

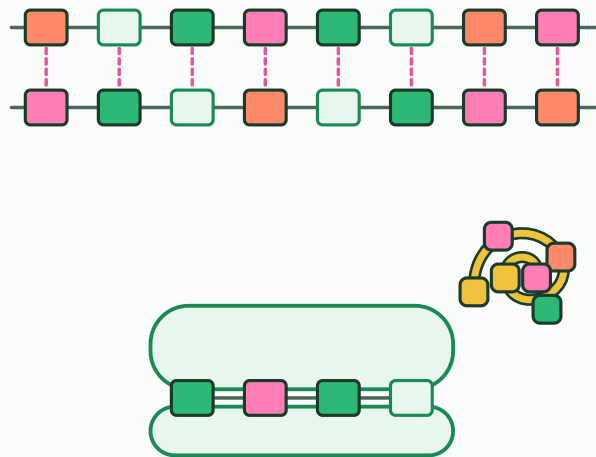
REVISION GUIDE

From one gene to one *protein*

Protein synthesis

Every protein you make starts as a message copied from one gene. Here is how a cell copies it, reads it three letters at a time and strings the chain that becomes a working protein, and what one wrong letter can do.

One protein



12 chapters

The interactive guide, with every animation:

biologybybradford.com/guides/ib-biology-d1-2-protein-synthesis



Contents

01	Copying a gene into RNA	4
02	Read for a lifetime, read when needed	7
03	Three kinds of RNA build a protein	10
04	Codon meets anticodon	12
05	A code written in threes	14
06	One codon at a time	17
07	One base, one amino acid	20
08	Five prime to three prime, both times HL	24
09	Where a gene starts, and DNA that codes for nothing HL	26
10	Capped, cut and tailed HL	29
11	Starting the chain HL	34
12	Finished, then recycled HL	38
	Key terms	42
	Check yourself	45
	Answers	46

By the end you can

- ☐ Explain how RNA polymerase uses one strand of a gene as a template, pairing U in the RNA with A on the template D1.2.1, D1.2.2
- ☐ Explain why a template can be read for a lifetime without changing, and why transcription is where a gene is switched on or off D1.2.3, D1.2.4
- ☐ Describe what mRNA, the two ribosome subunits and tRNA each do in translation D1.2.5, D1.2.6
- ☐ Pair a codon with its anticodon, and explain how pairing brings the right amino acid D1.2.7
- ☐ Explain why the code uses threes and what degenerate and universal mean, and use a codon table to deduce a polypeptide D1.2.8, D1.2.9
- ☐ Describe how the ribosome moves one codon at a time, joining each amino acid to the chain with a peptide bond D1.2.10
- ☐ Explain how one base change in the haemoglobin gene causes sickle cell anaemia D1.2.11
- ☐ Explain what 5' to 3' means for transcription and for translation D1.2.12
- ☐ Explain how transcription factors start transcription at a promoter, and name four kinds of DNA that code for no polypeptide D1.2.13, D1.2.14
- ☐ Describe how pre-mRNA is capped, tailed and spliced, and how alternative splicing makes several polypeptides from one gene D1.2.15, D1.2.16
- ☐ Describe how translation starts, and what the A, P and E sites do D1.2.17
- ☐ Explain how pre-proinsulin becomes insulin, and why proteasomes keep breaking proteins down D1.2.18, D1.2.19

Tick each one when you can do it without the book.

01

D1.2.1

D1.2.2

TRANSCRIPTION

Copying a gene into *RNA*

A **gene** is a stretch of DNA whose base sequence codes for a polypeptide. Proteins are not built where the DNA is kept, so the cell first makes a working copy of the gene in RNA. Making RNA with a DNA template is **transcription**, and the RNA that carries a gene's message to the ribosomes is **messenger RNA** (mRNA). In a eukaryotic cell this happens in the nucleus; in a prokaryote, in the cytoplasm.

One enzyme does the whole job. **RNA polymerase** binds at the start of a gene and parts the two DNA strands over a short stretch (it needs no helicase: that enzyme unzips DNA when the whole molecule is copied, in D1.1). Free RNA nucleotides pair with the exposed bases of one strand only, the **template strand**. The other strand is the **coding strand**, because the RNA ends up with its sequence. (You may meet them called antisense and sense.) The enzyme joins each new nucleotide to the last with a covalent bond, moves on, and lets go at the end of the gene.

Complementary base pairing chooses every RNA base. A on the template takes **uracil** (U), T takes A, C takes G and G takes C. The pairs are held by **hydrogen bonds**: weak enough to form and break as the enzyme passes, but specific, because only the right base fits. That is how the sequence is copied exactly. Behind the enzyme the RNA peels away and the DNA strands pair up again.

KEY POINTS

- The RNA is complementary to the template, and has the same sequence as the coding strand, with U where DNA has T.
- Only the template is read. The coding strand takes no part.

Which way the RNA grows is chapter 8, and how the enzyme finds the start of a gene is chapter 9.

KEY TERMS

gene

A length of DNA whose base sequence codes for a polypeptide, or for an RNA that does a job of its own.

transcription

Making an RNA copy of a gene, using one strand of the DNA as a template.

messenger RNA

RNA copied from a gene. It carries the gene's base sequence to a ribosome, where it is read.

RNA polymerase

The enzyme that makes RNA. It parts the two DNA strands over a short stretch, pairs free RNA nucleotides with one strand and joins them with covalent bonds.

template strand

The DNA strand that RNA polymerase reads. The RNA is built complementary to it.

coding strand

The DNA strand that is not read. Its base sequence matches the RNA, with T in place of U.

complementary base pairing

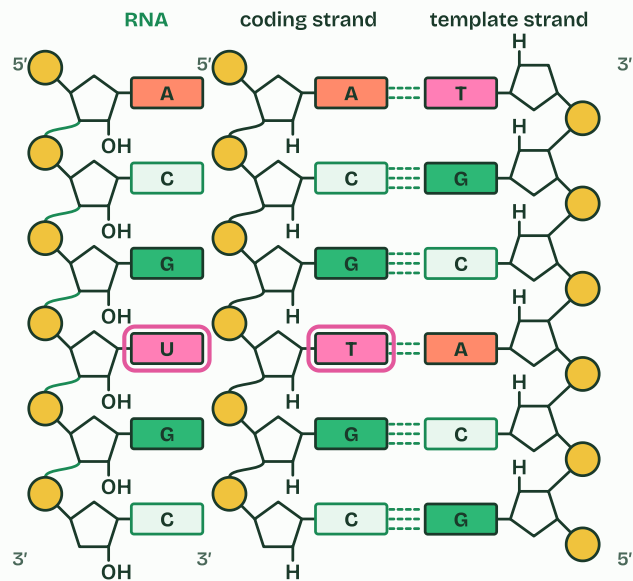
The rule that each base pairs with one particular other base: A with T (or U), and C with G.

uracil

The base U, found in RNA in place of thymine. It pairs with adenine.

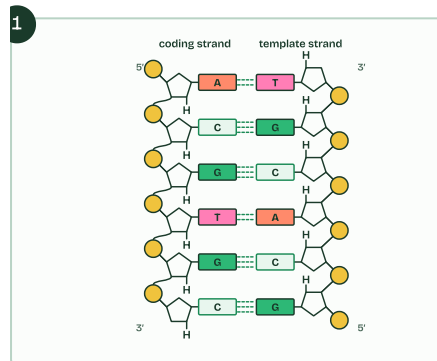
hydrogen bonds

Weak attractions between a slightly positive hydrogen atom on one molecule and a slightly negative atom on another.

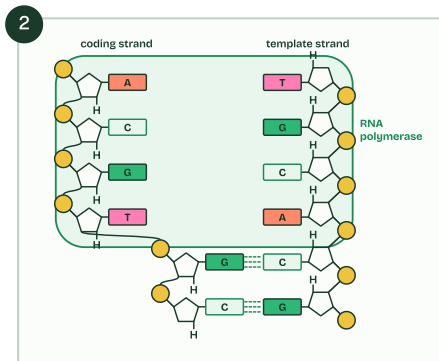


STEP BY STEP

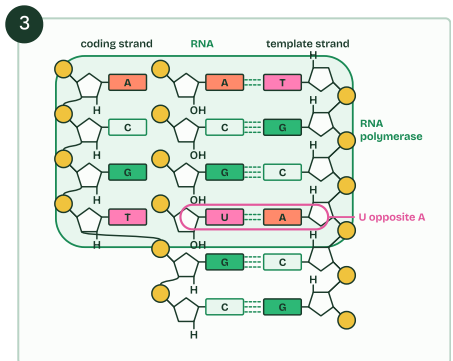
5 STEPS



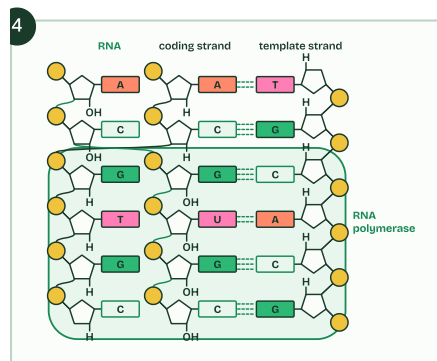
A gene: two strands of DNA, held by **hydrogen bonds**.



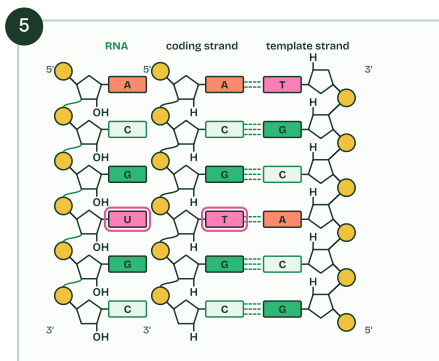
RNA polymerase parts the strands.



RNA nucleotides pair with the **template strand**: U opposite A.



The enzyme joins them into a strand and moves on; the DNA closes behind it.



The RNA has the **coding strand's** sequence, with U in place of T.

REMEMBER IT

Which base pairs with which in transcription

A Apples	U Under	C Cars	G Garage
A on the template pairs with U in the RNA	U in the RNA uracil, where DNA has T	C on the template pairs with G in the RNA	G on the template pairs with C in the RNA

WATCH OUT

RNA polymerase, not helicase, parts the DNA in transcription. And the RNA is not a copy of the template: it is complementary to it, and matches the coding strand (with U for T).

PREDICT

A gene's template strand reads T A C C T G. Which RNA does RNA polymerase make from it?

- (A) U A C C U G
- (B) A U G G A C
- (C) A T G G A C

Decide before you look. Answer on page 46.

02

D1.2.3

D1.2.4

STABLE TEMPLATES, GENE EXPRESSION

Read for a lifetime, read *when needed*

Transcription reads the template; it does not use it up. The hydrogen bonds open for a moment and close again, the covalent backbone is never broken, and no base is changed. So one gene can be transcribed again and again, and every copy of its mRNA matches.

That matters most in **somatic cells** that never divide again. Most of the nerve cells in the outer layer of your brain are as old as you are, and heart muscle cells are replaced only very slowly, so the genes in each have to be read for decades. Their base sequences must be **conserved**: held without change for the whole life of the cell. DNA suits the job, with two strands, a strong backbone and a home in the nucleus. (Cells also repair damage to DNA; that is D1.3.)

Every somatic cell of one person has the same **genome**, yet no cell uses all of its genes. A gene is expressed when its information is used to make its product. That is **gene expression**, and it has two main steps: transcription copies the gene into mRNA, and translation (chapter 3) uses the mRNA to build a polypeptide. A gene that is being transcribed is **switched on**, and one that is not is **switched off**. The more often it is transcribed, the more mRNA, and the more of its protein, the cell makes. Some genes are switched on and off as conditions change. Which genes a cell transcribes is what makes it a particular kind of cell: a pancreatic beta cell transcribes the insulin gene and a skin cell does not, so each is specialised for its own job.

