

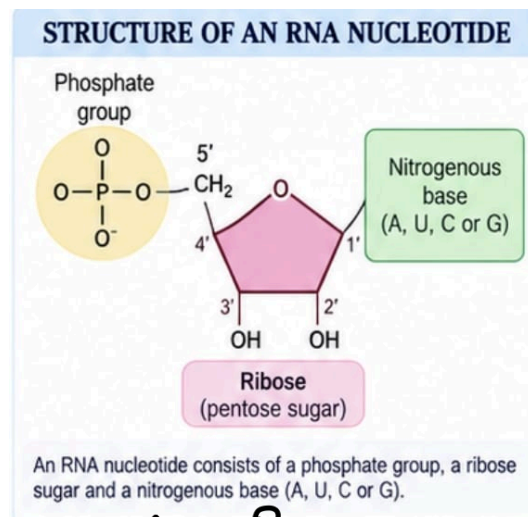
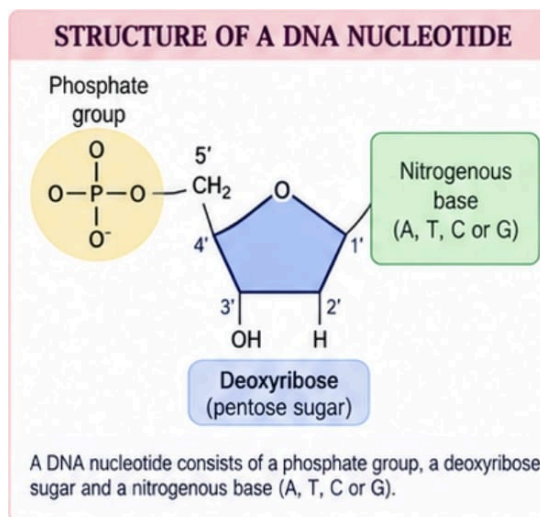
AS Biology 9700 • Nucleic Acids & Protein Synthesis

There are 2 types of nucleic acids: **Ribonucleic acid (RNA) & Deoxyribonucleic acid (DNA)**

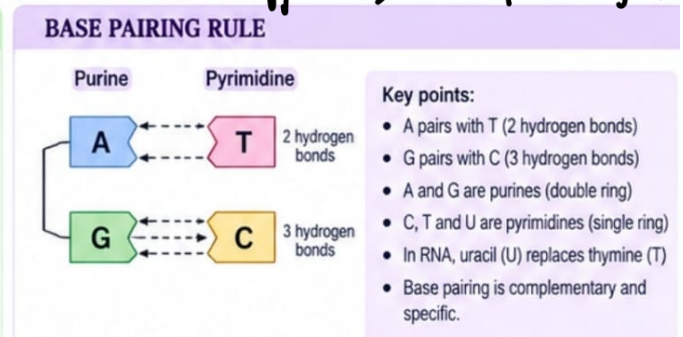
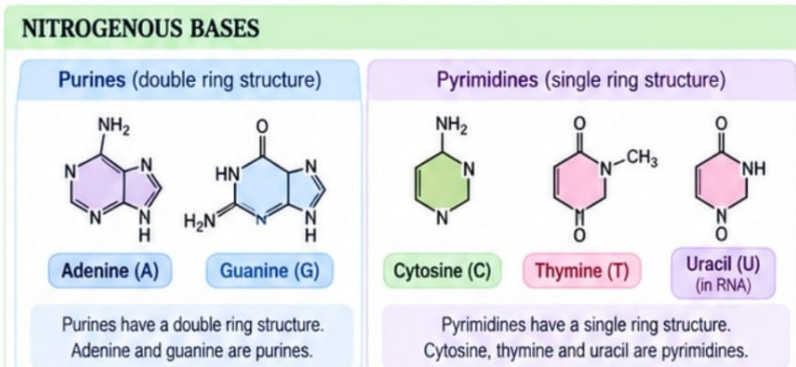
DNA	RNA
• Double stranded	• Single stranded
• Helical	• Non-helical
• Deoxyribose in nucleotide monomers	• Ribose in nucleotide monomers
• Does not contain uracil	• Does not contain thymine
• DNA is a larger molecule	• RNA is a smaller molecule
• Contains A, T, G, C	• Contains A, U, G, C
• Produced via DNA replication	• Produced via transcription

