MEGA LECTURE

IB DP BIOLOGY

Theme D: Continuity and Change

D1.2 Protein Synthesis

Revision Notes · Standard and Higher Level

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Original notes prepared for the IB Diploma Programme Biology course (first assessment 2025)

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What the syllabus requires

By the end of D1.2 you should be able to explain how the information stored in a gene is used to build a polypeptide, through the two stages of transcription and translation. Use this checklist as a final revision map; rows flagged (HL) are examined only at Higher Level.

Understanding	You should be able to...
Gene expression overview	Outline how a gene is transcribed to messenger RNA (mRNA) and then translated into a polypeptide (the central dogma).
Transcription	Describe how RNA polymerase uses one template DNA strand to build a complementary mRNA molecule 5′→3′, using U in place of T.
The genetic code	Explain that the code is read in **triplets (codons)**, and that it is degenerate, (almost) universal and non-overlapping.
Using a codon table	Deduce the amino acid sequence of a polypeptide from an mRNA sequence, and recognise start and stop codons.
Translation	Describe translation at the ribosome: codon–anticodon pairing, tRNA delivering amino acids, and peptide bond formation.
tRNA and ribosomes	Describe the role of tRNA (anticodon + amino acid) and the structure of the ribosome (two subunits, mRNA groove, binding sites).
Post-transcriptional modification (HL)	Explain intron removal / exon splicing, the 5′ cap and poly-A tail, and how alternative splicing lets one gene make several polypeptides.
Ribosome location (HL)	Relate free and bound (rough ER) ribosomes to the destination of the protein, and describe polysomes.

> **Exam note:** At SL you need the outline of transcription and translation plus confident use of a codon table. Intron/exon splicing, caps and tails, alternative splicing, polysomes and free-vs-bound ribosomes are all HL-only detail.

1. From gene to polypeptide — the overview

A **gene** is a length of DNA that carries the coded instructions for making one polypeptide (or a functional RNA). Proteins do almost all the work of a cell, but DNA never leaves the nucleus in a eukaryote, so the information must be copied into a mobile messenger and then decoded at the ribosome. This two-step flow of information is often called the **central dogma** of molecular biology:

DNA (gene) → transcription → mRNA → translation → polypeptide

Two distinct processes are involved, and it is worth fixing the difference between them at the outset:

- **Transcription** copies the base sequence of one strand of a gene into a complementary strand of **mRNA**. It happens in the **nucleus** and is catalysed by **RNA polymerase**.
- **Translation** reads the mRNA base sequence in groups of three (codons) and assembles the matching sequence of **amino acids** into a polypeptide. It happens at a **ribosome** in the cytoplasm.

The polypeptide then folds (and may be modified) into a functional protein, whose shape and job are ultimately determined by the base sequence of the original gene. In this way the genotype (DNA) is

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expressed as the phenotype (proteins).

	Transcription	Translation
Where (eukaryote)	Nucleus	Ribosome (cytoplasm or rough ER)
Template used	One DNA strand of the gene	mRNA
Product made	mRNA	Polypeptide (chain of amino acids)
Main enzyme / machine	RNA polymerase	Ribosome (with tRNA)
Language	Bases → bases	Bases (codons) → amino acids

> **Key idea:** Transcription changes DNA language into RNA language (still bases); translation changes RNA language into protein language (amino acids). The 'translator' is the genetic code, read three bases at a time.

2. Transcription — making mRNA

Transcription produces a single-stranded messenger RNA molecule that is complementary to one strand of the gene. It takes place in the nucleus (where the DNA is) and is carried out by the enzyme **RNA polymerase**.

