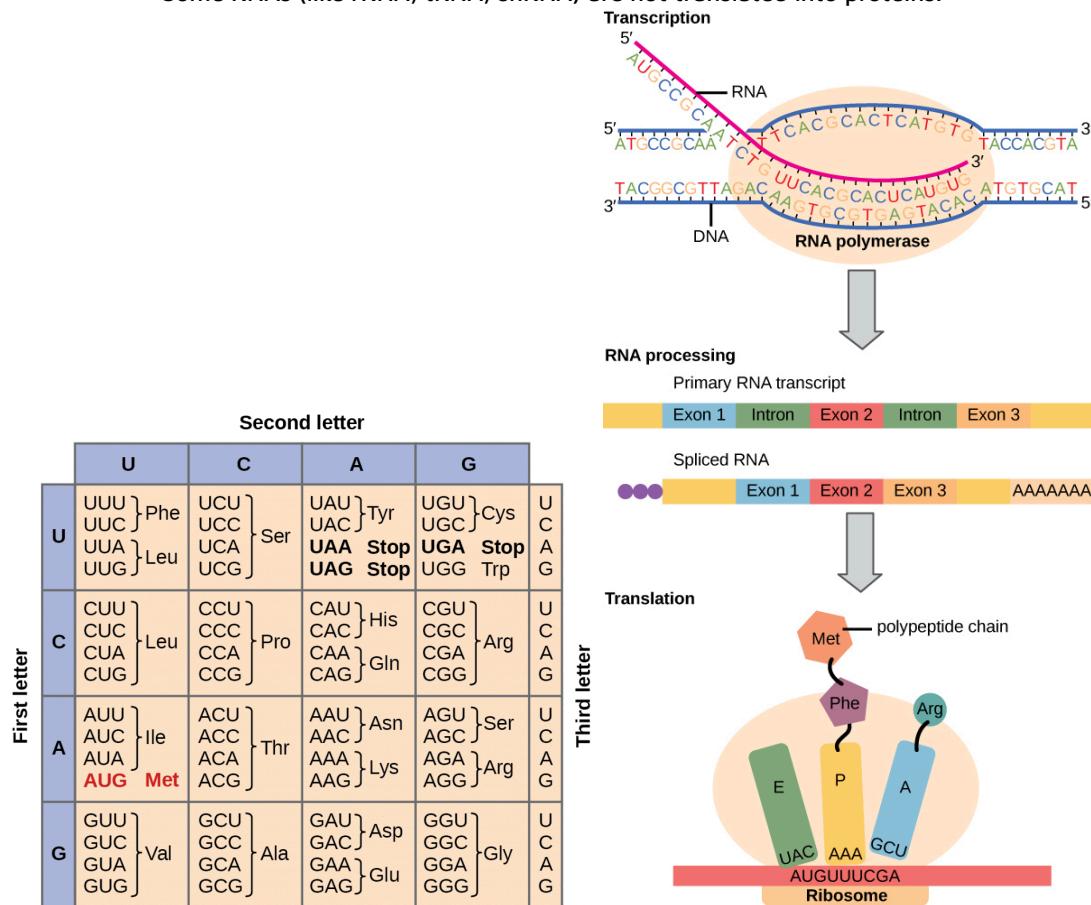
# Translation — Protein Synthesis

<https://www.youtube.com/watch?v=gG7uCskUOrA>

Translation is the process by which the mRNA sequence is decoded into a protein (a chain of amino acids).

It happens in the cytoplasm, where ribosomes and tRNA work together to make proteins.

- Converts nucleotide sequence (mRNA) → amino acid sequence (protein).  
Occurs on ribosomes (in cytoplasm or rough ER).  
Universal process – found in all organisms.  
tRNA, rRNA, and mRNA are the main players.
  - Some RNAs (like rRNA, tRNA, snRNA) are not translated into proteins.

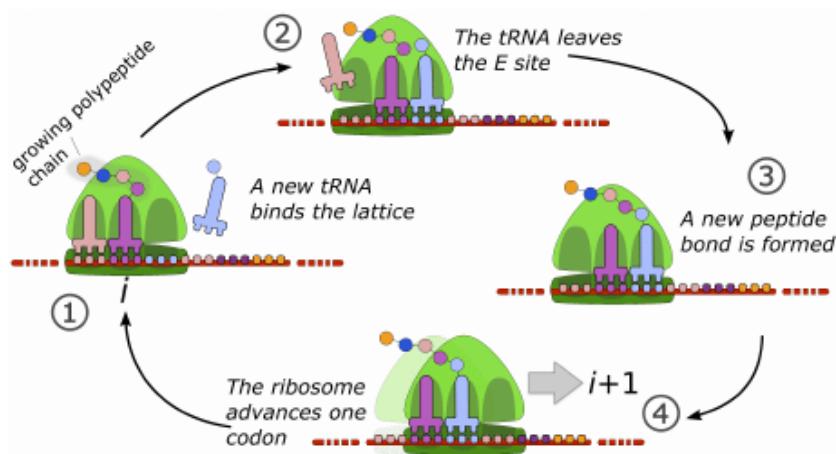


## Steps of Translation

Step	Description
Activation	Amino acids are attached ("charged") to their specific tRNAs by enzymes called aminoacyl-tRNA synthetases.
Initiation	The ribosome binds to mRNA and starts at the start codon (AUG).
Elongation	The ribosome moves along mRNA, adding amino acids one by one to form a polypeptide chain.

**Termination** The ribosome reaches a stop codon (UAA, UAG, UGA) → protein is released.

(Sometimes "activation" is not counted as a formal step.)



## Prokaryotic vs Eukaryotic Translation

Feature	Prokaryotes	Eukaryotes
Link with Transcription	Simultaneous (no nucleus)	Separate (in nucleus first)
mRNA Location	Cytoplasm	Nucleus (then cytoplasm)
Ribosome Size	70S (30S + 50S)	80S (40S + 60S)
Initiation	Cap-independent (Shine-Dalgarno sequence)	Mostly cap-dependent (Kozak sequence)
mRNA Stability	Unstable	Stable
mRNA Lifespan	Seconds-minutes	Hours-days
Cell Cycle Phase	Any	$G_1$ & $G_2$ phases
Speed	Fast	Slower
Release Factors	RF1, RF2	eRF
Initiation Factors	3	9



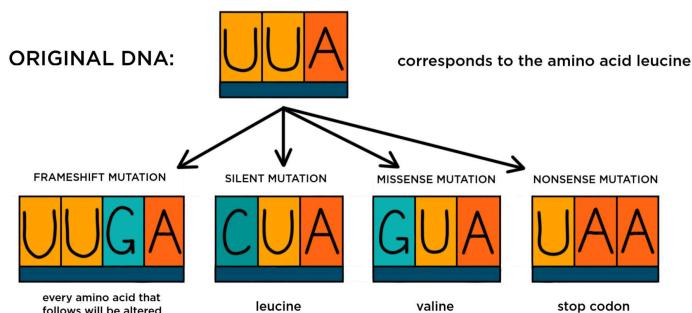
## The Genetic Code

- 3 mRNA bases = 1 codon = 1 amino acid.  
There are 64 codons but only 20 amino acids → some amino acids are coded by multiple codons (degeneracy).  
Start codon = AUG (Methionine). Stop codons = UAA, UAG, UGA.  
The genetic code links DNA/RNA sequences to amino acid sequences in proteins.