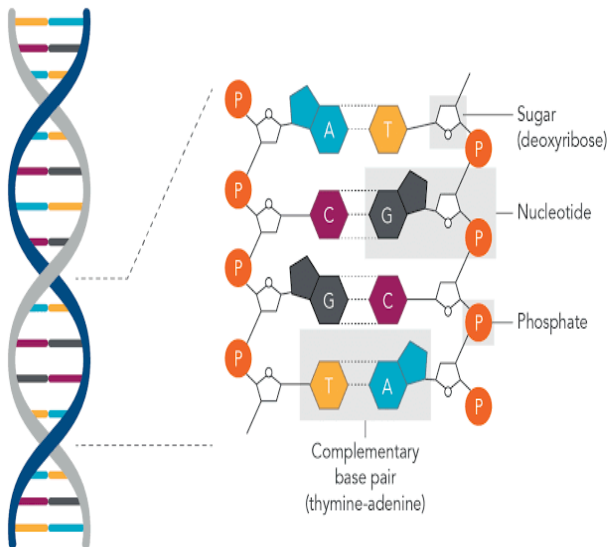
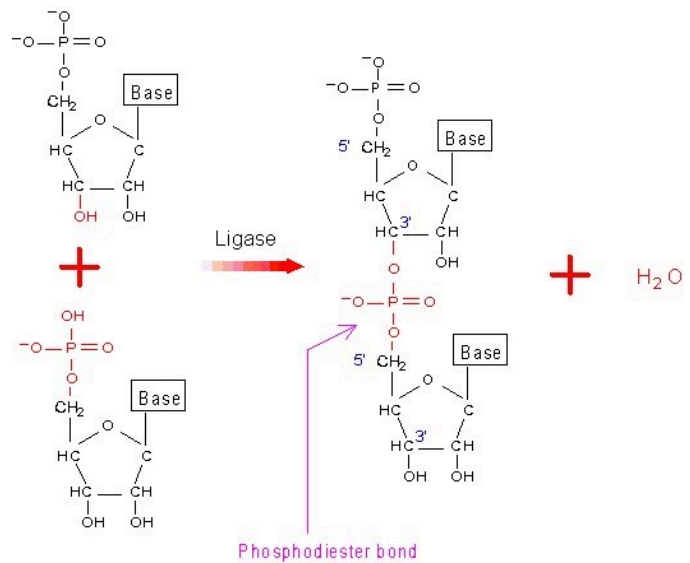
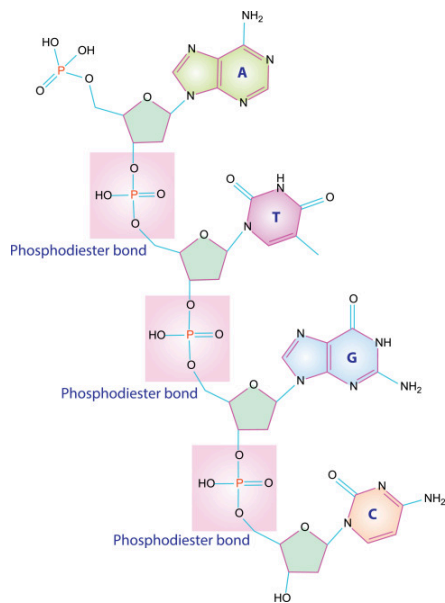
Nucleotide - basic unit/monomers of nucleic acid

A **nucleotide** consists of: **Phosphate group + pentose sugar + nitrogen-containing base**



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DNA Structure:

DNA consists of **two polynucleotide strands** arranged as a **double helix**.