Step by step

- **Initiation:** RNA polymerase binds to the DNA at the start of the gene (a promoter region) and unwinds the double helix, exposing the bases and breaking the hydrogen bonds over a short stretch.
- **Template strand:** only **one** of the two DNA strands is copied for any given gene — the **template** (antisense) strand. The other strand, the coding (sense) strand, is not transcribed but has the same sequence as the mRNA (with T where the mRNA has U).
- **Base pairing:** free RNA nucleotides pair with the exposed template bases following the complementary rules, except that **uracil (U) pairs with adenine instead of thymine**. So the template base A specifies U, T specifies A, C specifies G and G specifies C.
- **Elongation:** RNA polymerase joins the aligned RNA nucleotides together, building the mRNA in the 5′→3′ direction (reading the template 3′→5′). Behind the enzyme the DNA double helix re-forms.
- **Termination:** at the end of the gene RNA polymerase detaches and the completed mRNA molecule is released.

Because the mRNA is built against the template, it is a complementary copy of that template — and therefore an *identical* copy of the coding strand (with U for T). This is why the coding strand's sequence is the one usually quoted for a gene.

Strand / molecule	Example sequence (read 5′→3′)
DNA coding (sense) strand	A T G C C A T T C
DNA template (antisense) strand	read 3′→5′: T A C G G T A A G
mRNA transcript	A U G C C A U U C

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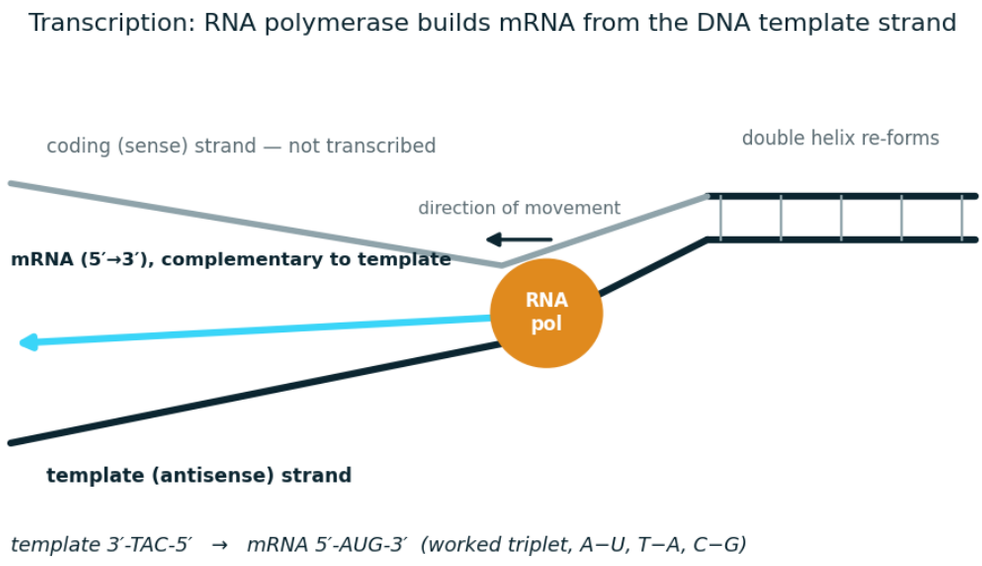


Figure 1. Transcription: RNA polymerase unwinds the DNA and builds mRNA 5′→3′ against the template strand; the worked triplet template 3′-TAC-5′ gives mRNA 5′-AUG-3′.

RNA versus DNA

The messenger is RNA, not DNA, and differs from it in three ways you should be able to state: RNA contains the sugar **ribose** (not deoxyribose); RNA uses the base **uracil (U)** in place of thymine; and RNA is **single-stranded**.

> **Exam trap:** Only the template strand is transcribed, but the mRNA ends up matching the *coding* strand. If a question gives you the coding strand, just swap every T for U to get the mRNA — do not also complement it.

3. The genetic code

The **genetic code** is the set of rules by which the base sequence of mRNA specifies the amino acid sequence of a polypeptide. Its key properties are examined regularly, so learn the vocabulary precisely.