KEY POINTS

- Transcription reads a template without changing it, so one gene gives many identical mRNAs.
- Not all genes are expressed in a cell at one time, and transcription is where a gene is switched on or off.

How a gene is switched on at its promoter is chapter 9.

KEY TERMS

somatic cells

Body cells: any cell of an organism except the cells that make eggs or sperm.

conserved

Kept unchanged over a long time, for the whole life of a cell or through many generations.

genome

All the DNA of a cell or organism, with all its genes.

gene expression

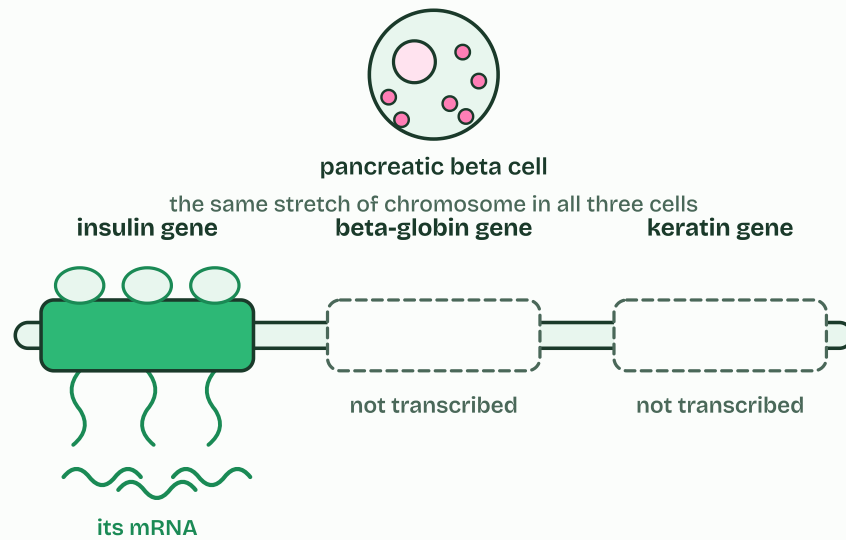
The use of the information in a gene to make its product, starting with transcription.

switched on

Being transcribed, so that its product is made.

switched off

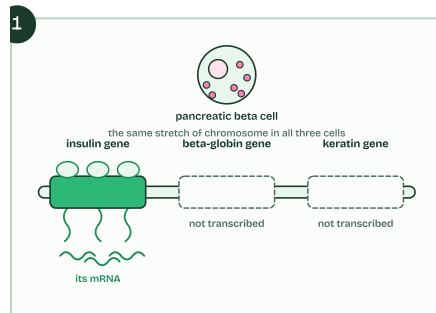
Not being transcribed, so that its product is not made.



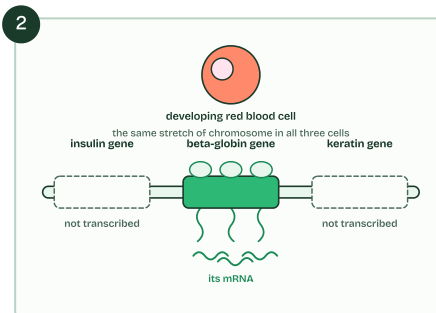
The same three genes sit in every one of these cells. Which one is being copied changes from cell to cell.

SWITCH IT

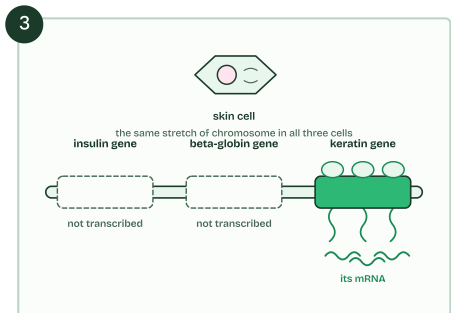
3 SETTINGS



Pancreatic beta cell



Developing red blood cell



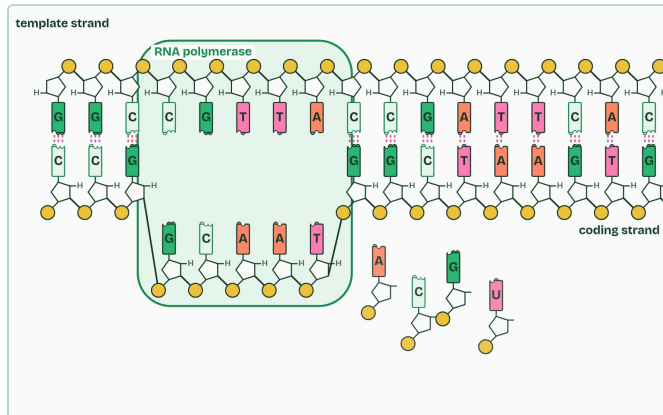
Skin cell

ANIMATION · ONE GENE, COPIED

4 MOMENTS

1

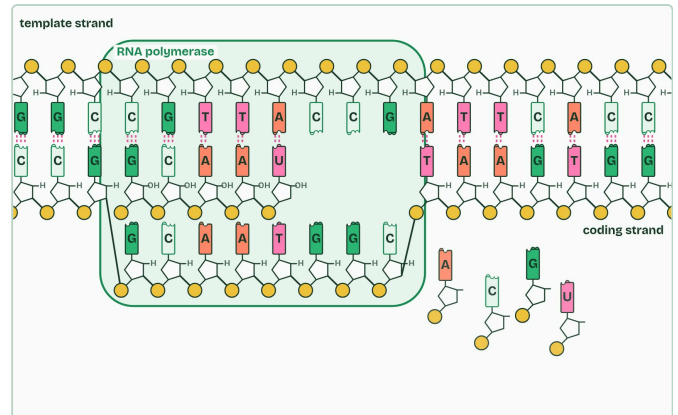
RNA BASES: 0



RNA polymerase unzips a short stretch of the gene: the hydrogen bonds holding its bases together give way.

2

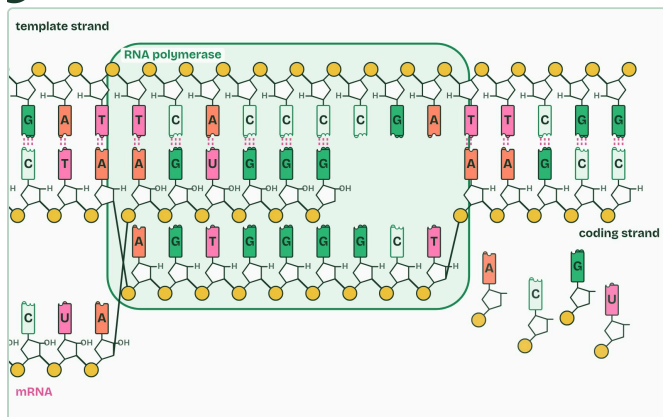
RNA BASES: 5



Free RNA nucleotides pair with the template by complementary base pairing, U opposite A.

3

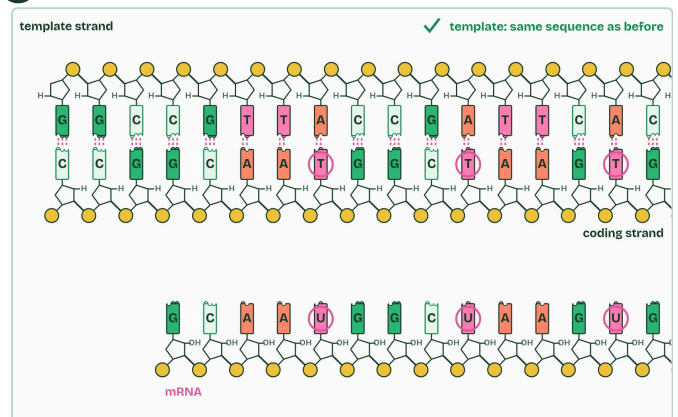
RNA BASES: 16



Behind the enzyme the RNA peels off and the DNA closes up again.

4

MRNA MADE: 1



The RNA has the coding strand's sequence, with U in place of T. The template has not changed.

Watch it move, and change it as it runs: biologybybradford.com/guides/ib-biology-d1-2-protein-synthesis#read-again

WATCH OUT

Different cells do not have different genes. They have the same genes and transcribe different ones.

PREDICT

A nerve cell in your brain is 60 years old and has never divided. Its genes have been transcribed all that time. What has happened to their base sequences?

- (A) Used up at the first reading, then remade
- (B) Read many times, and a little worn down
- (C) Read many times, and still the same

Decide before you look. Answer on page 46.

03

D1.2.5 D1.2.6 TRANSLATION

Three kinds of *RNA* build a protein

Translation makes a **polypeptide** whose order of **amino acids** is set by the base sequence of an mRNA. It happens at **ribosomes**, some free in the cytoplasm and some on the rough endoplasmic reticulum.

A ribosome is made of **ribosomal RNA (rRNA)** and protein, in two parts. The mRNA binds to the **small subunit**. The **large subunit** can hold two tRNAs at once, side by side, and it joins their amino acids (the rRNA is what speeds up that joining).

Transfer RNA (tRNA) molecules are short, single strands of RNA that fold back on themselves into a compact shape. Each carries one particular amino acid at one end, and has three exposed bases at the other, its anticodon, which chapter 4 is about. There are many kinds of tRNA, at least one for every amino acid.

So the three kinds of RNA share the work. The mRNA, a long single strand whose bases are read in threes, carries the message, the rRNA in the ribosome holds it and joins the amino acids, and the tRNAs bring the amino acids in. What holds the message in place, base to base, is hydrogen bonds again.

KEY POINTS

- mRNA binds to the small subunit of the ribosome.
- Two tRNAs can bind at the same time, in the large subunit.

KEY TERMS**translation**

Making a polypeptide by reading the codons of an mRNA: the base sequence sets the amino acid sequence.

polypeptide

A chain of amino acids joined by peptide bonds.

amino acids

The monomers of polypeptides. Twenty kinds are used in cells, each with a different R group.

ribosomes

Structures in the cytoplasm that read mRNA and join amino acids into polypeptides. Each is made of rRNA and protein, in two subunits.

ribosomal RNA (rRNA)

RNA that, with protein, makes up the two subunits of a ribosome.

small subunit

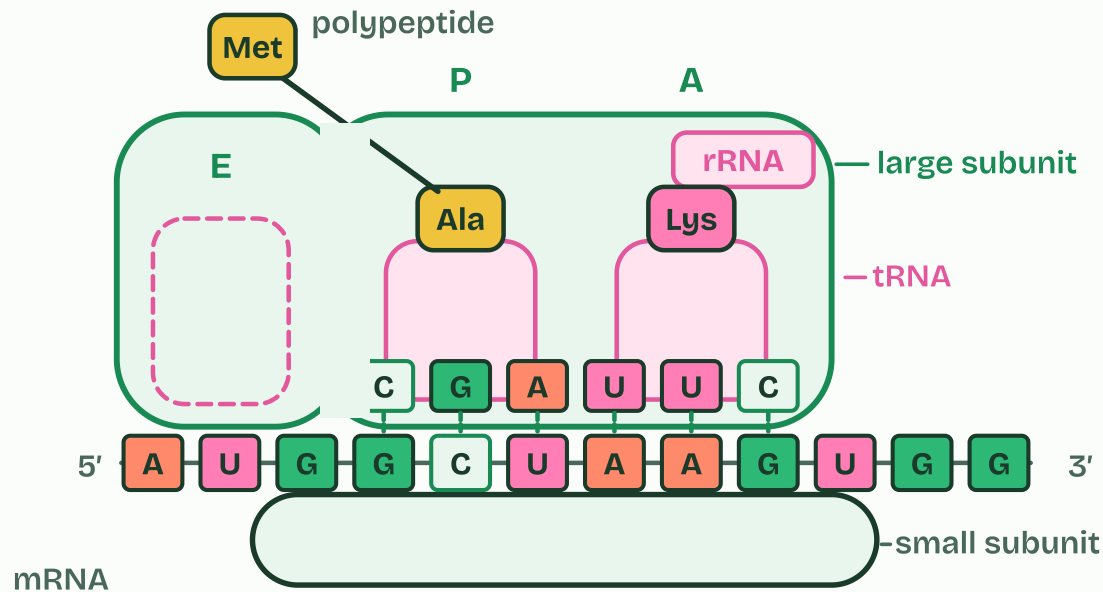
The smaller part of a ribosome. The mRNA binds to it.

large subunit

The larger part of a ribosome. It can hold two tRNAs at once and joins their amino acids.