Two strands are **antiparallel**

One strand runs **5' → 3'**

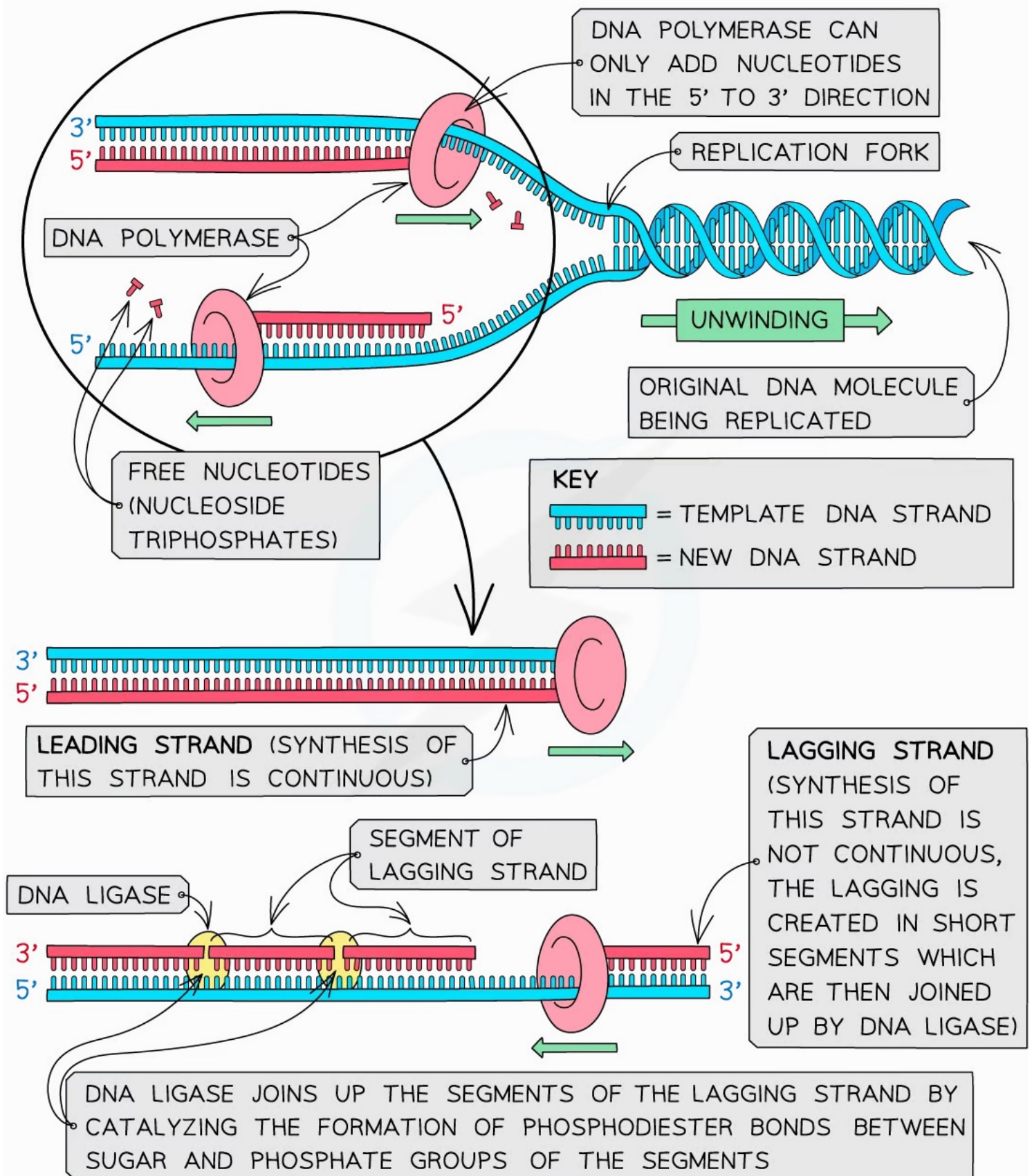
Other runs **3' → 5'**

Each strand contains nucleotides joined together by **phosphodiester bonds** forming the **sugar-phosphate backbone**. Bases face towards the centre of the molecule joined by H bonds according to the complementary base pairing.

DNA Replication (5-7 marks)

- semi conservative process
- DNA helicase unwinds and unzips the DNA by breaking "Hydrogen bonds" between the 2 strands.
- Both the DNA strands serve as a template for the formation of new strands.
- DNA polymerase can only synthesize new strand in the $5' \rightarrow 3'$ direction using activated nucleotides.
- A pairs with T via 2 hydrogen bonds
C pairs with G via 3 hydrogen bonds.
- DNA polymerase synthesizes new strands from the 2 template strands by catalysing condensation reactions between deoxyribose sugars and phosphate groups of adjacent nucleotides within the new strands creating the sugar phosphate backbone of the new DNA strands.
- DNA polymerase cleaves (breaks off) the 2 extra phosphate groups and uses the energy that is released to create the phosphodiester bonds between adjacent nucleotides. → active process
- Hydrogen bonds form between the complementary base pairs of the template and new DNA strands.
- DNA ligase joins the Okazaki fragments of the lagging strand.