- **Triplet / codon:** the bases are read in non-overlapping groups of three. Each triplet of mRNA bases is a **codon** that specifies one amino acid (or a stop signal). With four possible bases there are 4^3 = **64** codons.
- **Degenerate (redundant):** there are 64 codons but only about 20 amino acids, so **most amino acids are specified by more than one codon**. For example, GGU, GGC, GGA and GGG all code for glycine.
- **Universal (almost):** the same codons specify the same amino acids in nearly all organisms, from bacteria to humans. This shared code is strong evidence of common ancestry and is what makes genetic engineering across species possible. (A few minor exceptions exist, e.g. in mitochondria.)
- **Non-overlapping:** each base belongs to only one codon; the ribosome reads codon after codon without sharing bases between them.
- **Start and stop codons:** translation begins at the **start codon AUG** (which also codes for methionine) and ends at one of three **stop codons** — **UAA, UAG and UGA** — which code for no amino acid but signal 'end of polypeptide'.

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Reading frame

Because codons are read three bases at a time from a fixed starting point, the **reading frame** is the way the sequence is grouped into triplets. The start codon AUG sets the frame; from there the ribosome reads consecutive, non-overlapping triplets. Shifting the start point by one or two bases (a frameshift) regroups every codon downstream and usually produces a completely different, non-functional polypeptide.

For example, the same string read in two different frames gives different codons:

frame 1: AUG-CCU-UCA ×frame 2: A-UGC-CUU-CA

> **Common confusion:** 'Degenerate' does not mean the code is faulty. It means the redundancy is built in: several codons map to one amino acid. A useful consequence is that many single-base changes are 'silent' and change nothing.

4. Using an mRNA codon table (skill)

A codon table lets you convert any mRNA sequence into its amino acids. The table below is read from the **mRNA** (so it uses U, not T) and every codon is written 5′→3′. Find the first base down the left, then move across using the second and third bases. Amino acids are shown by their three-letter abbreviations.

mRNA codon	3rd = U	3rd = C	3rd = A	3rd = G
UU_	Phe	Phe	Leu	Leu
UC_	Ser	Ser	Ser	Ser
UA_	Tyr	Tyr	STOP	STOP
UG_	Cys	Cys	STOP	Trp
CU_	Leu	Leu	Leu	Leu
CC_	Pro	Pro	Pro	Pro
CA_	His	His	Gln	Gln
CG_	Arg	Arg	Arg	Arg
AU_	Ile	Ile	Ile	Met (start)
AC_	Thr	Thr	Thr	Thr
AA_	Asn	Asn	Lys	Lys
AG_	Ser	Ser	Arg	Arg
GU_	Val	Val	Val	Val
GC_	Ala	Ala	Ala	Ala
GA_	Asp	Asp	Glu	Glu
GG_	Gly	Gly	Gly	Gly

How to read the table

- Split the mRNA into codons starting at the first AUG (the start codon).
- For each codon, take the first base (row), then the second and third bases (column) to read off the amino acid.

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• Stop when you reach UAA, UAG or UGA — the polypeptide ends there and the stop codon itself adds no amino acid.

Worked skill — read a short mRNA

Translate the mRNA 5′ – A U GG C UU A UG G AU A A – 3′.

Split into codons: AUG | GCU | UAU | GGA | UAA.

AUG = Met (start); GCU = Ala; UAU = Tyr; GGA = Gly; UAA = STOP.

Polypeptide = **Met – Ala – Tyr – Gly** (four amino acids; the stop codon ends the chain and is not counted).

5. Translation — building the polypeptide

Translation is the decoding of the mRNA codons into a sequence of amino acids at the ribosome. It requires three players: the **mRNA** (the message), **transfer RNA (tRNA)** molecules (which bring the amino acids) and the **ribosome** (which holds everything together and forms the bonds).

Codon–anticodon pairing

Each tRNA carries a specific amino acid at one end and displays a triplet of bases called an **anticodon** at the other. The anticodon is **complementary and antiparallel** to a codon on the mRNA. When a codon and its matching anticodon pair by hydrogen bonds, the correct amino acid is automatically delivered to the right place — this is how the base sequence controls the amino acid sequence.