Transfer RNA (tRNA)

Small RNA molecules that each carry one particular amino acid and have three exposed bases, the anticodon, that pair with an mRNA codon.



A ribosome part way along an mRNA: two tRNAs are in place, a short chain hangs from one of them, and the next codon waits.

Small subunit Holds the mRNA in place on the ribosome.

Large subunit Holds two tRNAs at a time and joins their amino acids together.

tRNA Transfer RNA. Each kind brings one particular amino acid, and has three exposed bases at its foot.

Polypeptide The growing chain of amino acids, hanging from one of the tRNAs.

mRNA The message: the gene's base sequence, copied in the nucleus. The ribosome reads it three bases at a time.

rRNA Ribosomal RNA. With proteins, it makes up both subunits, and it is the rRNA that speeds up the joining of amino acids.

Amino acid One of 20 kinds, carried on the top end of a tRNA.

WATCH OUT

Ribosomes do not make amino acids. They join the amino acids that tRNAs bring.

PREDICT

The large subunit holds two tRNAs at the same moment. Why two, and not one?

- (A) So one brings the codon and one the amino acid
- (B) So one amino acid can be joined to the next
- (C) So each tRNA can check the other's anticodon

Decide before you look. Answer on page 46.

04

D1.2.7 CODONS AND ANTICODONS

Codon meets *anticodon*

The mRNA is read three bases at a time. Each group of three is a **codon**. A tRNA carries a matching group of three exposed bases at one end, its **anticodon**, and one particular amino acid at the other end.

In the ribosome an anticodon pairs with a codon by complementary base pairing, held by hydrogen bonds: A with U and C with G. A tRNA whose anticodon fits stays long enough for its amino acid to be joined to the chain, and any other tRNA drifts away again. So the right amino acid arrives because the right tRNA pairs, and each kind of tRNA always carries the same amino acid, which is what keeps the code accurate.

Anticodons contain U, never T, because a tRNA is RNA. There is a neat consequence: an anticodon has the same bases as the template strand's triplet for that codon, with U where DNA has T. Take the codon GCU: its anticodon is CGA, on a tRNA that carries alanine. At higher level you also write the ends: the codon is 5'-GCU-3' and the anticodon 3'-CGA-5'.

KEY POINTS

- A codon sits on mRNA, an anticodon on tRNA.
- Pairing is complementary, A with U and C with G, so a codon decides which tRNA fits.

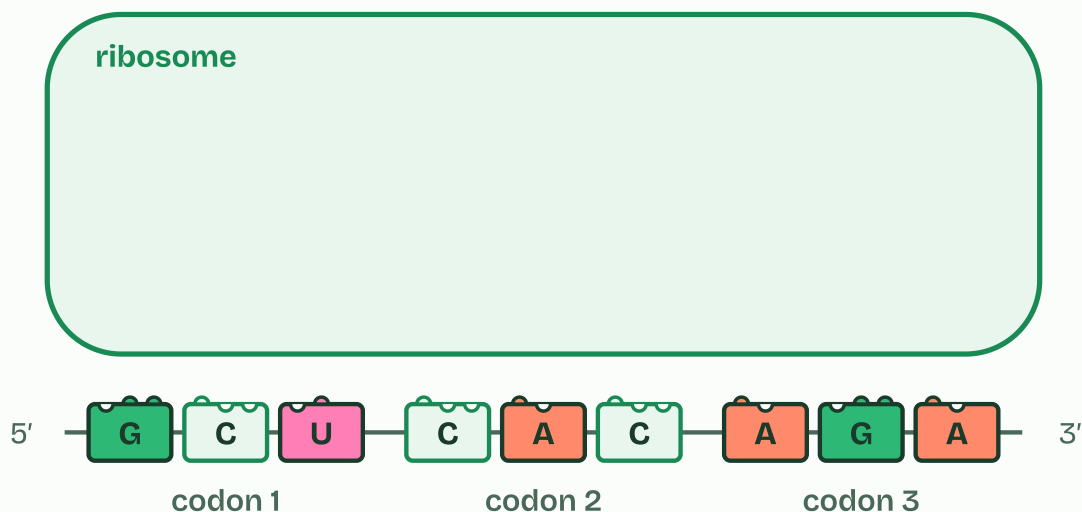
KEY TERMS

codon

A group of three bases on an mRNA that codes for one amino acid (or a stop).

anticodon

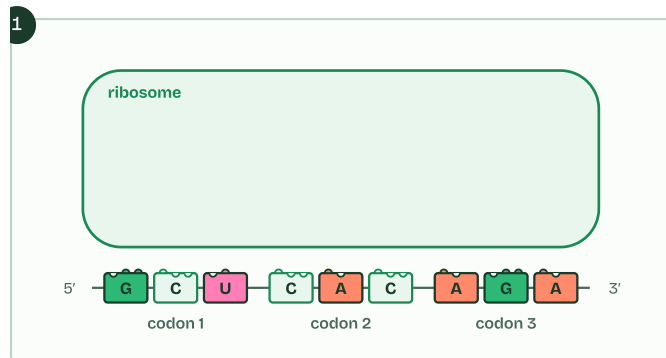
The three exposed bases of a tRNA, complementary to an mRNA codon.



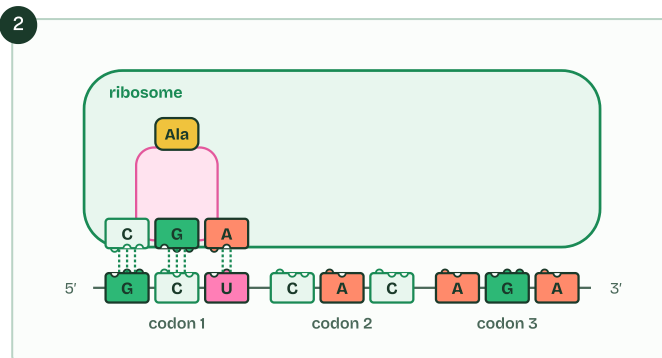
Each base's pairing edge has knobs and notches: a knob fits a notch, a flat edge fits a flat edge. The same rule decides which tRNA fits each codon. (A real ribosome holds two tRNAs at a time and moves on; here each codon keeps its tRNA so you can compare them.)

SWITCH IT

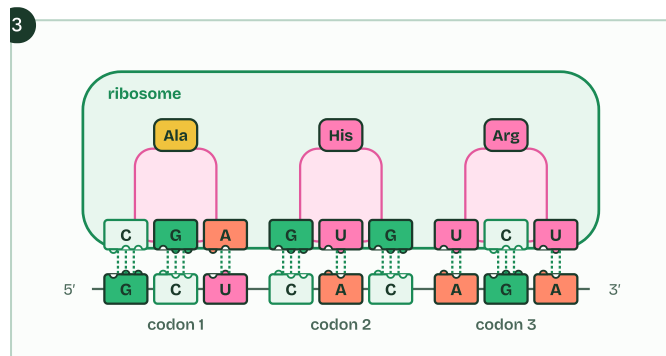
3 SETTINGS



Three codons, a rack of tRNAs



One tRNA docked



Each codon has found its tRNA

WATCH OUT

Codons are on mRNA and anticodons are on tRNA. DNA has neither: its triplets are just triplets.

PREDICT

A codon reads U G G. Which anticodon pairs with it?

- (A) A C C
- (B) T C C
- (C) U G G

Decide before you look. Answer on page 46.

05

D1.2.8 D1.2.9 THE GENETIC CODE

A code written in *threes*

The **genetic code** says which amino acid each codon stands for. A cell uses four bases and twenty amino acids. One base for each amino acid gives only 4 meanings, and two bases give $4 \times 4 = 16$, still too few. Three bases give $4 \times 4 \times 4 = 64$, more than enough. So the code is a **triplet code**.

Of the 64 codons, 61 code for amino acids. The other three, UAA, UAG and UGA, are **stop codons**: they code for nothing and end the chain. AUG codes for methionine and is also the **start codon**, where translation begins. With 61 codons for 20 amino acids, most amino acids have more than one codon, so the code is **degenerate**: leucine, serine and arginine have six each, methionine and tryptophan only one. Degenerate never means ambiguous, because no codon stands for two amino acids.

The code is also **universal**: almost every living thing reads each codon as the same amino acid, from bacteria to people. A few small exceptions exist (the mitochondria of vertebrates, ours included, read UGA as tryptophan), but they are rare. A code this arbitrary, shared by all life, points to one common ancestor (A1.2.10). It is also why bacteria given the human insulin gene make human insulin, which is how insulin for people with diabetes is made.

KEY TERMS

genetic code

The rules that say which amino acid each codon stands for.

triplet code

A code in which each codon is three bases long.

stop codons

Codons that code for no amino acid and end translation: UAA, UAG and UGA.

start codon

The codon AUG, where translation begins. It codes for methionine.

degenerate

Having more than one codon for most amino acids. A codon never stands for two amino acids.

universal

Shared by almost all living things: a codon means the same amino acid in nearly every organism.

reading frame

The way the bases of an mRNA are grouped into codons. A different start gives different codons.

20 amino acids



each small block is one base:



Each column is one amino acid (the shapes on top), and the blocks stacked under it are the codons that stand for it. At three bases, the last column holds the stop codons.

SLIDE IT

3 SETTINGS

1

20 amino acids

each small block is one base:

2

20 amino acids

each small block is one base:

Bases in each codon 1

Bases in each codon 2

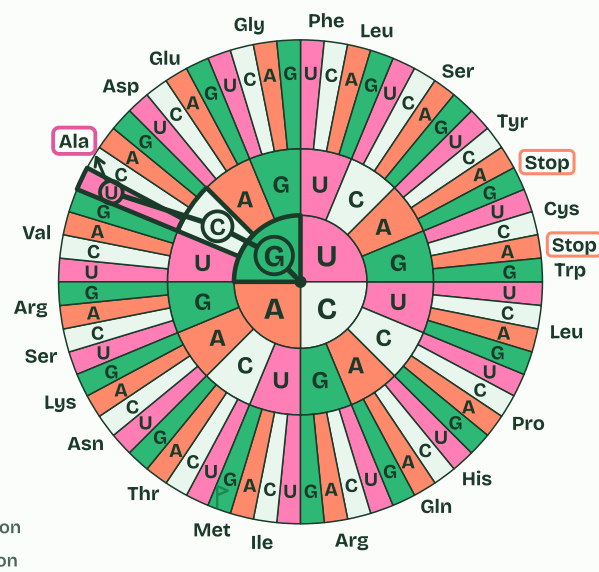
3

20 amino acids

each small block is one base:

stop

Bases in each codon 3



Tap three bases, or an amino acid. Paste a strand to translate it, or start a round of ten under it to practise reading the code.

STEP BY STEP

3 STEPS

1

1st	2nd	3rd
UUU	Phe	
UUC	Phe	
UUA	Leu	
UUG	Leu	
CUU	Leu	
CUC	Leu	
CUA	Leu	
CUG	Leu	
AUU	Ile	
AUC	Ile	
AUA	Ile	
AUG	Met	start
GUU	Val	
GUC	Val	
GUA	Val	
GUG	Val	

2

1st	2nd	3rd
UUU	Phe	
UUC	Phe	
UUA	Leu	
UUG	Leu	
CUU	Leu	
CUC	Leu	
CUA	Leu	
CUG	Leu	
AUU	Ile	
AUC	Ile	
AUA	Ile	
AUG	Met	start
GUU	Val	
GUC	Val	
GUA	Val	
GUG	Val	

3

The **genetic code**: 64 codons, read from the first base to the third.