Codons = 3-nucleotide sequences in RNA that specify an amino acid.

- Total codons: 64
  - 61 → amino acids
  - 3 → stop codons (signal end of translation)
- Degenerate code: Some amino acids are coded by multiple codons (redundancy), but each codon only codes for one amino acid (no ambiguity).
  - Example:
    - Glutamic acid → GAA, GAG
    - Leucine → UUA, UUG, CUU, CUC, CUA, CUG
    - Serine → UCA, UCG, UCC, UCU, AGU, AGC
- Fault tolerance: Redundancy helps prevent errors from point mutations.

## What Are Point Mutations?



- Number of amino acids: 21 universally, 22nd (pyrrolysine, Pyl) in some Archaea & Bacteria.



## Ribosomes

- Made of rRNA + proteins.
- Sites:
  - A site: Accepts incoming aminoacyl-tRNA.
  - P site: Holds growing peptide chain.
  - E site: Exit for empty tRNA.
- Prokaryotes: 70S (30S + 50S)  
Eukaryotes: 80S (40S + 60S)  
Mitochondria & chloroplasts: 70S (like prokaryotes)

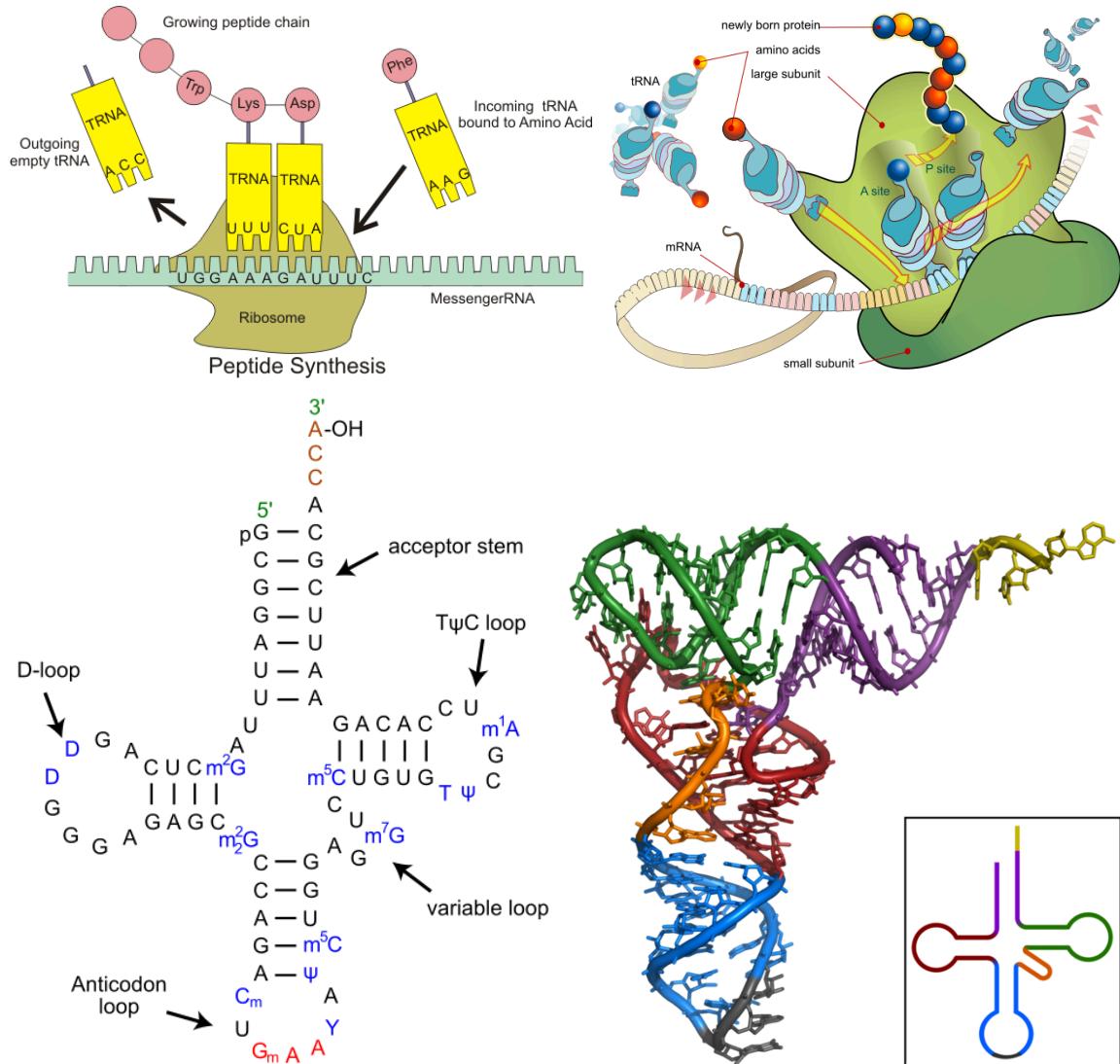


## Transfer RNA (tRNA)

- Small RNA molecules that bring amino acids to ribosomes.
- Each tRNA:
  1. Has an anticodon (matches mRNA codon).  
Has a 3' CCA site (binds amino acid).

- tRNA charging:

1. Amino acid activated by AMP.  
Attached to its tRNA by aminoacyl-tRNA synthetase.  
AMP released → charged tRNA ready for translation.



[https://bio.libretexts.org/Bookshelves/Introductory\\_and\\_General\\_Biology/General\\_Biology\\_\(Boundless\)/15.3%3A\\_Genes\\_and\\_Proteins/15.11%3A\\_Ribosomes\\_and\\_Protein\\_Synthesis\\_-\\_The\\_Mechanism\\_of\\_Protein\\_Synthesis](https://bio.libretexts.org/Bookshelves/Introductory_and_General_Biology/General_Biology_(Boundless)/15.3%3A_Genes_and_Proteins/15.11%3A_Ribosomes_and_Protein_Synthesis_-_The_Mechanism_of_Protein_Synthesis)

Translation is the process by which the sequence of mRNA is used to build a protein.  
It happens in the cytoplasm using ribosomes, tRNAs, and enzymes.

- ♦ Main Components
  - mRNA (messenger RNA):  
Carries the genetic code from DNA to ribosomes.
  - Ribosomes:  
Made of rRNA + proteins.  
Have two subunits:

Organism	Small	Large	Total
Prokaryote	30S	50S	70S

Eukaryote      40S      60S      80S

- Small subunit binds mRNA.  
Large subunit makes peptide bonds.