The three stages

- **Initiation:** the small ribosomal subunit binds the mRNA and moves to the **start codon AUG**. The first tRNA, carrying methionine and bearing the anticodon UAC, pairs with AUG. The large subunit then joins to complete the ribosome.
- **Elongation:** a second tRNA whose anticodon matches the next codon binds alongside the first. The ribosome catalyses a **peptide bond** between the two amino acids. The ribosome then moves one codon along the mRNA (**translocation**); the now-empty tRNA leaves and is recharged, and the next tRNA arrives. Codon by codon the polypeptide grows.
- **Termination:** when the ribosome reaches a **stop codon** (UAA, UAG or UGA) no tRNA matches it; instead the completed polypeptide is released, and the ribosome separates from the mRNA.

The polypeptide is always assembled from its first amino acid (the N-terminus, methionine) to its last, in the same order as the codons are read 5′→3′ along the mRNA.

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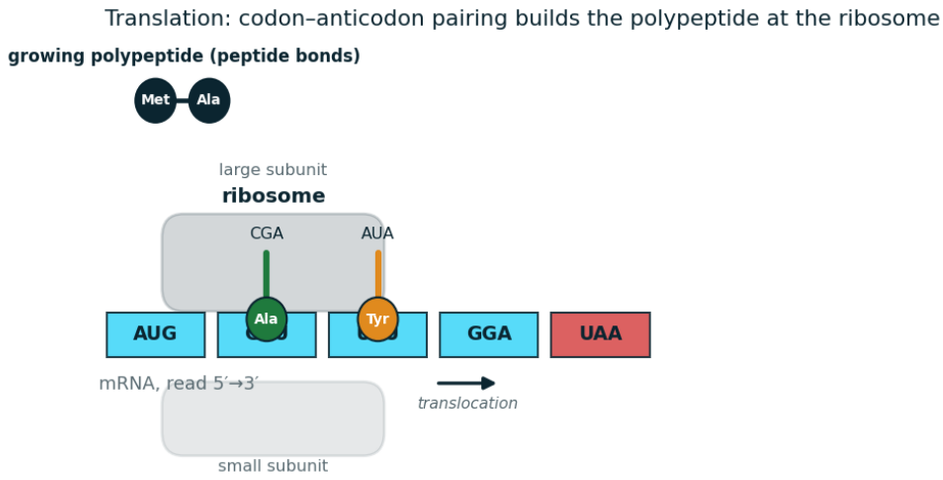


Figure 2. Translation at the ribosome: successive tRNAs pair anticodon-to-codon, the ribosome catalyses a peptide bond at each step, and translocation moves the ribosome one codon along the mRNA.

> **Key idea:** Peptide bonds are **condensation** reactions between the amino group of one amino acid and the carboxyl group of the next, catalysed by the ribosome. The order of amino acids (the primary structure) is dictated entirely by the order of codons.

6. tRNA and ribosome structure

Transfer RNA (tRNA)

A tRNA is a small, single-stranded RNA molecule that folds back on itself into a roughly cloverleaf (or L) shape held by internal base pairing. Two regions matter for translation:

- an **anticodon** — a triplet of exposed bases that pairs with a complementary mRNA codon;
- an **amino-acid attachment site** at the 3′ end, where the specific amino acid corresponding to that anticodon is covalently attached.

There is a different tRNA (with its own anticodon) for each amino acid, and enzymes load each tRNA with the correct amino acid — so a tRNA acts as a physical adaptor translating between the language of bases and the language of amino acids.

The ribosome

A ribosome is made of ribosomal RNA (rRNA) and protein, assembled into **two subunits** — a large one and a small one — that clamp around the mRNA during translation. Its important structural features are:

- a **groove** or channel on the small subunit through which the mRNA is threaded and moved one codon at a time;
- **tRNA binding sites** on the large subunit (commonly labelled the A, P and E sites) that hold two tRNAs side by side so their amino acids can be joined;
- a catalytic region that forms the **peptide bond** between adjacent amino acids (this activity is carried out by rRNA, making the ribosome a ribozyme).