Find the **first** base, then the **second**, then the **third**: GCU is alanine.

The **wheel** holds the same code, read from the centre out.

PREDICT

Why can the code not use pairs of bases for each amino acid?

- (A) Pairs would be read too slowly by the ribosome
- (B) Pairs cannot form hydrogen bonds with any anticodon
- (C) Pairs give only 16 codons for 20 amino acids

Decide before you look. Answer on page 46.

06

D1.2.10 ELONGATION

One codon at a *time*

Once translation has started, the polypeptide grows by a cycle that repeats for every codon. This is **elongation**, and it is the part of translation this chapter follows. How translation starts is chapter 11.

KEY POINTS

- A tRNA whose anticodon pairs with the codon in the free place binds, bringing its amino acid.
- The ribosome joins the chain to that amino acid with a **peptide bond**. This is a **condensation** reaction, so a molecule of water is released, and the chain now hangs from the newest tRNA.
- The ribosome moves one codon, three bases, along the mRNA, towards its 3' end.
- The tRNA that handed over the chain leaves, free to collect another amino acid.

KEY TERMS

elongation

The stage of translation in which the polypeptide grows by one amino acid for each codon read.

peptide bond

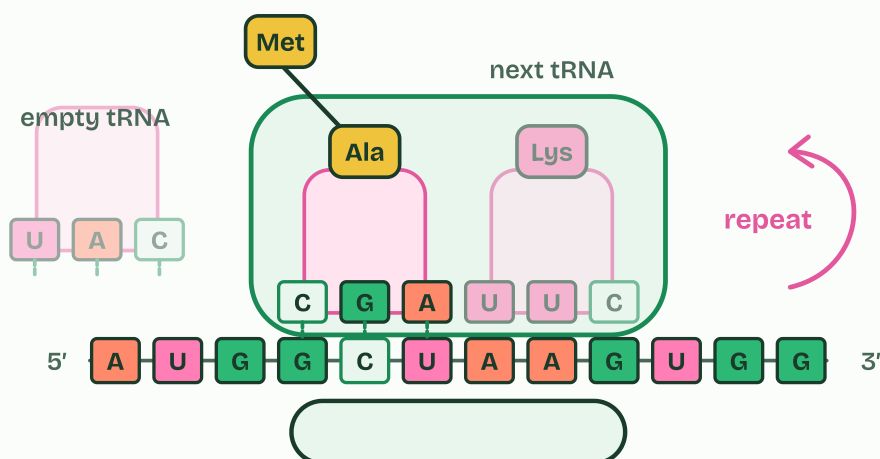
The covalent bond between the carbon of one amino acid and the nitrogen of the next. It holds a polypeptide together.

condensation

A reaction that joins two molecules and releases a molecule of water.

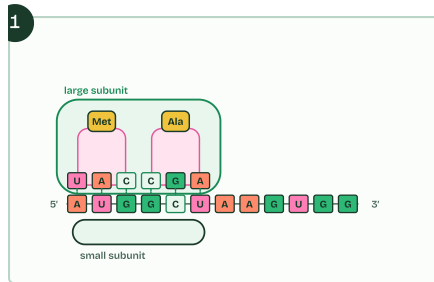
The chain grows by one amino acid for every codon, in the order of the codons. A human ribosome adds about five amino acids a second, so a protein of 300 amino acids takes about a minute. At a stop codon no tRNA pairs, and the polypeptide is released.

Two kinds of bond do two jobs here. Hydrogen bonds hold codon and anticodon together for a moment. Peptide bonds, which are covalent, hold the chain together for good.

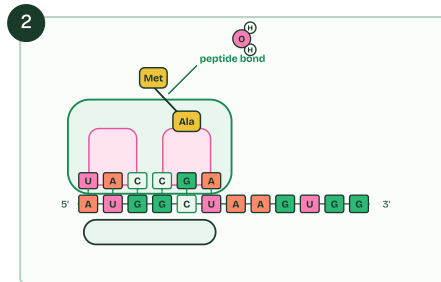


STEP BY STEP

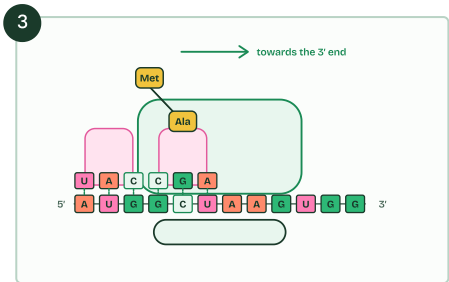
4 STEPS



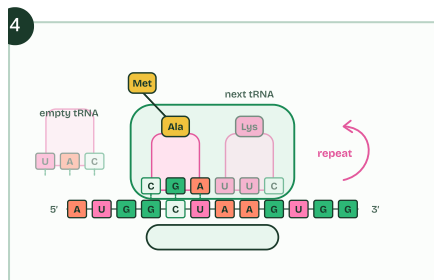
The next tRNA **pairs** with the open codon.



A **peptide bond** joins the chain to its amino acid.



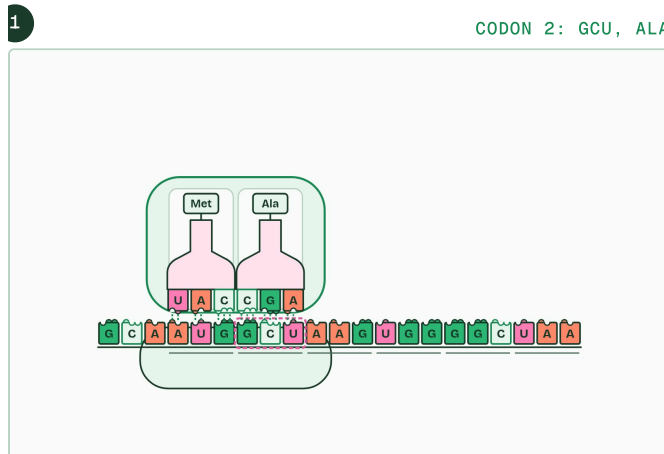
The ribosome **moves** one codon along.



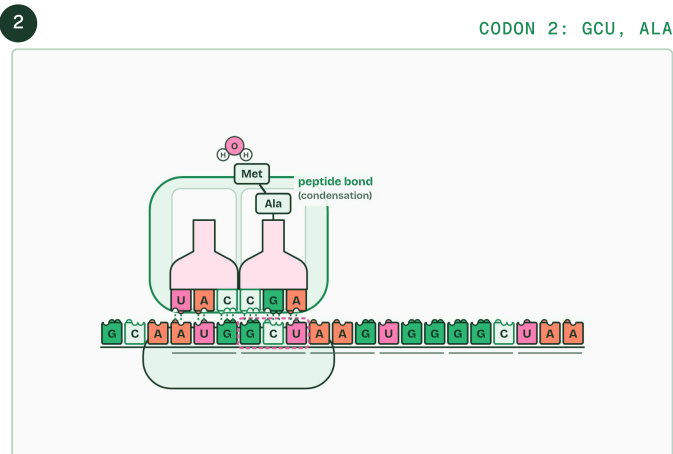
The empty tRNA **leaves**. Repeat.

ANIMATION · ONE CODON AT A TIME

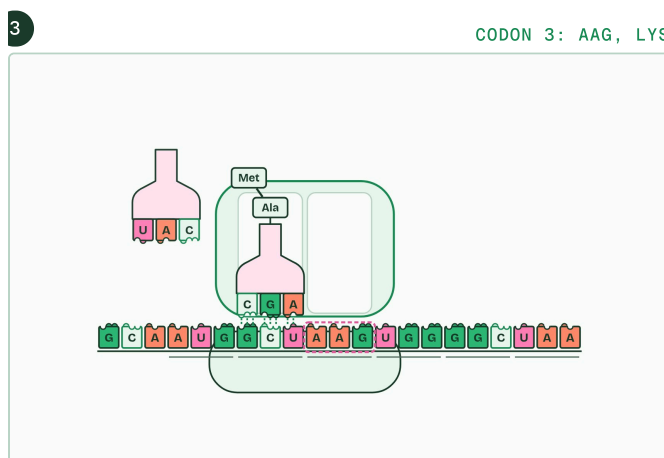
4 MOMENTS



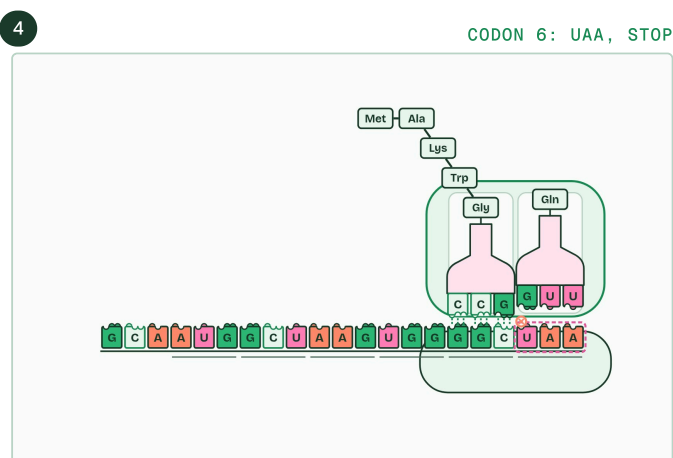
A tRNA whose anticodon pairs with the codon brings the right amino acid.



A peptide bond joins the chain to the new amino acid.



The ribosome moves along one codon, and the empty tRNA leaves to collect another amino acid.



At a stop codon no tRNA fits, and the polypeptide is released.

Watch it move, and change it as it runs: biologybybradford.com/guides/ib-biology-d1-2-protein-synthesis#elongation

WATCH OUT

Amino acids in the chain are joined by peptide bonds, not hydrogen bonds. The hydrogen bonds are between codon and anticodon, and they break as each tRNA leaves.

PREDICT

A polypeptide is 150 amino acids long. How many codons did the ribosome read to make it, counting the codon that ended it?

- ☐ A 150
- ☐ B 151
- ☐ C 450

Decide before you look. Answer on page 46.

07

D1.2.11 MUTATIONS THAT CHANGE PROTEIN STRUCTURE

One base, one *amino acid*

A **mutation** is a change in the base sequence of a gene. A **point mutation** changes one base, and the commonest kind is a **base substitution**: one base swapped for another, which changes one codon. What that does to the polypeptide depends on the new codon. If it stands for the same amino acid, the mutation is **silent**, which the code's degeneracy allows. If it stands for a different amino acid, it is **missense**. If it is a stop codon, it is **nonsense**, and the chain ends early, usually too short to work. (Bases added or lost, and what causes mutations, are D1.3.)

Sickle cell anaemia is the guide's example of a point mutation that changes a protein. **Haemoglobin** carries oxygen in red blood cells. In the gene for its beta chain, codon 6 on the coding strand changes from GAG to GTG (on the template strand, CTC becomes CAC), so the mRNA codon changes from GAG to GUG and glutamic acid (Glu) becomes valine (Val). (The positions are counted from the first amino acid of the finished chain, which is valine, because the starting methionine is removed. Counted from the start codon this is the seventh codon.)

One amino acid matters because of where it sits. Glu is charged and hydrophilic, and Val is non-polar. Position 6 lies on the outside of the haemoglobin molecule, so the valine makes a non-polar patch there that sticks to a pocket on a neighbouring molecule. When oxygen is low, the molecules join into long stiff fibres that bend red blood cells into sickle shapes. The sickled cells block small blood vessels, which causes pain and damage to organs, and they are destroyed early, so the person has too few red blood cells, which is **sickle cell anaemia**. The haemoglobin itself still carries oxygen: the harm comes from the fibres, and from the cells' shape and short life.