2. tRNA binding sites in ribosome:

- A site: accepts new aminoacyl-tRNA  
P site: holds growing chain  
E site: exit site for empty tRNA

3. Polysome: one mRNA being read by many ribosomes at once.

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3. tRNA (Transfer RNA):

- Brings amino acids to ribosome.  
Has anticodon (matches mRNA codon) and acceptor arm (binds amino acid).  
61 codons code for amino acids, 3 are stop codons.  
Start codon (AUG) = Methionine (Met).
- 

4. Aminoacyl tRNA Synthetase:

- Enzyme that attaches the correct amino acid to its tRNA.  
Uses ATP energy.
- 

 Steps of Translation

1. Initiation

● Prokaryotes:

- 30S subunit binds mRNA at Shine-Dalgarno sequence. (5' — AGGAGG — NNNN — AUG — 3')  
fMet-tRNA binds start codon (AUG).  
50S subunit joins → forms 70S ribosome.

● Eukaryotes:

- 40S subunit + Met-tRNAs + initiation factors (eIFs) bind to 5' cap of mRNA.  
Scans mRNA for AUG start codon.  
60S subunit joins → forms 80S ribosome.

Feature	Prokaryotes	Eukaryotes
Sequence	Shine-Dalgarno (AGGAGG)	Kozak ((GCC)RCCATGG)
Location	5–10 bases before AUG	Surrounds the AUG
Recognized by	16S rRNA (of 30S ribosome)	eIFs & 40S ribosome
Function	Positions AUG correctly	Helps ribosome identify AUG during scanning

Mechanism	Base pairing with rRNA	Scanning from 5' cap
<p><b>2. Elongation</b></p> <ul style="list-style-type: none"> <li>• New aminoacyl-tRNA enters A site.</li> <li>• Peptidyl transferase links amino acids (forms peptide bond).</li> <li>• Ribosome moves (translocates) to the next codon (A → P → E).</li> <li>• Empty tRNA exits; process repeats.</li> </ul>		
<p><b>3. Termination</b></p> <ul style="list-style-type: none"> <li>• Stop codon (UAA, UAG, or UGA) enters A site.</li> <li>• No tRNA fits → release factors bind.</li> <li>• New protein is released, and ribosome disassembles.</li> <li>• </li> </ul>		<p>The diagram illustrates the three stages of ribosomal function:</p> <ul style="list-style-type: none"> <li><b>Initiation:</b> Shows the ribosome with the initiator tRNA at the P site (peptidyl site) and the aminoacyl site (A). The exit site (E) is empty. The 5' start codon (AUG) is at the A site. The amino acid chain begins with methionine.</li> <li><b>Elongation:</b> Shows the ribosome translocating along the mRNA strand. The aminoacyl site (A) has moved to the P site, and the exit site (E) has moved to the A site. A new tRNA has entered the A site. The amino acid chain now includes methionine, arginine, and threonine. The 5' codon is now at the exit site (E). The text explains that peptide bonds are formed between amino acids and linked onto the tRNA in the A site, then the ribosome translocates in the 5' to 3' direction, allowing the tRNA in the P-site to exit and the tRNA in the A-site to move to the P-site.</li> <li><b>Termination:</b> Shows the ribosome at the end of the mRNA strand. The exit site (E) is filled with a release factor. The amino acid chain is complete. The text indicates that the ribosome disassembles and releases the new protein.</li> </ul>

## Protein Folding and Post-Translational Processing

### 1. Protein Folding

- After translation, proteins emerge from the ribosome as linear amino acid chains.
- To function, they must adopt a native conformation: a stable 3D structure that determines biological activity.
- Denaturation occurs when proteins lose their native structure due to:
  - Heat
  - Extreme pH, which disrupts hydrogen bonds and weak interactions.
- Denatured proteins are not completely random; they often exist in partially folded, intermediate states.
- Chaperones (helper molecules) assist proteins that cannot fold spontaneously, preventing aggregation during folding.

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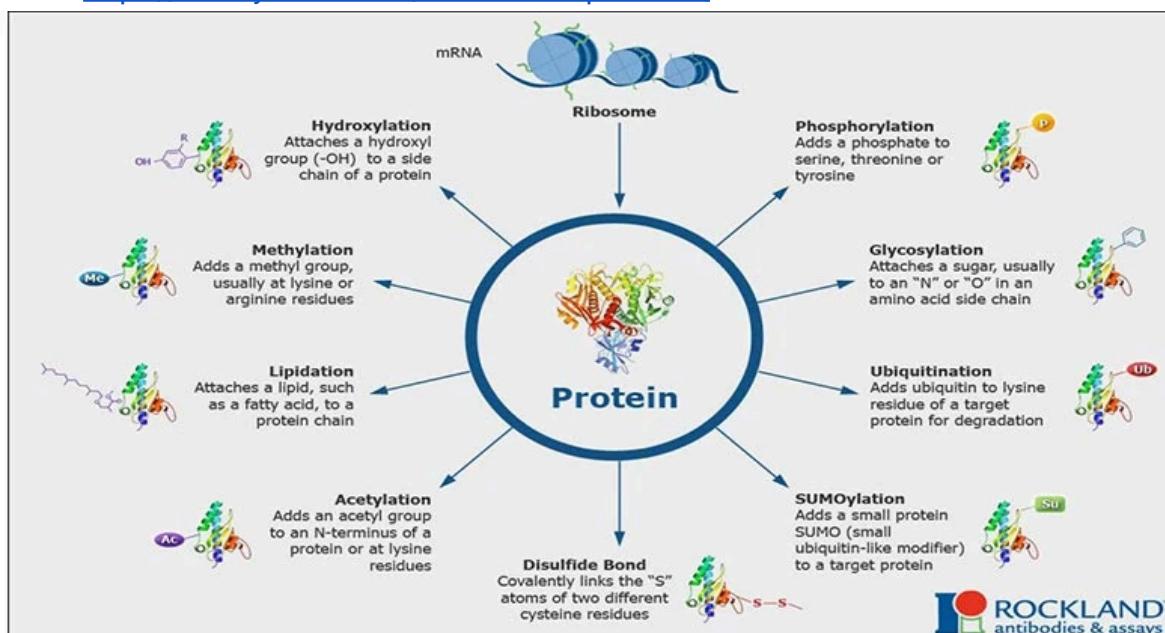
### 2. Protein Modification and Targeting

- Proteins may undergo chemical modifications during or after translation.
  - Signal sequences: short amino acid tails that act as “addresses” to target proteins to specific cellular compartments (e.g., mitochondria, chloroplasts).
  - Once the protein reaches its destination, the signal sequence is usually removed.
  - Example: amino-terminal sequences can direct proteins to mitochondria or chloroplasts in plants.
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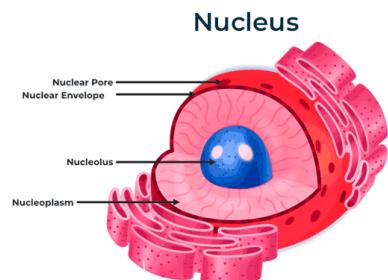
### 3. Protein Misfolding

- Correct folding is critical for proper protein function.
- Misfolding can cause genetic disorders:
  - Cystic fibrosis: Deletion of Phe508 in CFTR → improper folding → defective chloride channel.
  - Collagen disorders: Mutations affect folding → defective connective tissue.
- Prions: misfolded proteins that can cause degenerative brain diseases.
  - Examples: mad cow disease, kuru, Creutzfeldt-Jakob disease
  - These diseases are spongiform encephalopathies (brain riddled with holes).
  - Prions are normal brain proteins that misfold; they cannot reproduce independently.