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Molecule	Job in translation
mRNA	Carries the coded message as a sequence of codons read 5′→3′.
tRNA	Adaptor: anticodon pairs with a codon; 3′ end carries the matching amino acid.
Ribosome (rRNA + protein)	Holds mRNA and tRNAs together; catalyses peptide bond formation; moves along the mRNA.

> **Codon vs anticodon:** A **codon** is a triplet on the mRNA; an **anticodon** is the complementary triplet on the tRNA. Codon UAC pairs with anticodon AUG (antiparallel). Do not confuse the two — it is a very common slip.

7. Post-transcriptional modification (HL)

In eukaryotes the mRNA made directly by transcription is not yet ready to be translated. This immature transcript, called **pre-mRNA** (or primary transcript), is processed inside the nucleus before it leaves for the cytoplasm.

Introns and exons — RNA splicing

A eukaryotic gene contains coding regions called **exons** interrupted by non-coding regions called **introns**. The whole gene is transcribed, so the pre-mRNA contains both. During **RNA splicing**:

- the **introns are removed** and the **exons are joined** together in order, producing a shorter, continuous coding sequence (mature mRNA);
- only the spliced exon sequence is then translated, so introns do not appear in the final polypeptide.

Helpful memory aid: **ex**ons are **ex**pressed; **int**rons stay **in** the nucleus (they are cut out and degraded).

The 5′ cap and poly-A tail

Two further modifications protect and stabilise the mRNA:

- a **5′ cap** (a modified guanine nucleotide) is added to the front of the transcript;
- a **poly-A tail** (a long run of adenine nucleotides) is added to the 3′ end.

The cap and tail protect the mRNA from being broken down by enzymes, help it to be exported from the nucleus, and help the ribosome recognise and bind it in the cytoplasm.

Alternative splicing

Because splicing joins exons together, a cell can join **different combinations of exons** from the same pre-mRNA. This is called **alternative splicing**, and it means that **one gene can produce several different mature mRNAs**, and hence several different polypeptides. Alternative splicing greatly increases the number of proteins an organism can make from its limited number of genes, and it allows different cell types to make different versions of a protein.

Polysomes

A single mRNA is usually being translated by **several ribosomes at once**, spaced along its length. This cluster of ribosomes on one mRNA is a **polysome** (or polyribosome). It lets a cell make many copies of a polypeptide from one mRNA molecule quickly and efficiently.

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Free versus bound ribosomes

Translation happens on two populations of ribosomes, and where a ribosome sits is linked to the destination of the protein it makes:

- **Free ribosomes** float in the cytoplasm and mainly make proteins that will be used **inside the cell** — for example enzymes of the cytosol, or proteins for the nucleus, mitochondria and chloroplasts.
- **Bound ribosomes**, attached to the **rough endoplasmic reticulum**, mainly make proteins that will be **secreted** from the cell, inserted into membranes, or sent to lysosomes. These proteins enter the ER, are processed, and are packaged (often via the Golgi apparatus) for export.

> **Exam framing (HL):** 'One gene, several proteins' is best explained by **alternative splicing**. 'Where is a protein made?' is answered by free (stays in the cell) versus bound / rough ER (secreted or membrane) ribosomes.

8. Putting it together: base sequence to protein

Every exam skill in this topic is a version of the same chain of logic, running from the gene to the finished polypeptide. Learn to move confidently in both directions along it:

DNA template → mRNA codons → tRNA anticodons → amino acids → polypeptide

Worked flow — tracking one gene

Stage	Sequence
DNA template strand (read 3′→5′)	T A C A A A G G G A T T
mRNA (transcription; 5′→3′, U for T)	A U G U U U C C C U A A
Codons	AUG | UUU | CCC | UAA
tRNA anticodons	UAC | AAA | GGG | (none)
Amino acids (translation)	Met | Phe | Pro | STOP
Polypeptide	Met – Phe – Pro

Reading the table upward is just as important: given a polypeptide you can work back to possible codons (remembering the code is degenerate, so several DNA sequences could produce the same protein).