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TRANSCRIPTION

Transcription is the process of using the **DNA sequence** of a gene to synthesise a **complementary mRNA molecule**.

DNA → mRNA

Where? Nucleus (in eukaryotes)

Main enzyme: RNA polymerase

1 DNA unwinds

Hydrogen bonds between bases break and the DNA double helix unwinds.

2 RNA polymerase binds

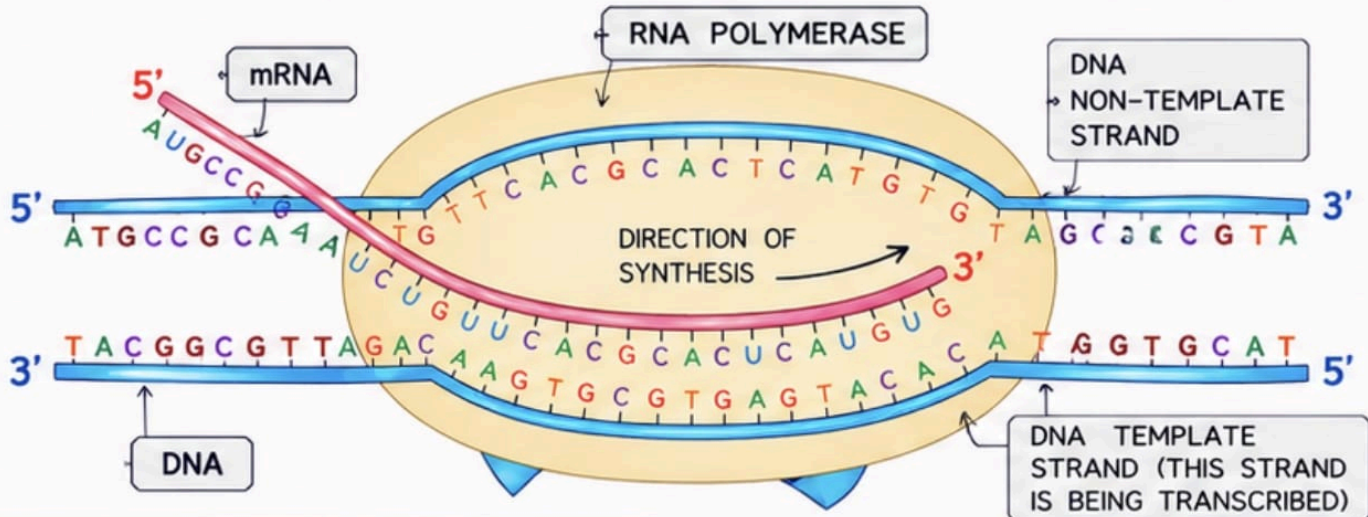
RNA polymerase binds to the DNA at the start of a gene.

3 Complimentary RNA nucleotides are added

RNA polymerase matches RNA nucleotides to the template strand using base pairing (A-U, T-A, C-G, G-C) and joins them by phosphodiester bonds.

4 mRNA is produced

When the gene has been transcribed, the mRNA molecule detaches from the DNA and leaves the nucleus (in eukaryotes).



KEY

- = mRNA sugar-phosphate backbone
- = DNA sugar-phosphate backbone

Base pairing in transcription

DNA template base	mRNA base
A	U
T	A
C	G
G	C

Key points:

- Only one strand of DNA is transcribed (template strand).
- The other strand is the non-template (coding) strand.
- mRNA is complementary to the template strand.
- mRNA has uracil (U) instead of thymine (T).
- In eukaryotes, the initial RNA transcript (primary transcript) is processed (introns removed, exons joined) before leaving the nucleus.
- mRNA then moves to a ribosome for translation.

Template vs non-template strand

Template (transcribed) strand	Non-template (coding) strand
Used by RNA polymerase	Not used as template
Complementary to mRNA	Same sequence as mRNA (except T is replaced by U)
Also called transcribed strand	Also called non-transcribed or coding strand

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The initial RNA molecule formed during transcription is called the **primary transcript**. In eukaryotes, it contains both **exons and introns**. Introns are **non-coding sequences** that are removed during RNA processing, while exons are **coding sequences** that are joined together. Therefore, the primary transcript is processed by removing the introns and joining the exons together to form **mature mRNA**. The mature mRNA then leaves the nucleus and moves to a **ribosome**, where it is used during translation to produce a polypeptide. The process is known as **splicing**.