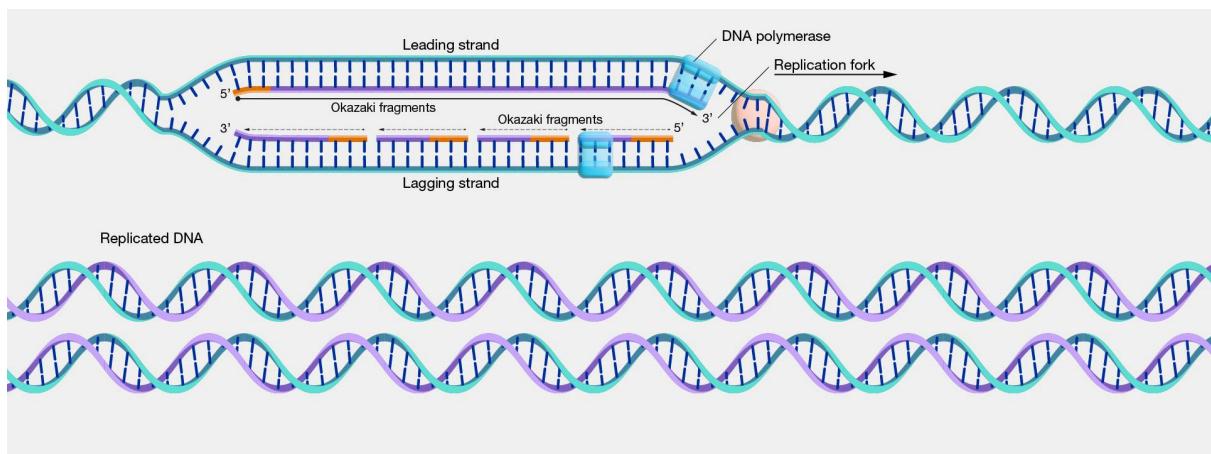
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- Proteins must fold into native 3D structures to be functional.  
Chaperones help prevent aggregation and assist in proper folding.  
Signal sequences guide proteins to their correct cellular location.  
Misfolded proteins can lead to diseases such as cystic fibrosis and prion diseases.  
Understanding folding can help develop therapies for genetic and neurodegenerative disorders.
  - <https://www.youtube.com/watch?v=bKlpDtJdK8Q>



Features	Nucleus	Nucleolus
Location	Organelle present in the cell, bounded by the nuclear envelope	Sub-organelle present inside the nucleus, not bounded by a membrane
Composition	Contains genetic material (DNA)	contains RNA
Structure	Bounded by the nuclear envelope, with inner and outer membranes	Not bounded by any membrane
Size	Largest organelle in eukaryotic cells	Largest sub-organelle in the nucleus
Presence	Present in all eukaryotic cells except RBCs and Sieve Tube	Found only in higher eukaryotes
Volume	Occupies a significant portion of the cell	Occupies 25 per cent of the volume of the nucleus
Function	The control centre of the cell stores genetic material (DNA). Controls DNA replication during the cell cycle	Involved in ribosome biogenesis, nuclear detention, and assembling the signal recognition particles.
Transcription	Site of DNA transcription into hnRNA and mRNA	Involved in transcription of DNA into rRNA



**DNA replication** is the process of copying the DNA in a cell so that each new cell gets a complete set of genetic information. Before a cell divides, it must duplicate its entire genome, which contains nearly three billion DNA base pairs. DNA polymerases are the molecules that carry out this copying process. It takes several hours to replicate all the DNA in a human cell. After replication, the cell has double the amount of DNA, which is then split between the parent and daughter cells, making them genetically identical.



DNA replication is the process by which a double-stranded DNA molecule is copied to produce two identical molecules. This ensures that when a cell divides, both daughter cells have the same genetic information.

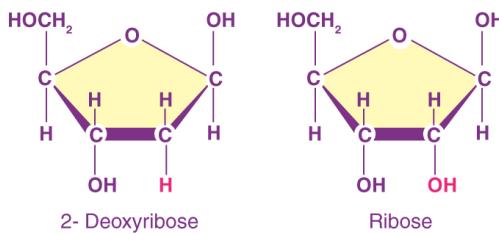
Replication happens in three main steps:

1. Separation of Strands: The DNA double helix uncoils at a specific site called the origin. Proteins like helicase break the bonds between the DNA strands, separating them. A replication fork is a Y-shaped structure that forms when a DNA double helix splits into two strands.

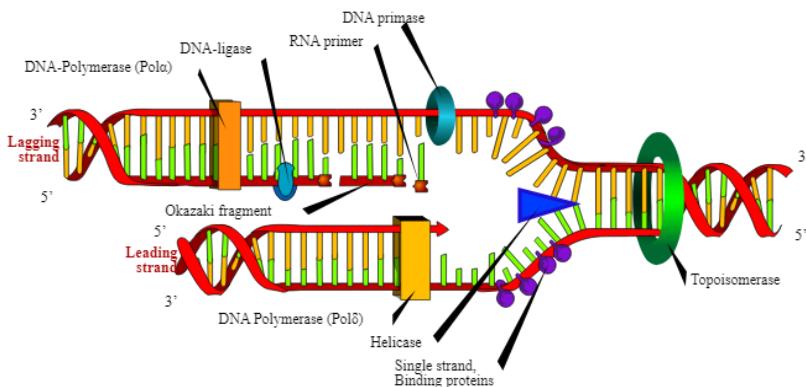


2. Priming: DNA primase creates short RNA primers to provide a starting point for DNA polymerase, which builds new DNA strands. Since DNA polymerase can only

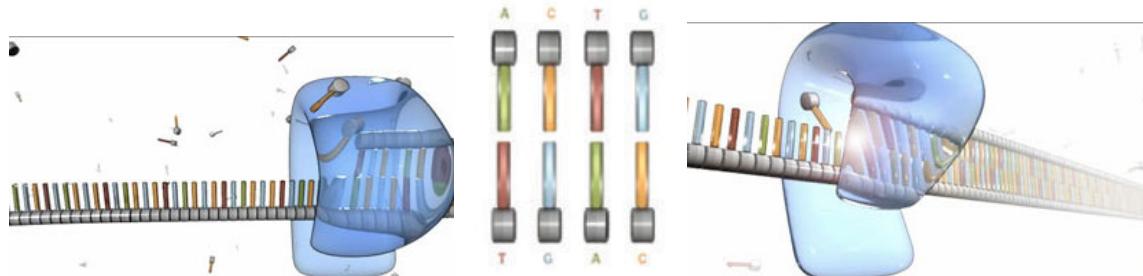
add nucleotides to an existing strand, the RNA primer serves as a "primer" to kickstart DNA replication on a single-stranded DNA template.