KEY TERMS

mutation

A change in the base sequence of a gene.

point mutation

A mutation that changes a single base.

base substitution

A point mutation in which one base is swapped for another. It changes one codon.

silent

A substitution that does not change the amino acid, because the new codon codes for the same one.

missense

A substitution that changes one amino acid in the polypeptide.

nonsense

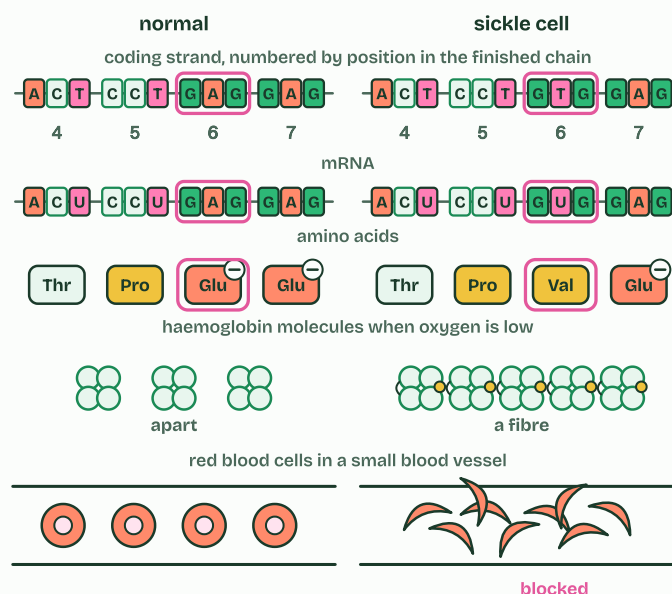
A substitution that makes a stop codon, so the chain ends early.

haemoglobin

The protein in red blood cells that carries oxygen.

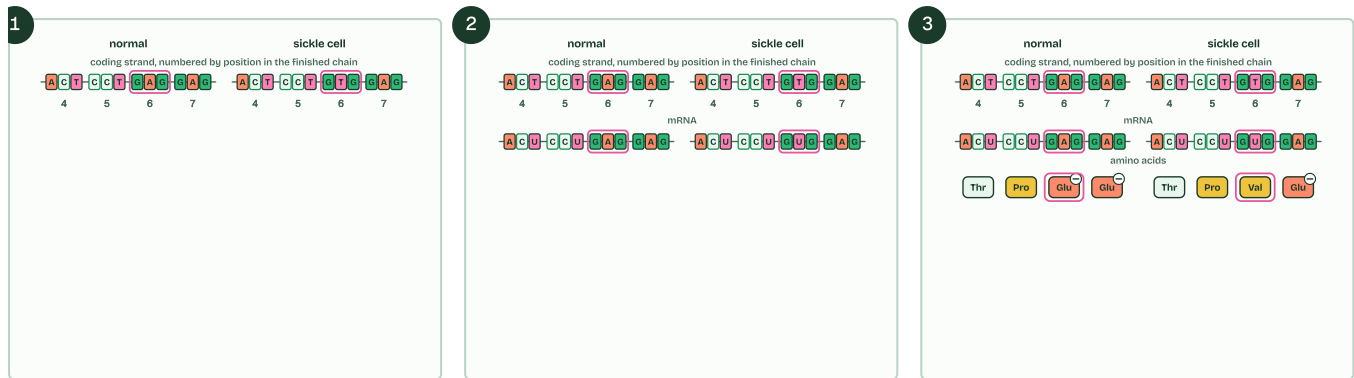
sickle cell anaemia

An inherited disease in which a changed haemoglobin forms fibres that bend red blood cells into sickles, block small vessels and are destroyed early.



STEP BY STEP

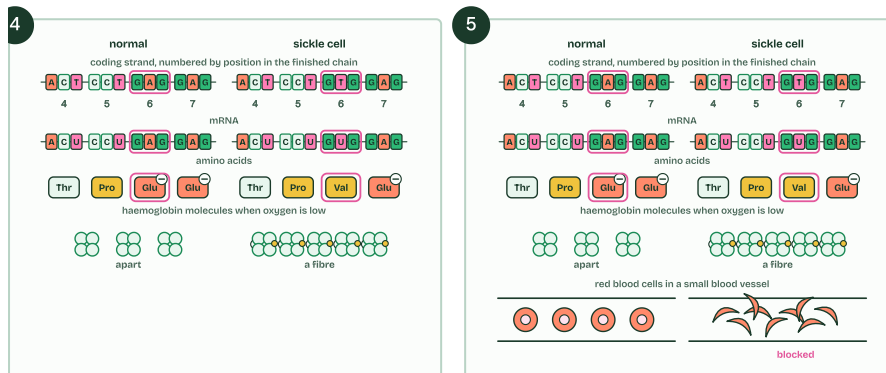
5 STEPS



One base differs in the gene for haemoglobin's beta chain.

So one **codon** in the mRNA differs.

So one **amino acid** differs: **valine** for glutamic acid.



The non-polar valine makes the molecules stick into **fibres**.

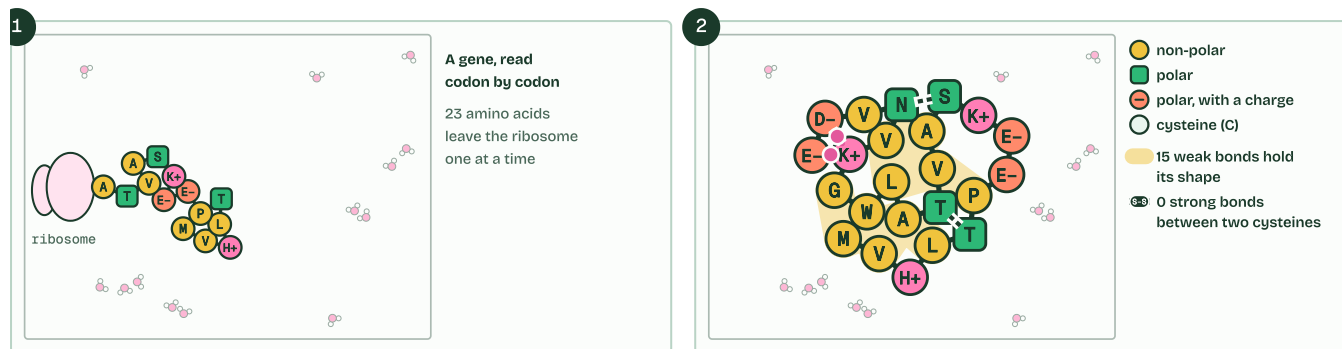
Fibres bend the cells into sickles that block small vessels.

- non-polar
- polar
- polar, with a charge
- cysteine (C)
- 15 weak bonds hold its shape
- 0 strong bonds between two cysteines

Fold the start of the beta-globin gene, make the sickle cell change, fold both and make a second copy of each.

STEP BY STEP

2 STEPS

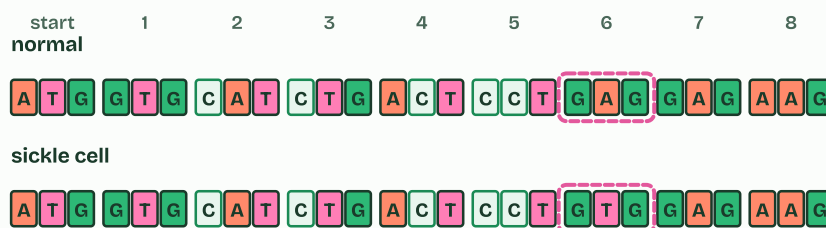


The gene is transcribed and translated: Its 23 amino acids are joined by 22 peptide bonds: one of 20^{23} (about 8×10^{29}) possible chains this long. A ribosome makes the chain one amino acid at a time, and it starts to fold as it comes out.

It folds into a shape of its own, held by **weak bonds** between its side chains.

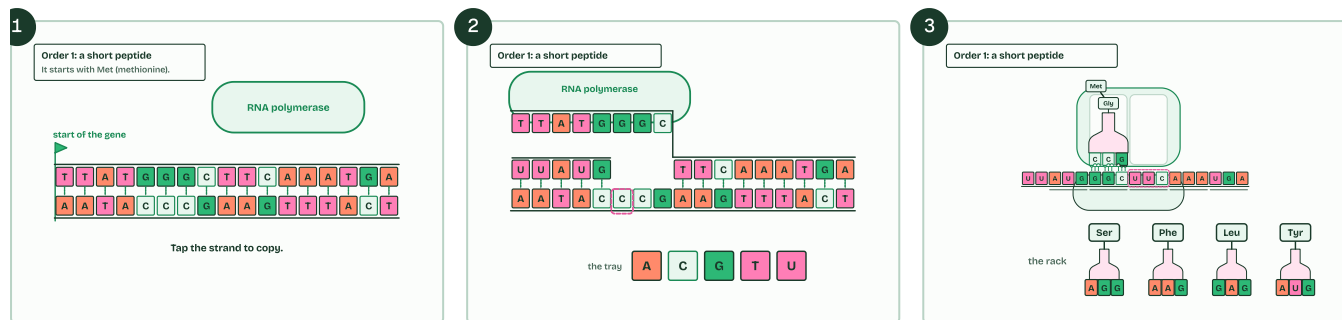
Clinic sample

Two alleles of one gene

normal, amino acid 6 sickle cell, amino acid 6

STEP BY STEP

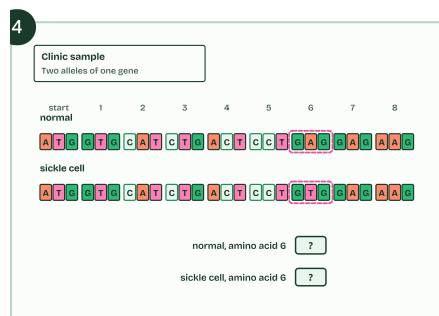
4 STEPS



Which strand will you copy?

Pick the base that pairs: RNA has U, not T.

Which tRNA's anticodon pairs with this codon?



One base differs. What does it do to the protein?

REMEMBER IT

What a substitution can do

S Same	S Swapped	S Stopped
Silent the same amino acid	Missense a different amino acid	Nonsense a stop codon: the chain ends early

WATCH OUT

A mutation changes the gene, not the protein directly: the changed protein follows from the changed codon. And not every substitution changes the protein.

PREDICT

In a gene, one base changes so that an mRNA codon GAA becomes GAG. What happens to the polypeptide?

- (A) Glu is replaced by another amino acid
- (B) The chain stops at that codon
- (C) No change: GAG also codes for Glu

Decide before you look. Answer on page 46.

08

D1.2.12 HL DIRECTIONALITY

Five prime to three prime, *both times*

From A1.2 you know that the carbons of a nucleotide's sugar are numbered 1' to 5'. A strand has a **5' end**, where the last nucleotide has a phosphate on its carbon 5', and a **3' end**, where the last nucleotide has a free OH on its carbon 3'. So every strand has a direction.

5' to 3' transcription means that RNA polymerase joins the 5' phosphate of each incoming RNA nucleotide to the 3' OH at the end of the growing RNA (the sugar is ribose, because this is RNA). The new link is a covalent bond, the same sugar-phosphate bond that forms the backbone of a strand (A1.2). A nucleotide can only be added at the 3' end, so the RNA is built from its 5' end to its 3' end. The template runs the opposite way to the RNA, so the polymerase reads the template 3' to 5'. The coding strand runs the same way as the RNA, which is why its sequence, written 5' to 3', matches the mRNA's.

Translation runs 5' to 3' too. The ribosome starts near the mRNA's 5' end and moves towards its 3' end, so the codons are read in that order, and the first amino acid of the polypeptide comes from the codon nearest the 5' end. Direction matters: read the other way, the same bases make different codons and a different polypeptide, and the start codon is found only by moving 5' to 3' from the 5' end (chapter 11). By convention a sequence is written 5' to 3', left to right, unless it is labelled otherwise.