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What is translation?

Translation is the process in which the base sequence of mRNA is used to determine the sequence of amino acids in a **polypeptide**.

TRANSLATION

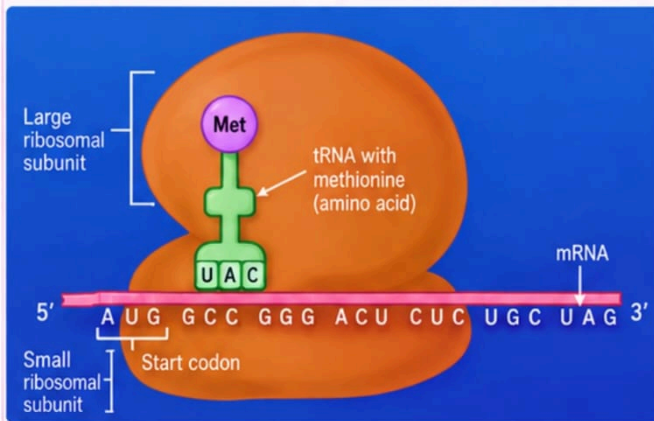
mRNA to polypeptide

Where? Cytoplasm (at ribosomes)

Main structures: ribosomes, tRNA, mRNA
Uses the genetic code (triplets of bases/codons)
mRNA is read in the 5' → 3' direction

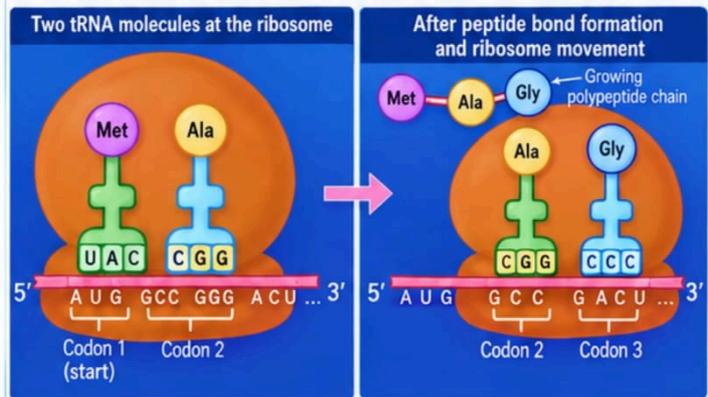
1 INITIATION

- The small ribosomal subunit binds to the mRNA.
- The start codon (AUG) is recognised.
- A tRNA with a complementary anticodon (UAC) carrying methionine binds to the start codon.
- The large ribosomal subunit then joins, forming a complete ribosome.



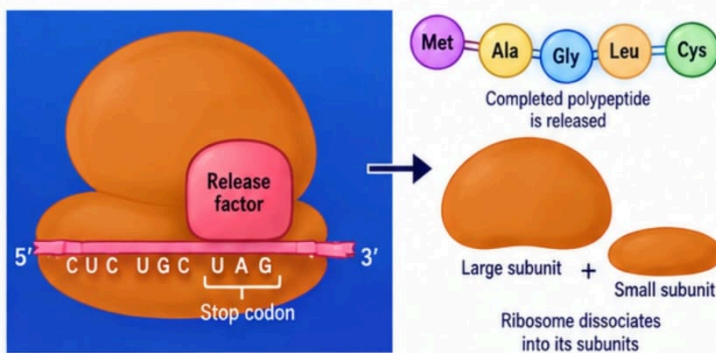
2 ELONGATION

- A second tRNA with a complementary anticodon binds to the next codon.
- The ribosome catalyses the formation of a peptide bond between the adjacent amino acids.
- The ribosome then moves one codon along the mRNA (5' → 3').
- The first (empty) tRNA leaves and a new tRNA enters.
- This process is repeated, adding amino acids to the growing polypeptide chain.



3 TERMINATION

- When a stop codon (UAA, UAG or UGA) is reached, no tRNA binds.
- A release factor binds to the stop codon.
- The polypeptide is released and the ribosome dissociates into its subunits.