> **Watch the direction:** The template is read 3′→5′ so that the mRNA is built 5′→3′. The mRNA and the DNA coding strand share the same sequence (U for T). Anticodons are the antiparallel complement of the codon.

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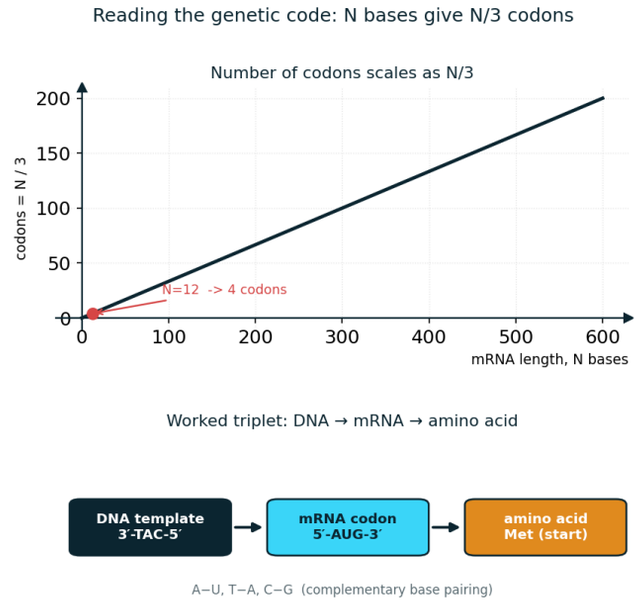


Figure 3. Codon count scales as N / 3 for an mRNA of N bases; the 12-base template above (TAC AAA GGG ATT) gives 12 / 3 = 4 codons, matching the worked flow table, and the worked triplet DNA → mRNA → amino acid confirms AUG codes for Met (start).

9. Worked examples

Worked example 1 — transcribe DNA to mRNA

A gene's template (antisense) strand reads 3′ – T A CG G AT T CA C T – 5′. Write the mRNA transcript with its polarity.

Pair each template base with its RNA partner (A–U, T–A, C–G, G–C), reading the template 3′→5′ so the mRNA is built 5′→3′:

mRNA: 5′ – A U GC C UA A GU G A – 3′

Check: template T→A, A→U, C→G gives AUG; and remember RNA uses **U**, never T.

Worked example 2 — translate mRNA using the codon table

Translate 5′ – A U GC C UA A GU G A – 3′ (the transcript from Example 1) into amino acids.

Codons: AUG | CCU | AAG | UGA.

AUG = Met (start); CCU = Pro; AAG = Lys; UGA = STOP.

Polypeptide = **Met – Pro – Lys**. The chain has three amino acids; translation stops at UGA.

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Worked example 3 — give the tRNA anticodon

The mRNA codon is 5′ – G C A – 3′. State (a) the amino acid it codes for and (b) the anticodon of the tRNA that delivers it.

(a) From the table, GCA = **Ala** (alanine).

(b) The anticodon is complementary and antiparallel to the codon. Codon 5′-GCA-3′ pairs with anticodon 3′-CGU-5′, i.e. written 5′→3′ it is **5′-UGC-3′**. (Pair G−C, C−G, A−U.)

Worked example 4 — effect of a base substitution

An mRNA codon UAU (Tyr) is altered by a single base change. Give the consequence if it becomes (a) UAC, (b) UAA, (c) UCU.

(a) UAC = **Tyr** — still tyrosine. This is a **silent** mutation: the code is degenerate, so the amino acid is unchanged.

(b) UAA = **STOP** — a **nonsense** mutation: translation ends early and the polypeptide is truncated, usually non-functional.