RNA primers are used in DNA replication because DNA polymerase can only add nucleotides to an existing chain with a free 3'-OH group, which RNA primers provide. DNA polymerase can't start DNA synthesis on its own, so it needs a short RNA primer to begin the process.



3. DNA Assembly: The enzyme DNA polymerase attaches to the primer and adds new nucleotides to form a complementary strand.



The new strand is created by matching each nucleotide with its complement: A pairs with T, and C pairs with G. Replication is fast. In bacteria like *E. coli*, it happens at 1,000 nucleotides per second, while in humans, it's about 50 nucleotides per second. The two strands of DNA are replicated differently: one (leading strand) is made continuously, while the other (lagging strand) is made in small fragments that are later joined together.

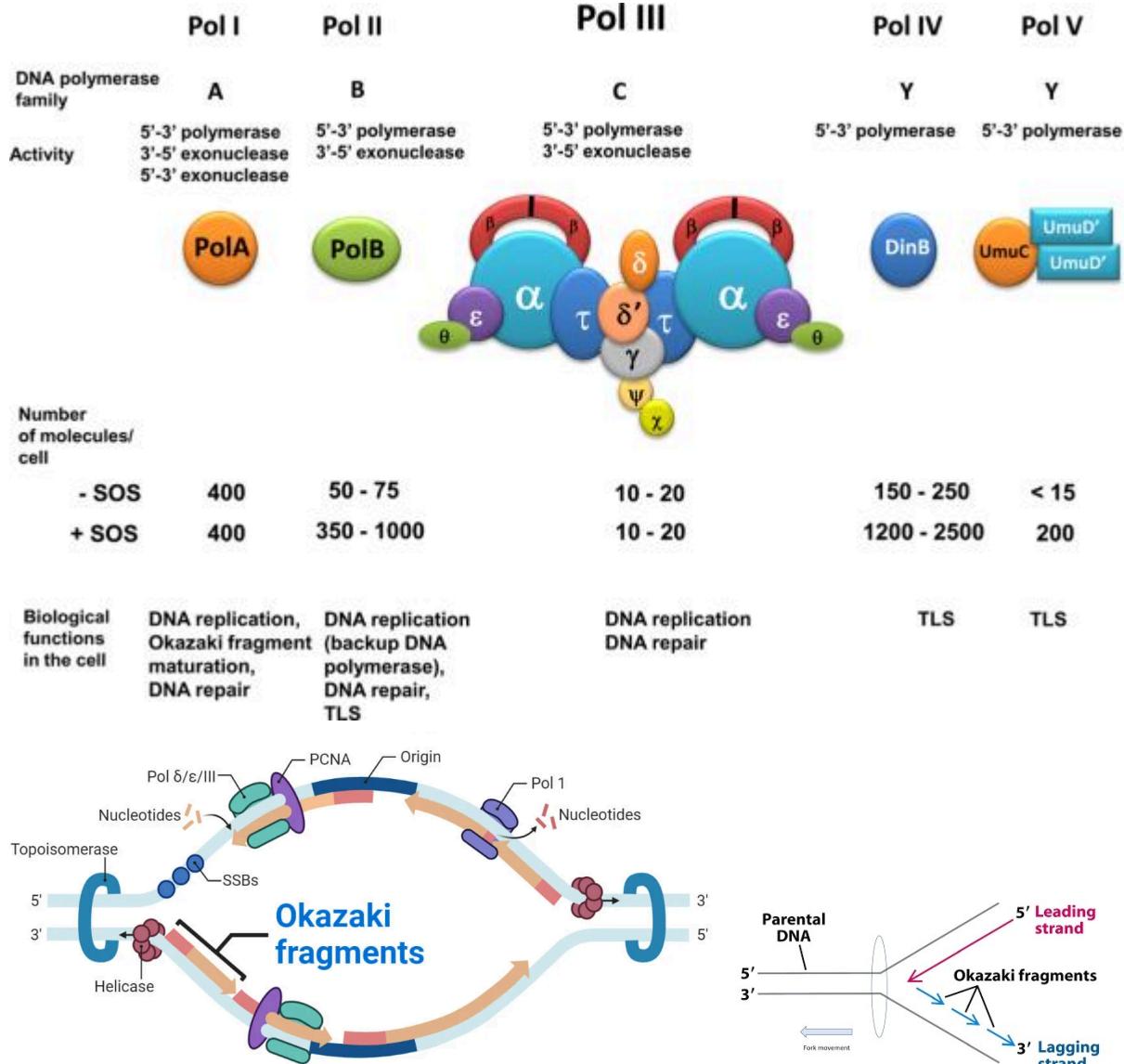
The five DNA polymerases of *E. coli* and some of their relevant properties.

High accuracy in DNA replication is crucial for maintaining genetic stability and preventing harmful mutations. The error rate during DNA replication is extremely low, around **1 in a billion to 1 in 100 billion base pairs**. Achieving this low error rate involves several mechanisms, especially in the model organism *Escherichia coli* (*E. coli*), where the primary enzyme involved is DNA polymerase III (Pol III).

Here are the key points about DNA replication fidelity in *E. coli*:

1. Pol III is the main enzyme responsible for DNA replication, but it is supported by other DNA polymerases in the process.
2. Pol II acts as a back-up proofreader for Pol III, helping to correct errors made during replication.

- Pols IV and V do not significantly contribute to replication accuracy under normal conditions, but can help with fidelity if expressed at higher levels. They primarily function on the lagging strand.
- Pol I plays a smaller role, mainly in filling in gaps during the formation of Okazaki fragments on the lagging strand. Translesion DNA synthesis (TLS) is a direct mechanism of bypassing unrepaired DNA lesions