Key molecules involved

mRNA

- Carries genetic information from DNA
- Read in 5' → 3' direction
- Contains codons (triplets of bases)

tRNA

- Carries a specific amino acid
- Has an anticodon complementary to the mRNA codon
- Different tRNA for each amino acid

Ribosome

- Site of translation
- Consists of a large and a small subunit
- Catalyses peptide bond formation

Some stop codons

UAA
UAG
UGA

Key points to remember

- ✓ mRNA is read 5' → 3'.
- ✓ Anticodon on tRNA is complementary to codon on mRNA.
- ✓ Two tRNA molecules are present in the ribosome at a time.
- ✓ Peptide bonds form between adjacent amino acids.
- ✓ Translation starts at AUG and ends at a stop codon (UAA, UAG or UGA).
- ✓ The result is a polypeptide with a specific sequence of amino acids.

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Key points

- A gene mutation is a change in the sequence of base pairs in a DNA molecule.
- It can occur due to substitution, insertion or deletion of nucleotide(s).
- It may alter the amino acid sequence and hence the structure and function of the polypeptide.

GENE MUTATIONS

A change in the sequence of base pairs in DNA that may result in an altered polypeptide

Why do mutations occur?

- Errors during DNA replication
- Exposure to mutagens (e.g. UV radiation, ionising radiation, certain chemicals)
- Some viruses
- Can be spontaneous or induced

Types of gene mutations

Substitution

One base pair is replaced by another.

Original DNA:

A T G C C A

Mutated DNA:

A T G T C A

Insertion

One or more base pairs are added.

Original DNA:

A T G C C A

Mutated DNA:

A T G A C C A

Deletion

One or more base pairs are removed.

Original DNA:

A T G C C A

Mutated DNA:

A T C C A

Effect on the polypeptide

- A mutation may have no effect, alter one amino acid, produce a stop codon (shorter polypeptide), or cause a frameshift (if insertion or deletion is not a multiple of 3), which can significantly alter the polypeptide.
- The effect depends on the type and position of the mutation.

The genetic code is degenerate

- Most amino acids are coded for by more than one codon.
- Therefore, some mutations (especially substitutions) may not change the amino acid, and the polypeptide remains the same.

Examples and their effects

Type of mutation	Example (DNA → mRNA → amino acid)	Effect on polypeptide	Explanation
Substitution	No effect (silent mutation) DNA: T T T → T T C mRNA: A A A → A A A Amino acid: Lys → Lys	No change in polypeptide.	Both codons code for the same amino acid (due to degeneracy of the genetic code).
	Different amino acid (missense mutation) DNA: G A G → G T G mRNA: C U C → C A C Amino acid: Leu → His	Altered amino acid in polypeptide.	A different amino acid is coded for, which may alter the polypeptide's structure and function.
	Stop codon (nonsense mutation) DNA: T A C → T A A mRNA: A U G → A U U Amino acid: Met → Stop	Shorter polypeptide (truncated).	A stop codon is formed, so translation terminates early.
Insertion (frameshift mutation)	DNA: A T G C C A → A T G A C C A mRNA: U A C G G U → U A C U G G U Amino acid: Tyr Gly → Tyr Trp ...	Many different amino acids from the point of mutation.	If the number of bases inserted is not a multiple of 3, the reading frame shifts, altering all subsequent codons.
Deletion (frameshift mutation)	DNA: A T G C C A → A T C C A mRNA: U A C G G U → U A G G U Amino acid: Tyr Gly → Stop	Altered polypeptide (usually non-functional).	If the number of bases deleted is not a multiple of 3, the reading frame shifts, often producing a stop codon.

Frameshift mutation (example)

Deletion of one base:

Original sequence:

A T G C C A G T T A C G
Met Pro Val Thr

After deletion:

A T C C A G T T A C G ...
Ile Gln Leu ...

All codons after the mutation are changed, leading to a completely different polypeptide.

Summary of effects

Type of mutation	Possible effects on polypeptide
Substitution	- No change (same amino acid) - Different amino acid - Stop codon (shorter polypeptide)
Insertion	- If not a multiple of 3 → frameshift (alters many amino acids) - Usually non-functional polypeptide
Deletion	- If not a multiple of 3 → frameshift (alters many amino acids) - Usually non-functional polypeptide

A small change in the genetic code can make a big difference.