(c) UCU = **Ser** — a **missense** mutation: one amino acid is replaced by a different one, which may or may not change the protein's function.

Worked example 5 — order the steps of translation

Put these events into the correct order: peptide bond forms between adjacent amino acids; ribosome reaches a stop codon and releases the polypeptide; small subunit binds mRNA and locates the start codon AUG; tRNA anticodon pairs with the next codon; ribosome translocates one codon along.

Correct order: **small subunit binds mRNA and finds AUG → tRNA anticodon pairs with the next codon → peptide bond forms → ribosome translocates one codon** → (repeat) → **stop codon reached; polypeptide released**.

Worked example 6 — from coding strand to protein

A gene's **coding** (sense) strand reads 5′ – A T GG U*... — in fact 5′ – A T GT T TG G CT A A – 3′. Give the mRNA and the polypeptide.

The mRNA has the **same sequence as the coding strand**, with U replacing every T:

mRNA: 5′ – A U GU U UG G CU A A – 3′

Codons AUG | UUU | GGC | UAA give Met | Phe | Gly | STOP, so the polypeptide is **Met – Phe – Gly**. Note we simply swapped T for U — we did not complement the coding strand.

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Worked example 7 — a frameshift mutation

The mRNA 5′ – A U GA A UG C UU A A – 3′ normally codes Met – Asn – Ala. Predict the effect of inserting one extra G immediately after the start codon.

Insertion shifts the reading frame. The new mRNA reads AUG | GAA | UGC | UUA | A...

AUG = Met; GAA = Glu; UGC = Cys; UUA = Leu — every codon after the insertion is changed, so the amino acid sequence downstream is completely different.

This is a **frameshift**: because codons are read in a fixed, non-overlapping frame, adding or deleting a base regroups all later triplets and usually destroys the protein.

Common pitfalls

- Complementing the *coding* strand to get the mRNA. The mRNA matches the coding strand — just replace T with U. Only the *template* strand is complemented.
- Forgetting that RNA uses **uracil (U)**, not thymine. mRNA and tRNA never contain T.
- Confusing **codon** (on mRNA) with **anticodon** (on tRNA), or forgetting the anticodon is antiparallel to the codon.
- Treating the code as one-codon-per-amino-acid. It is **degenerate**: most amino acids have several codons, so many base changes are silent.
- Counting the stop codon as an amino acid. Stop codons (UAA, UAG, UGA) code for *no* amino acid — they only end translation.
- Saying introns are translated. Introns are removed by splicing before translation; only exons are expressed. (HL)
- Saying transcription happens at the ribosome. Transcription is in the nucleus (RNA polymerase); translation is at the ribosome.

10. The three RNAs of protein synthesis

Protein synthesis depends on three types of RNA, all transcribed from DNA but each with a distinct job. Being able to compare them cleanly is a common short-answer question.

RNA type	Structure	Role in protein synthesis
Messenger RNA (mRNA)	Long, single-stranded; a copy of the gene read in codons.	Carries the coded message from the gene (nucleus) to the ribosome; read 5′→3′ codon by codon.
Transfer RNA (tRNA)	Small, folded (cloverleaf/L shape); has an anticodon and an amino-acid site.	Brings the correct amino acid to the ribosome; its anticodon pairs with an mRNA codon.
Ribosomal RNA (rRNA)	Combined with protein to form the two ribosomal subunits.	Structural and catalytic core of the ribosome; forms the peptide bonds (a ribozyme).

All three are made by transcription, but only mRNA is translated into a polypeptide; tRNA and rRNA are functional RNAs that never leave the RNA form.

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> **Exam tip:** If asked to compare the RNAs, structure each answer around three points: where it is used, what it is made of, and what it does. mRNA = message; tRNA = adaptor; rRNA = machine.