KEY TERMS

5' end

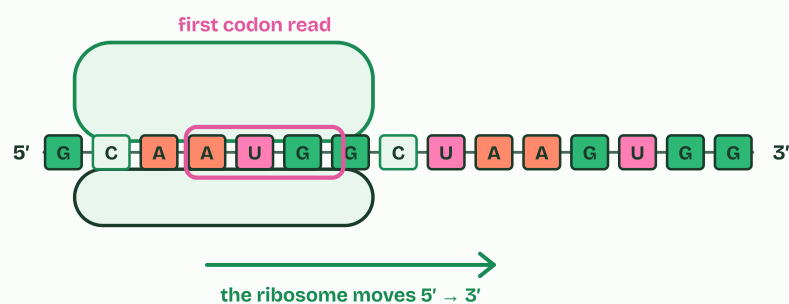
The end of a strand where the last nucleotide has a free phosphate on its carbon 5'.

3' end

The end of a strand where the last nucleotide has a free OH on its carbon 3'.

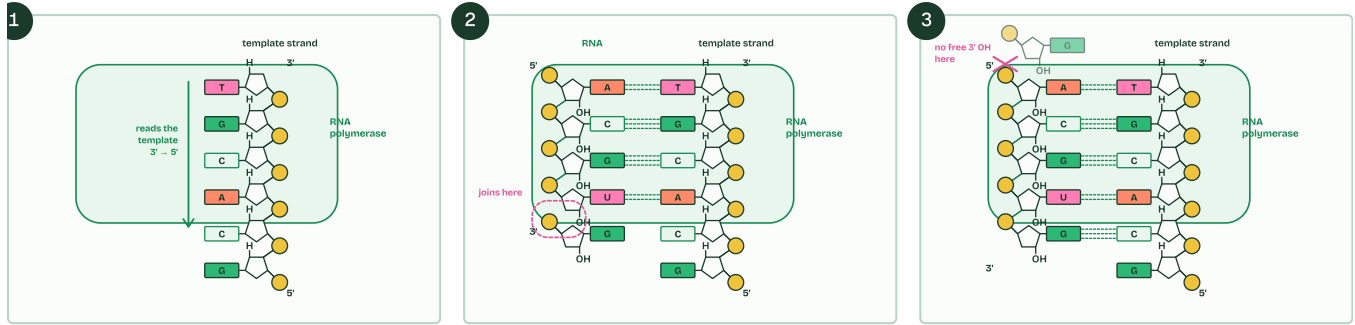
5' to 3'

The direction of a strand: from its 5' end to its 3' end. RNA is built this way, and mRNA is read this way.



STEP BY STEP

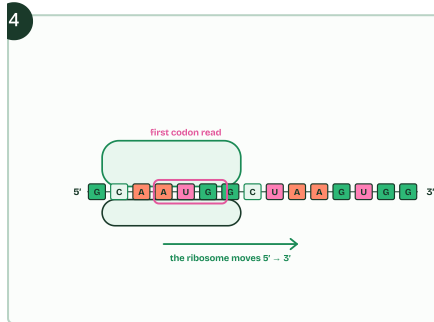
4 STEPS



The polymerase reads the **template 3' to 5'**.

Each new nucleotide joins the RNA's **3' end**.

Nothing can join at the 5' end.



The ribosome reads the mRNA **5' to 3'** too.

WATCH OUT

5' and 3' name carbons of the sugar. The polymerase moves along the template from its 3' end towards its 5' end, while the RNA it makes grows 5' to 3': two directions, one movement.

PREDICT

A template strand reads 3'-TACAAGCGT-5'. Written 5' to 3', what is the mRNA?

- (A) 5'-ACGCUUGUA-3'
- (B) 5'-AUGUUCGCA-3'
- (C) 5'-UACAAGCGU-3'

Decide before you look. Answer on page 46.

D1.2.13 HL

D1.2.14 HL

PROMOTERS AND NON-CODING DNA

09

Where a gene starts, and DNA that codes for *nothing*

The **promoter** is a stretch of DNA just before the part of a gene that is transcribed. It is not transcribed itself. It is where transcription starts.

Transcription factors are proteins that attach to the promoter, and RNA polymerase can bind and start only when the right ones are in place (you do not have to name any). Which factors a cell makes decides which of its genes are transcribed: that is the switch from chapter 2. Some factors promote transcription and others block it. The promoter is a whole region, not one named sequence.

Non-coding sequences are stretches of DNA that code for no polypeptide. In humans only about 1 to 2% of the genome codes for polypeptides, and the rest includes:

KEY POINTS

- **regulators of gene expression:** promoters, and other sequences where factors bind;
- **introns:** stretches inside a gene that are transcribed but cut out of the RNA (chapter 10);
- **telomeres:** repeats of a short sequence (TTAGGG in humans) at each end of a chromosome, which protect the genes near the ends when the DNA is copied;
- genes for rRNA and tRNA: they are transcribed, and the RNA is the product. It is never translated.

Non-coding does not mean useless. Every one of these has a job, and none of them codes for a polypeptide.

KEY TERMS**promoter**

A region of DNA just before a gene, where transcription factors and RNA polymerase bind to start transcription. It is not itself transcribed.

transcription factors

Proteins that bind to DNA at a promoter, or other regulatory sequences, and control whether a gene is transcribed.

Non-coding sequences

DNA that codes for no polypeptide, such as promoters, introns, telomeres and genes for rRNA and tRNA.

regulators of gene expression

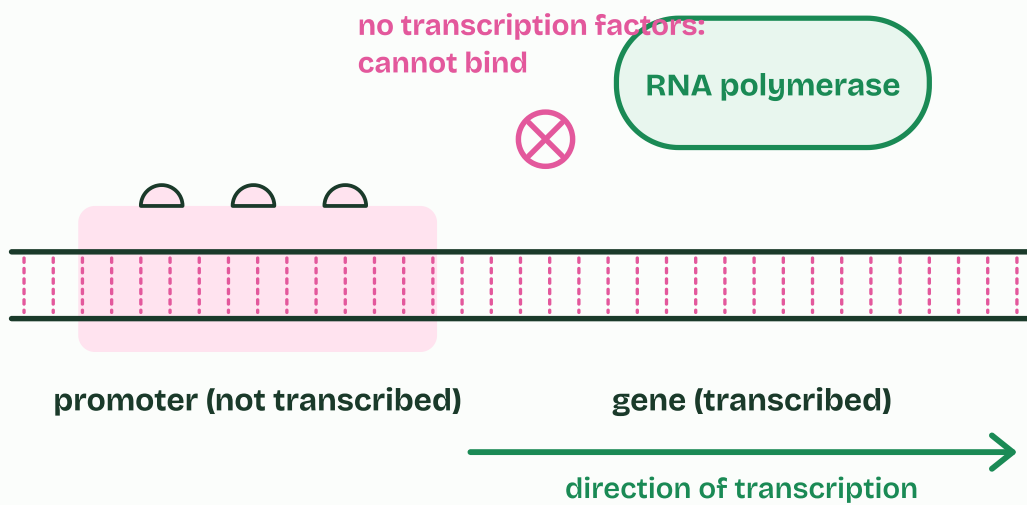
Sequences where transcription factors bind, such as promoters, that control how often a gene is transcribed.

introns

Stretches inside a gene that are transcribed but cut out of the RNA before it is used.

telomeres

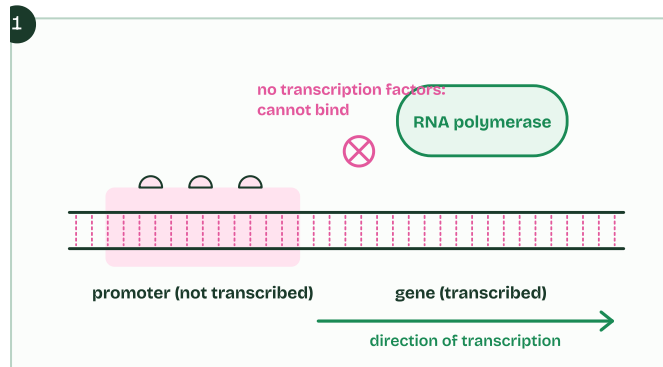
Repeats of a short sequence at the ends of a chromosome. They protect the genes near the ends from being lost each time the DNA is copied.



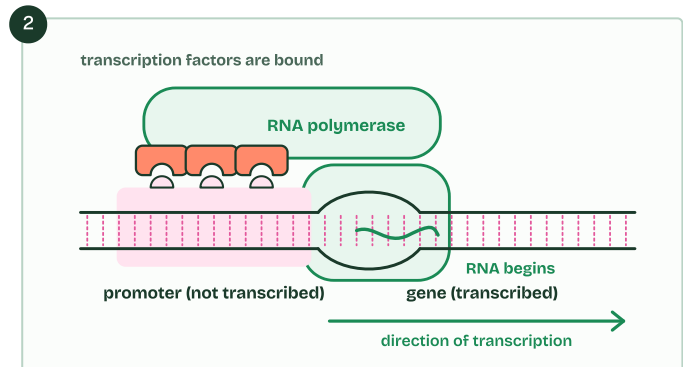
The promoter (pale pink band) is DNA just before the gene. Its bumps are where transcription factors fit.

SWITCH IT

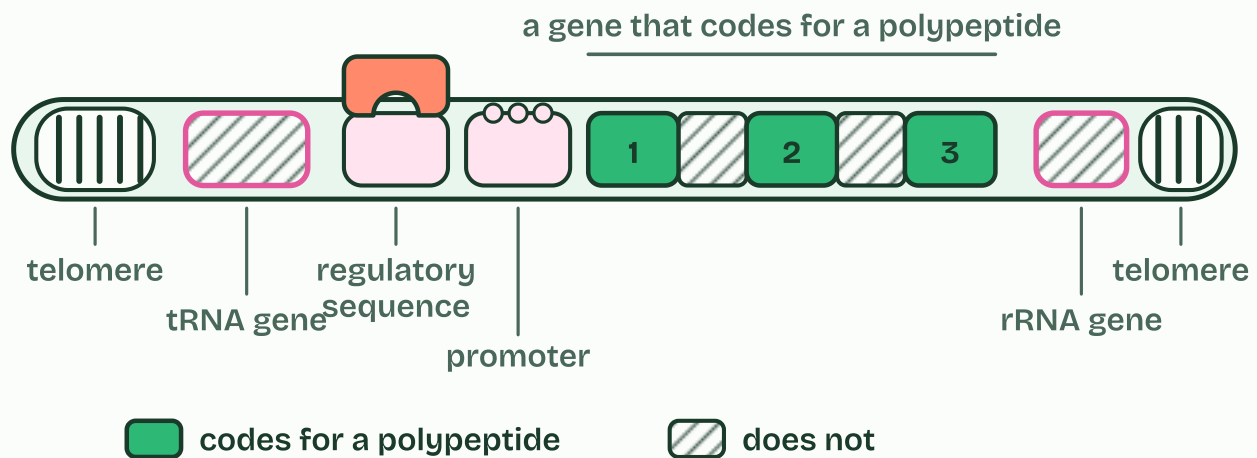
2 SETTINGS



Absent



Present



One stretch of chromosome, drawn to show kinds of DNA, not to scale. Only the exons code for the polypeptide.

Telomere Many repeats of a short sequence (TTAGGG in humans) at each end of a chromosome. They protect the genes near the end from being lost when the DNA is copied, and code for no polypeptide.

Regulatory sequence Another stretch where transcription factors bind and change how often the gene is transcribed. It is not transcribed.

Exon Transcribed and kept in the mRNA: it codes for part of the polypeptide.

Exon Transcribed and kept in the mRNA: it codes for part of the polypeptide.

Exon Transcribed and kept in the mRNA: it codes for part of the polypeptide.

Telomere Many repeats of a short sequence (TTAGGG in humans) at each end of a chromosome. They protect the genes near the end from being lost when the DNA is copied, and code for no polypeptide.

tRNA gene Transcribed into tRNA, which is never translated: the RNA is the product. It is a gene, but it codes for no polypeptide.

Promoter Where transcription factors and RNA polymerase bind, just before the gene. It is not transcribed.

Intron Transcribed, then cut out of the RNA before it is used. It codes for nothing.

Intron Transcribed, then cut out of the RNA before it is used. It codes for nothing.

rRNA gene Transcribed into rRNA, which makes up the ribosomes. It is never translated.