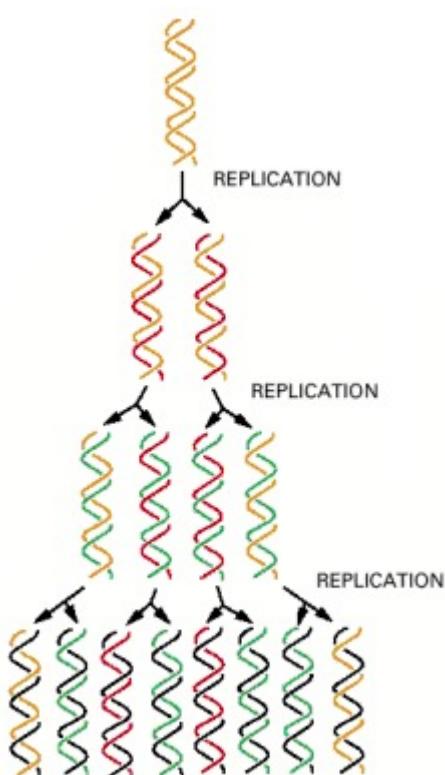
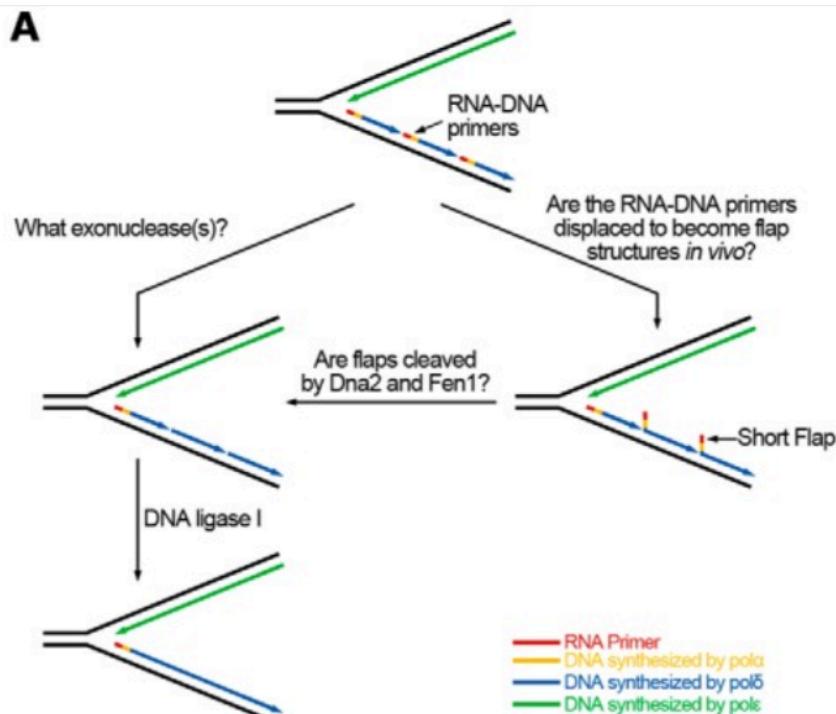
Okazaki fragments are short DNA segments formed on the lagging strand during replication. In 1968, Reiji and Tsuneko Okazaki discovered Okazaki fragments while studying bacteriophage DNA replication in *E. coli*. In bacteria and bacteriophage T4, Okazaki fragments are about 1000 to 2000 nucleotides long, while in eukaryotes, they are about 150 to 200 nucleotides long. Each fragment has an RNA primer at the start, and they are later connected by the enzyme DNA ligase to form the lagging strand during DNA replication.

The study investigates how RNA-DNA primers are removed from Okazaki fragments during DNA replication, focusing on different pathways. There are two proposed ways to remove these primers: the exonuclease pathway and the flap pathway. In the exonuclease pathway, the RNA-DNA primers are directly digested by enzymes like RNase H2 and Exo1. In the flap pathway, the RNA-DNA primers are first displaced,

creating "flap" structures. These flaps are then cut by endonucleases like Fen1 and Dna2.

<https://www.youtube.com/watch?v=TNKWgcFPHqw>

Exonucleases are enzymes that break down DNA by removing nucleotides from the ends of DNA strands. They are crucial for maintaining genome stability and play a role in DNA replication, repair, and cell metabolism. Exonucleolytic proofreading by DNA polymerase during DNA replication.



The semiconservative nature of DNA replication. In a round of replication, each of the two strands of DNA is used as a template for the formation of a complementary DNA strand. The original strands therefore remain intact through many cell generations.

A human chromosome has about 150 million nucleotide pairs. Replicating this DNA with a single replication fork moving at 50 nucleotides per second would take about 800 hours. To speed up the process, many replication forks work at the same time on each chromosome. These forks are grouped in clusters called replication units, with 20-80 origins. **Replication starts at different times during the cell cycle until all DNA is copied.** Within a replication unit, origins are spaced 30,000–300,000 nucleotide pairs apart. Replication forks move in opposite directions, forming a bubble and stopping when they meet other forks or the end of the chromosome. This allows many forks to replicate the DNA quickly and efficiently.

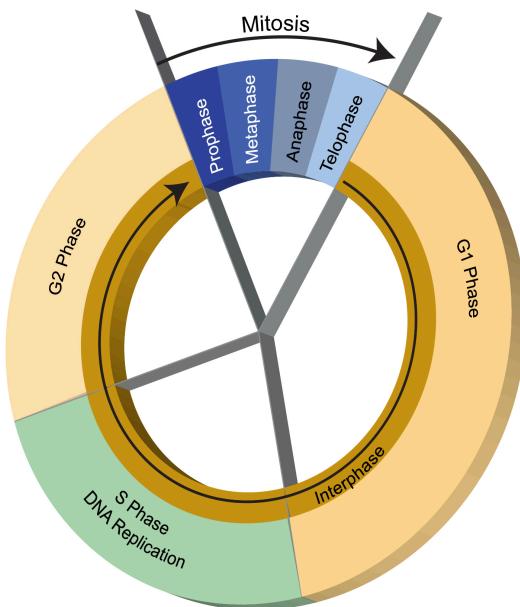
Topic	Prokaryotic DNA Replication	Eukaryotic DNA Replication
<b>Definition</b>	Prokaryotic DNA replication is the process by which a prokaryotic organism duplicates its entire genome in order to pass the second copy to a daughter cell.	Eukaryotic DNA replication is the process by which the eukaryotic genome duplicates prior to cell division.
<b>Occurrence</b>	Prokaryotic DNA replication is a continuous process.	Eukaryotic DNA replication occurs during the S phase of the cell cycle.
<b>Location</b>	Prokaryotic DNA replication takes place in the cytoplasm.	Eukaryotic DNA replication takes place in the nucleus.
<b>Type of DNA</b>	Prokaryotic DNA is circular and double-stranded.	Eukaryotic DNA is linear and double-stranded with ends.
<b>Amount of DNA</b>	There is a small amount of Prokaryotic DNA.	The amount of eukaryotic DNA is 50 times more than the amount of prokaryotic DNA.
<b>Packaging</b>	Prokaryotic DNA forms loop-like structures by wrapping around histone-like protein molecules.	Eukaryotic DNA forms nucleosomes and shows higher order packaging.
<b>Origin of Replication</b>	Prokaryotic DNA consists of a single origin of replication.	Eukaryotic DNA consists of multiple origins of replication (over 1000).
<b>DNA Polymerases</b>	Prokaryotic DNA replication is carried out by DNA polymerase I and III.	Eukaryotic DNA replication is carried by DNA polymerase $\alpha$ , $\delta$ , and $\epsilon$ .
<b>Size of the Okazaki Fragment</b>	The Okazaki fragments are comparatively large, 1000-2000 nucleotides in length.	The Okazaki fragments are small, around 100-200 nucleotides in length.
<b>DNA Gyrase</b>	DNA gyrase is involved in the prokaryotic DNA replication.	DNA gyrase is not required for the eukaryotic DNA replication.
<b>Rate of DNA replication</b>	Prokaryotic DNA replication is a rapid process and around 2000 nucleotides are added per second.	Eukaryotic DNA replication is a slow process and around 100 nucleotides are added per second.
<b>End Synthesis</b>	Prokaryotic DNA does not contain ends.	Telomerase is involved in the end synthesis in Eukaryotic DNA during the replication.
<b>Final Product of the Replication</b>	The final product of the prokaryotic DNA replication is two circular chromosomes.	The final product of the eukaryotic DNA replication is two sister chromatids.