Quick reference

Term / step	Summary
Central dogma	DNA → (transcription) → mRNA → (translation) → polypeptide.
Transcription	In nucleus; RNA polymerase copies the template strand into mRNA 5′→3′ (U for T).
Template strand	The one DNA strand that is transcribed; mRNA is its complement.
Codon	Triplet of mRNA bases specifying one amino acid; 64 codons in total.
Code properties	Degenerate, (almost) universal, non-overlapping, read in a fixed frame.
Start / stop	Start = AUG (Met). Stop = UAA, UAG, UGA (no amino acid).
Translation	At ribosome; codon–anticodon pairing; tRNA brings amino acids; peptide bonds form.
tRNA	Adaptor with an anticodon and its matching amino acid at the 3′ end.
Ribosome	Two subunits (rRNA + protein); mRNA groove; tRNA binding sites; forms peptide bonds.
Splicing (HL)	Introns removed, exons joined; alternative splicing → several proteins per gene.
Cap & tail (HL)	5′ cap and poly-A tail protect mRNA and aid export/translation.
Ribosome location (HL)	Free → proteins used in the cell; bound (rough ER) → secreted / membrane proteins.

Test yourself

Attempt these without notes; full answers follow. HL-only items are flagged.

1. Distinguish between transcription and translation, giving the location and product of each.

2. A DNA template strand reads 3′ – T A CG G GC A TA T C – 5′. Write the mRNA transcript with its polarity, then the polypeptide.

3. Explain what is meant by the statement that the genetic code is 'degenerate' and 'universal'.

4. State the start codon and the three stop codons, and explain what each signals.

5. The mRNA codon is 5′ – A A G – 3′. Give the amino acid and the tRNA anticodon.

6. Describe the roles of tRNA and the ribosome in translation.

7. (HL) Explain how RNA splicing occurs and how alternative splicing allows one gene to code for more than one polypeptide.

8. (HL) Explain the difference between free and bound ribosomes in terms of the destination of the proteins they make.

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Answers

1. **Transcription** occurs in the **nucleus** and produces **mRNA** from a DNA template (enzyme RNA polymerase). **Translation** occurs at a **ribosome** and produces a **polypeptide** from the mRNA (using tRNA). Transcription copies bases to bases; translation converts codons to amino acids.

2. Reading the template 3′→5′ and pairing (with U for T): mRNA = **5′ – A U GC C CG U AU A G – 3′**. Codons AUG | CCC | GUA | UAG give Met | Pro | Val | STOP, so the polypeptide is **Met – Pro – Val**.

3. **Degenerate:** most amino acids are coded by more than one codon (there are 64 codons but about 20 amino acids). **Universal:** the same codons specify the same amino acids in almost all organisms, evidence of a shared evolutionary origin.

4. Start codon = **AUG** (also codes for methionine); it sets the reading frame and marks where translation begins. Stop codons = **UAA, UAG, UGA**; they code for no amino acid and signal the end of the polypeptide.

5. AAG = **Lys** (lysine). The anticodon is antiparallel and complementary to the codon: codon 5′-AAG-3′ pairs with anticodon 3′-UUC-5′, i.e. **5′-CUU-3′**.

6. **tRNA** is an adaptor: its anticodon pairs with a complementary mRNA codon and its 3′ end carries the matching amino acid, so it delivers the correct amino acid to the ribosome. The **ribosome** holds the mRNA and tRNAs together, catalyses peptide bonds between adjacent amino acids, and moves along the mRNA codon by codon.

7. (HL) The pre-mRNA contains **exons** (coding) and **introns** (non-coding). In **splicing** the introns are removed and the exons are joined to make the mature mRNA. In **alternative splicing**, different combinations of exons are joined from the same pre-mRNA, so **one gene can yield several different mRNAs and polypeptides**.

8. (HL) **Free ribosomes** in the cytoplasm make proteins used **inside the cell** (e.g. cytosolic enzymes). **Bound ribosomes** on the **rough ER** make proteins destined to be **secreted, inserted into membranes, or sent to lysosomes**; these enter the ER and are packaged for export.

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