WATCH OUT

Non-coding is not the same as not transcribed. Introns and the genes for rRNA and tRNA are transcribed, while the promoter is not, and is never part of the mRNA. Telomeres code for no polypeptide.

PREDICT

A gene for a tRNA is transcribed in every cell, but its RNA is never translated. Is it coding or non-coding DNA?

- (A) Non-coding: its RNA is the product
- (B) Coding: anything transcribed counts as coding
- (C) Coding: a tRNA carries amino acids, so it codes

Decide before you look. Answer on page 47.

10

D1.2.15 HL D1.2.16 HL RNA PROCESSING AND ALTERNATIVE SPLICING

Capped, cut and *tailed*

In a eukaryotic cell, the RNA that RNA polymerase makes from a protein-coding gene is **pre-mRNA**. It is changed in the nucleus before it leaves, a stage called **post-transcriptional modification**, and the result is **mature mRNA**.

In **splicing**, the introns are cut out and the **exons** joined end to end, so the mature mRNA carries only sequence that codes for the polypeptide. The cut-out introns are broken down in the nucleus. The two ends are protected as well. A **5' cap**, a modified guanine nucleotide, is added to the 5' end, and a **poly-A tail**, a long run of adenine nucleotides (often about 200), to the 3' end.

The reason is that enzymes in the cytoplasm break RNA down from its ends. The cap and the tail protect, and so stabilise, the mRNA, which then lasts long enough to be translated many times. The cap also helps the ribosome find the mRNA's 5' end (chapter 11). Prokaryotes do not cap, tail or splice their mRNA in this way (most of their genes have no introns), and with no nucleus, translation can start before transcription has ended.

Alternative splicing: in many genes, which exons are kept can vary. Leave an exon out, or keep a different one, and the mature mRNA codes for a different polypeptide. So one gene can code for several polypeptides, and a cell's set of proteins is much larger than its number of genes: about 20,000 human protein-coding genes make many more proteins than that. You need no named example, and the gene in figure 10.2 is invented.

KEY TERMS

pre-mRNA

The first RNA made from a eukaryotic gene, with its introns still in. It is processed in the nucleus.

post-transcriptional modification

Changes made to an RNA after it is transcribed, such as capping, tailing and splicing.

mature mRNA

The finished mRNA, capped, tailed and spliced, that leaves the nucleus to be translated.

splicing

Cutting the introns out of pre-mRNA and joining the exons end to end.

exons

Parts of a gene that stay in the mature mRNA and code for the polypeptide.

5' cap

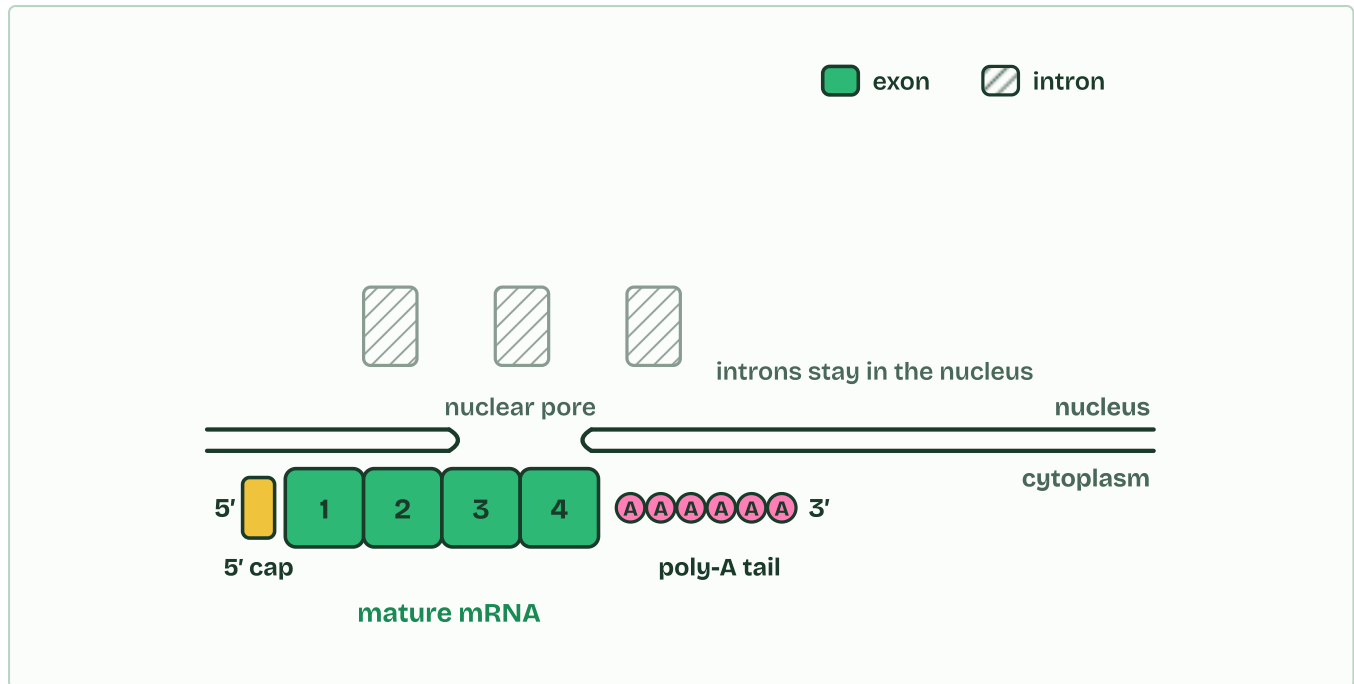
A modified guanine nucleotide added to the 5' end of an mRNA. It protects the mRNA and helps the ribosome find it.

poly-A tail

A long run of adenine nucleotides added to the 3' end of an mRNA, to protect it.

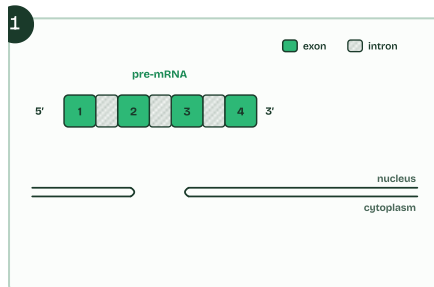
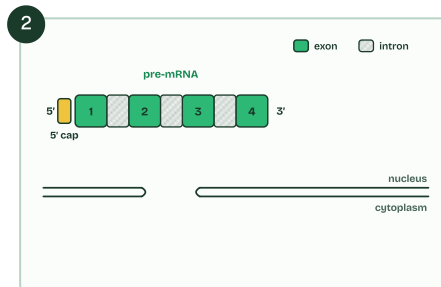
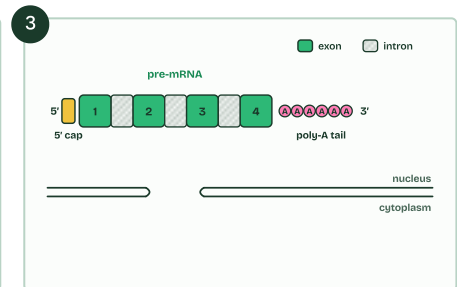
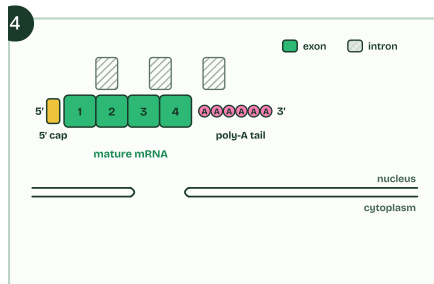
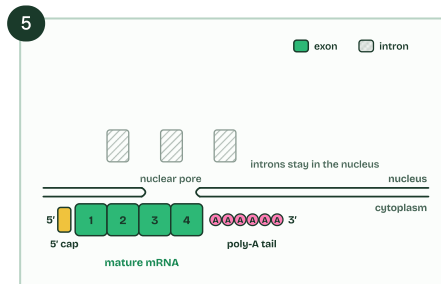
alternative splicing

Splicing the exons of one gene together in different combinations, so that one gene codes for more than one polypeptide.



STEP BY STEP

5 STEPS

Pre-mRNA: **exons** and **introns**.A **5' cap** is added.A **poly-A tail** is added.Introns are cut out and the exons **spliced** together.

Mature mRNA leaves the nucleus.

one gene,
as pre-mRNA



mature mRNA



polypeptide version 1

An invented gene. Each exon codes for four amino acids, and the colours follow each exon into the polypeptide.

SWITCH IT

2 SETTINGS

1

one gene,
as pre-mRNA



mature mRNA



polypeptide version 1

All four exons

2

one gene,
as pre-mRNA



mature mRNA



exon 2 is left out

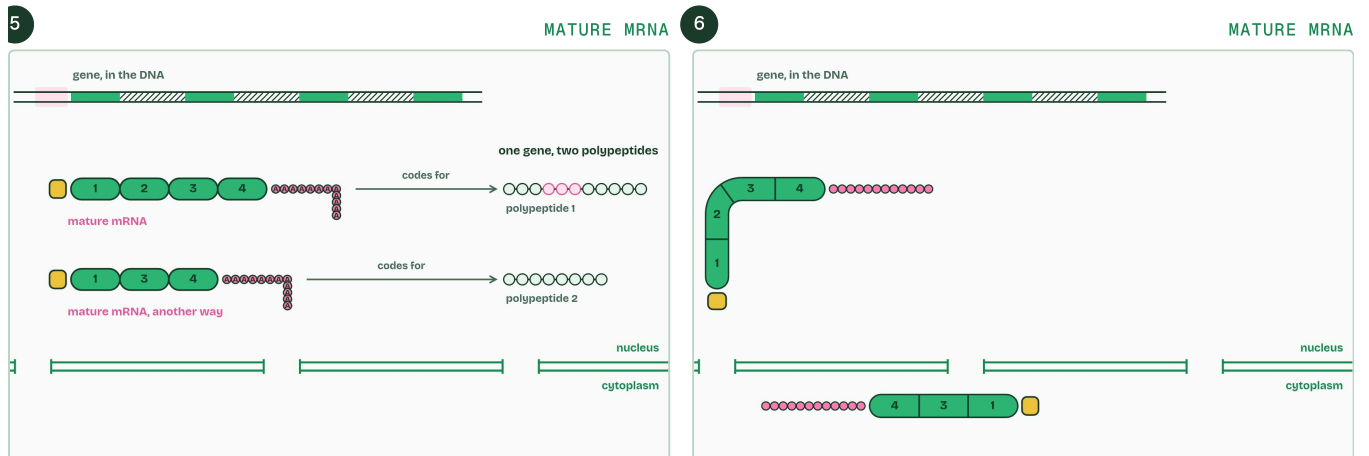
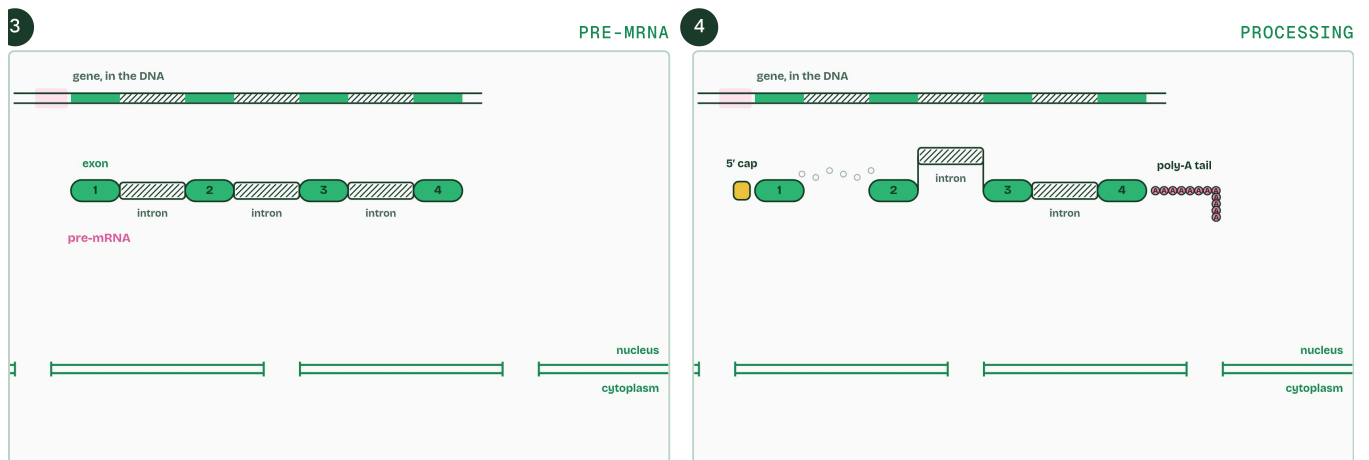
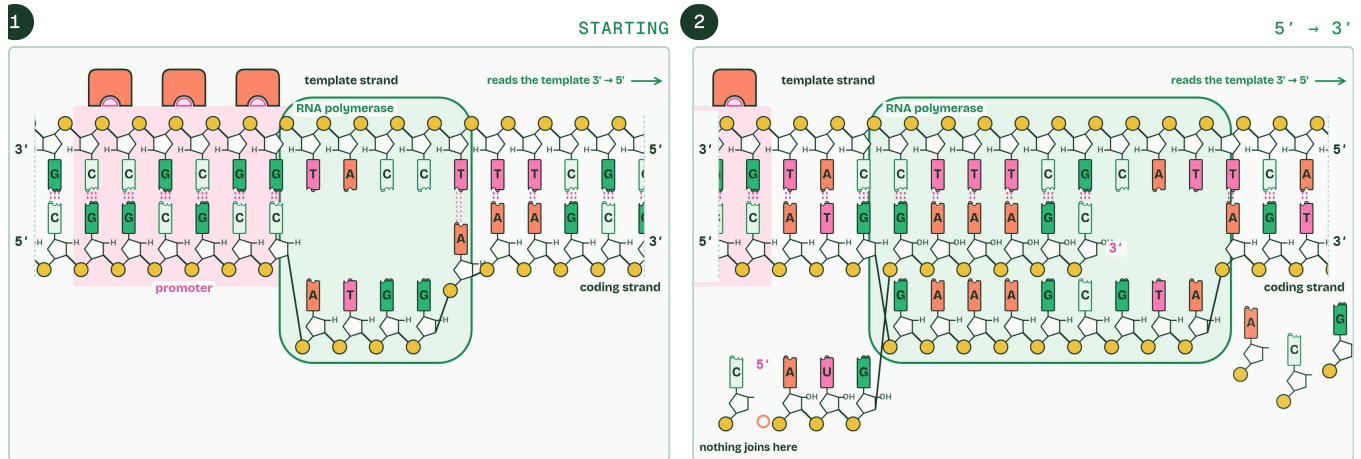