The cell cycle is the process through which a cell replicates and forms two new cells. It has four stages: G1/(Gap/Growth), S, G2, and M.

In G1, the cell prepares to divide. The cell prepares for division. At a point called the restriction point, the cell commits to division and enters S phase.

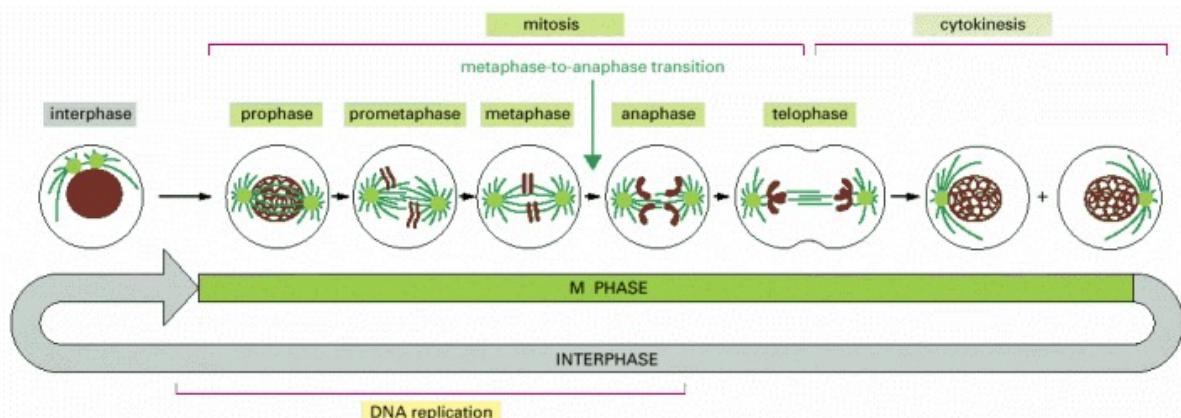
In the S phase, the cell copies its DNA (S stands for DNA synthesis). DNA is copied, and each chromosome now has two sister chromatids.

After that, in G2, the cell prepares for mitosis and cytokinesis by assembling the necessary materials.



of the cell cycle.

[https://www.youtube.com/watch?v=5bq1To\\_RKEo](https://www.youtube.com/watch?v=5bq1To_RKEo)



<https://www.youtube.com/watch?v=TNKWqcFPHqw&t=61s>

<https://www.youtube.com/watch?v=sX6LncNjTFU>

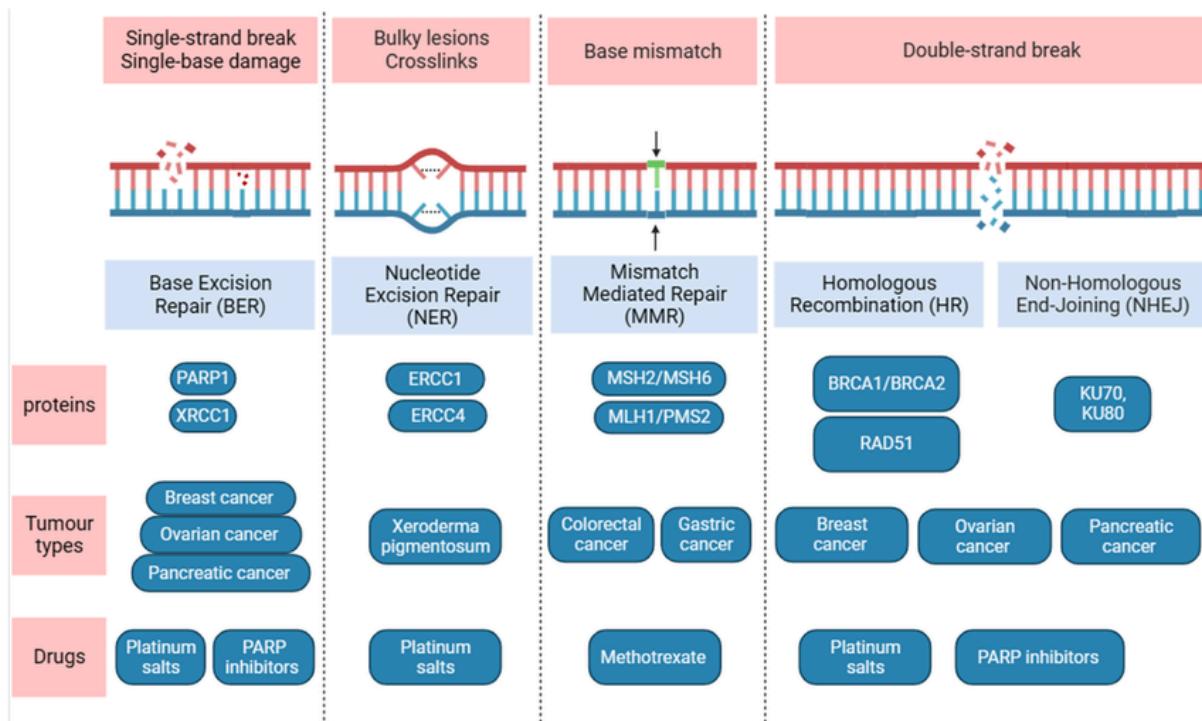
### Flow cytometry:

The cells were stained with a dye that fluoresces when bound to DNA, so the brightness indicates the amount of DNA in each cell. The cells are categorized into three groups: G1 phase (unreplicated DNA), G2 or M phase (fully replicated DNA, double the G1 amount), and S phase (DNA replication in progress, intermediate DNA content). The

graph shows that most cells are in G1 phase, indicating G1 lasts longer than G2 + M phases in this population.



<https://www.youtube.com/watch?v=xPk-kVTUH5c>

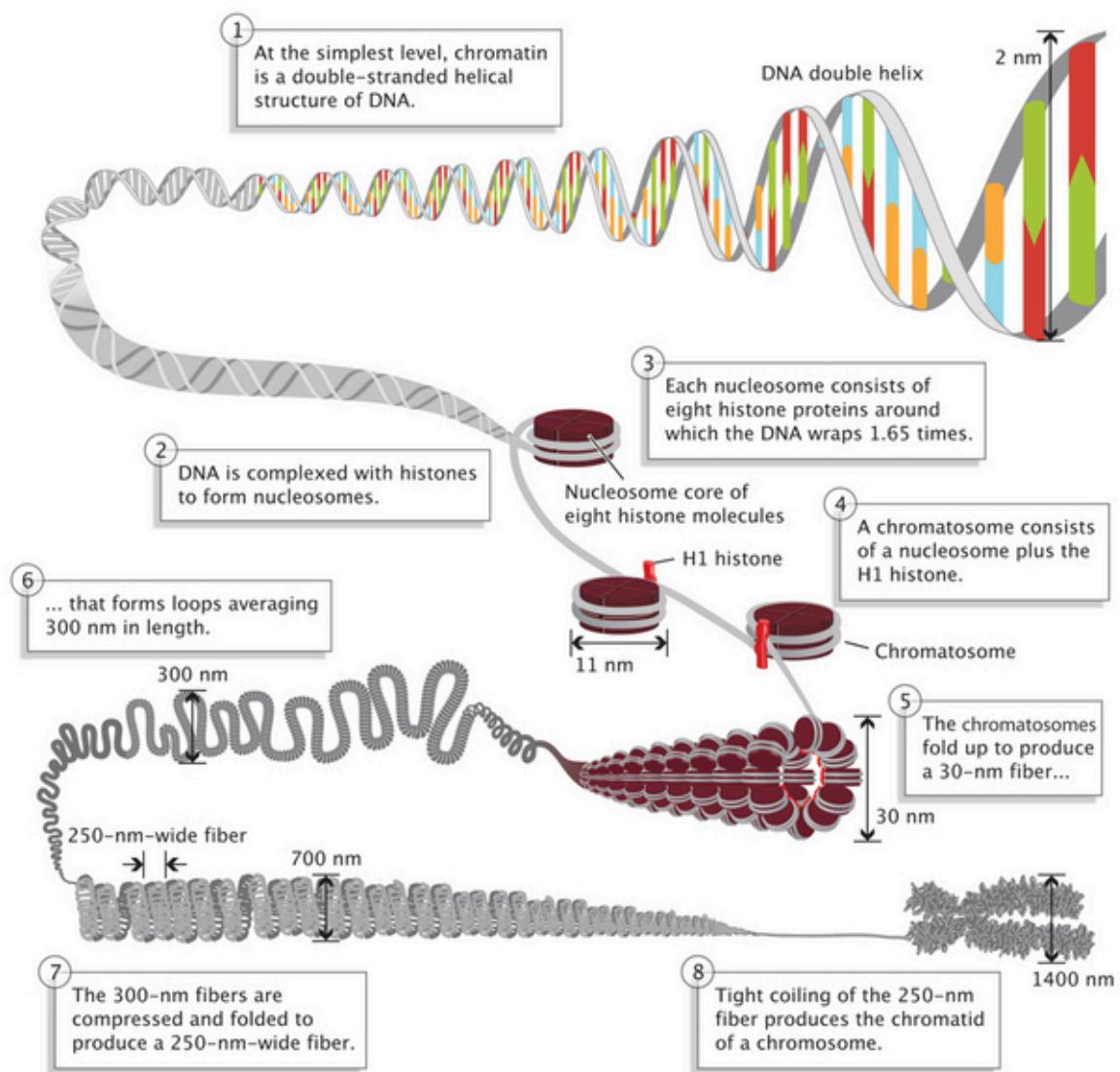


<https://www.youtube.com/watch?v=vP8-5Bhd2ag>

## Genome Complexity

Eukaryotic genomes are linear, unlike bacterial genomes, and follow the Watson-Crick double-helix structure. They are organized into nucleosomes, which are DNA-protein complexes that form chromosomes. While eukaryotic genomes vary in size and gene count, these factors don't necessarily indicate the organism's complexity.

DNA is tightly packed in several steps: it starts as a double helix, wraps around nucleosomes, forms fibers, and eventually compacts into chromosomes. Despite differences in genome size, **complexity** isn't linked to genome size or gene number.



Having more protein-coding genes doesn't always mean an organism is more **complex**. Eukaryotic genomes create complexity in other ways, mainly through how **genes** are expressed. One key example is **alternative splicing**, where a single gene can produce multiple **proteins** by rearranging its parts (exons). This means that, even though humans have around 20,000 protein-coding genes, they could produce over 500,000 different proteins.

**Q1:** Which of the following correctly shows the flow of genetic information in cells?

- A. RNA → DNA → Protein
- B. DNA → RNA → Protein
- C. Protein → DNA → RNA
- D. DNA → Protein → RNA

**Q2:** If one gene produces many RNA copies, and each RNA can make many proteins, what feature of gene expression is this illustrating?

- A. Redundancy
- B. Amplification
- C. Mutation
- D. Silencing

**Q3:** Why do cells produce some proteins in large amounts and others in tiny amounts?

- A. DNA sequence differences
- B. Gene expression efficiency
- C. RNA folding
- D. Random chance

**Q4:** Which of these is a feature unique to RNA?

- A. Double-stranded helix
- B. Thymine (T) base
- C. Ribose sugar
- D. Genetic storage

**Q5:** Which type of RNA can fold into 3D shapes and act like an enzyme?

- A. tRNA
- B. mRNA
- C. rRNA
- D. Catalytic RNA

**Q6:** Transcription is the process of:

- A. Making DNA from RNA
- B. Making RNA from DNA
- C. Making protein from RNA
- D. Making RNA from protein

**Q7:** RNA polymerase differs from DNA polymerase because it:

- A. Requires a primer
- B. Does not require a primer
- C. Makes DNA instead of RNA
- D. Works only in mitochondria

**Q8:** During transcription, RNA is synthesized in which direction?

- A. 3' → 5'
- B. 5' → 3'
- C. Both directions
- D. Randomly

**Q9:** What signals in DNA tell RNA polymerase where to start and stop transcription?

- A. Enhancers and silencers
- B. Promoters and terminators
- C. Exons and introns
- D. Telomeres and centromeres

**Q10:** Which RNA carries the genetic code to make proteins?

- A. tRNA
- B. rRNA
- C. mRNA
- D. snRNA

**Q11:** Which RNA helps remove introns during splicing?

- A. rRNA

- B. snRNA
- C. tRNA
- D. miRNA

Q12: Unlike bacteria, eukaryotic transcription:

- A. Occurs in cytoplasm
- B. Requires multiple RNA polymerases
- C. Is coupled directly to translation
- D. Produces circular RNA

Q13: Which eukaryotic RNA polymerase transcribes protein-coding genes?

- A. Pol I
- B. Pol II
- C. Pol III
- D. Pol IV

Q14: Which protein recognizes the TATA box in eukaryotic promoters?

- A. TFIIH
- B. TBP (in TFIID)
- C. RNA Pol I
- D. Mediator

Q15: What is the first modification of eukaryotic pre-mRNA?

- A. Poly-A tail
- B. Splicing
- C. 5' Capping
- D. Export from nucleus

Q16: During splicing, what is removed from pre-mRNA?

- A. Exons
- B. Introns
- C. 5' cap
- D. Poly-A tail

Q17: Alternative splicing allows:

- A. One gene to produce multiple protein isoforms
- B. Only one protein per gene
- C. RNA to leave the nucleus without processing
- D. Ribosomes to bind directly to DNA

Q18: Which of these is mainly RNA in catalytic function during splicing?

- A. U2 and U6 snRNAs
- B. DNA polymerase
- C. RNA polymerase II
- D. TFII proteins

Q19: Which structure is the main site for rRNA synthesis and ribosome assembly?

- A. Cajal body
- B. Nucleolus
- C. Chromosome territory
- D. Nuclear pore

Q20: Mature mRNAs are exported only if they are:

- A. Capped, spliced, and polyadenylated
- B. Single-stranded
- C. Attached to DNA
- D. Bound to snRNAs only