polypeptide version 2

Leave out exon 2

ANIMATION · FROM PROMOTER TO MATURE MRNA

6 MOMENTS



Watch it move, and change it as it runs: biologybybradford.com/guides/ib-biology-d1-2-protein-synthesis#processing

REMEMBER IT

Introns and exons

I
In**Introns**

cut out and broken down in the nucleus

E
Exit**Exons**

joined, and leave in the mature mRNA

WATCH OUT

Introns are cut out of the RNA, not out of the gene: the DNA keeps them. And alternative splicing changes which exons are kept, not the gene's sequence.

PREDICT

A gene has four exons. Exons 1 and 4 are always kept, and exons 2 and 3 can each be kept or left out. How many different mature mRNAs can it make?

- ☐ A 2
- ☐ B 8
- ☐ C 4

Decide before you look. Answer on page 47.

11

D1.2.17 HL INITIATION OF TRANSLATION

Starting the *chain*

Initiation is how translation starts. It happens in this order:

KEY POINTS

- the small subunit attaches to the mRNA at its **5' terminal**, its 5' end (in eukaryotes the 5' cap helps);
- it moves along the mRNA, 5' to 3', to the first AUG, the start codon (the short stretch before it is not translated);
- the **initiator tRNA**, anticodon UAC, carrying methionine, pairs with AUG;
- the large subunit joins, so the ribosome is complete, with the initiator tRNA in the P site;
- another tRNA, matching the next codon, binds in the A site.

The large subunit has three places for tRNAs, and they are used all through elongation. The **A site** is where each new tRNA arrives with its amino acid. The **P site** holds the tRNA carrying the growing chain, which is joined by a peptide bond to the amino acid in the A site. The **E site** is where an empty tRNA goes when the ribosome moves one codon, and where it leaves from. After each move the tRNA that carried the chain is in the P site, and the A site is free over the next codon.

Every new polypeptide begins with methionine, because the start codon codes for it, but in many proteins that methionine is removed afterwards. Haemoglobin's beta chain, for example, begins with valine in the finished protein, which is why chapter 7 counted from there.

KEY TERMS

initiation

The first stage of translation: the ribosome assembles on the mRNA at the start codon, with the initiator tRNA in place.

5' terminal

The 5' end of an mRNA, where its first nucleotide lies.

initiator tRNA

The tRNA that starts translation. Its anticodon is UAC, it carries methionine, and it pairs with the start codon AUG.

A site

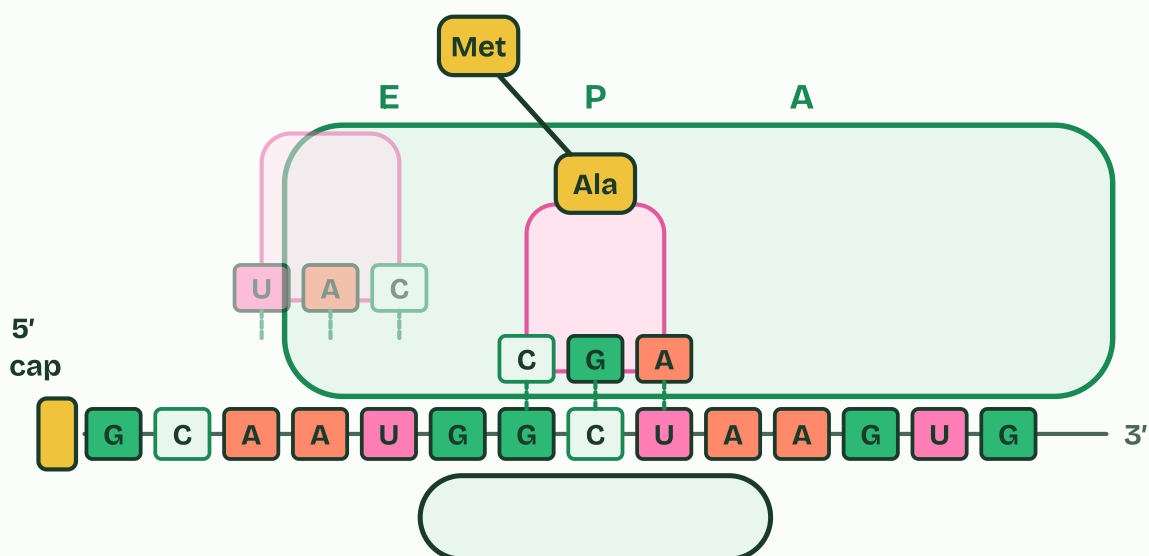
The place in the ribosome where each new tRNA arrives with its amino acid.

P site

The place in the ribosome that holds the tRNA carrying the growing chain.

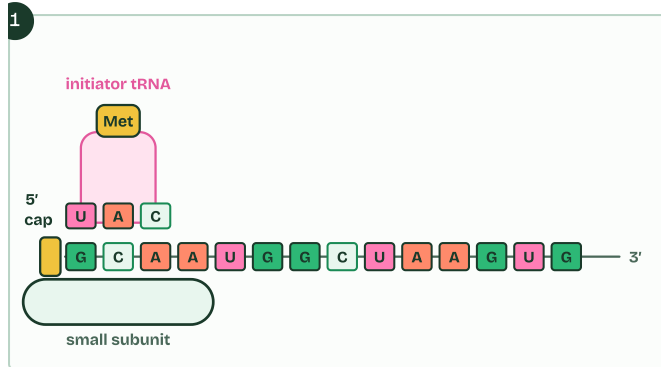
E site

The place in the ribosome where an empty tRNA goes after the ribosome moves one codon, and from where it leaves.

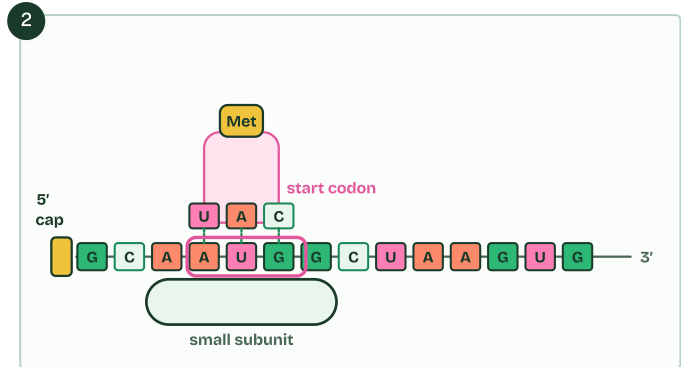


STEP BY STEP

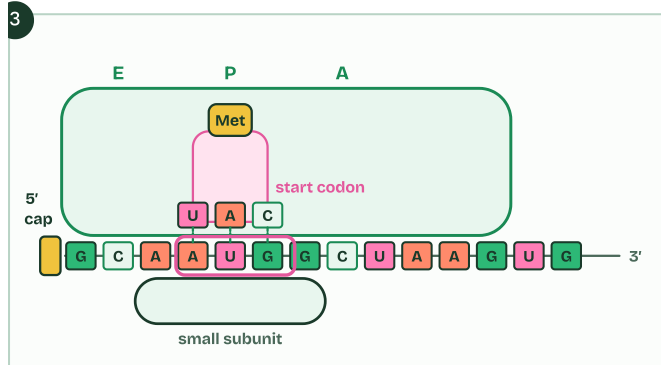
6 STEPS



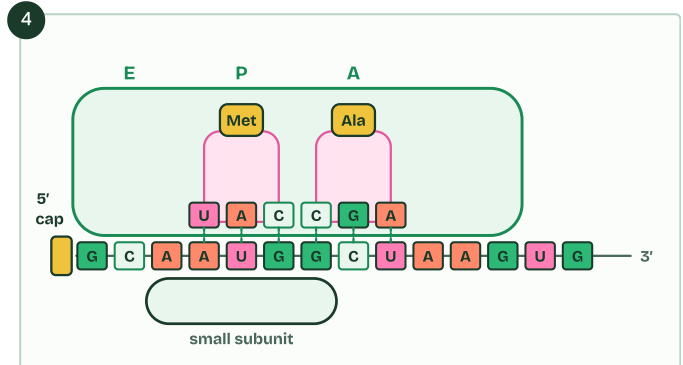
The **small subunit** attaches at the mRNA's 5' end.



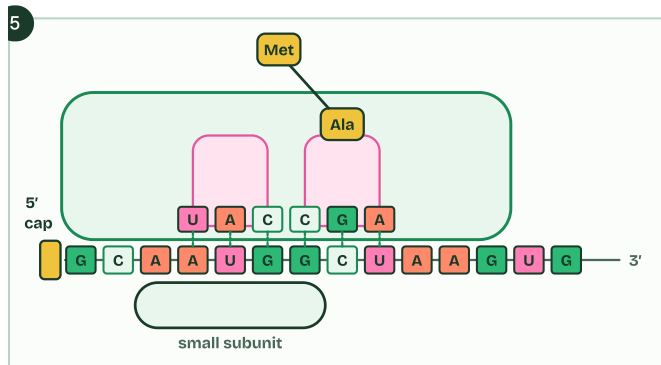
It moves to the **start codon**, AUG, where the **initiator tRNA** pairs.



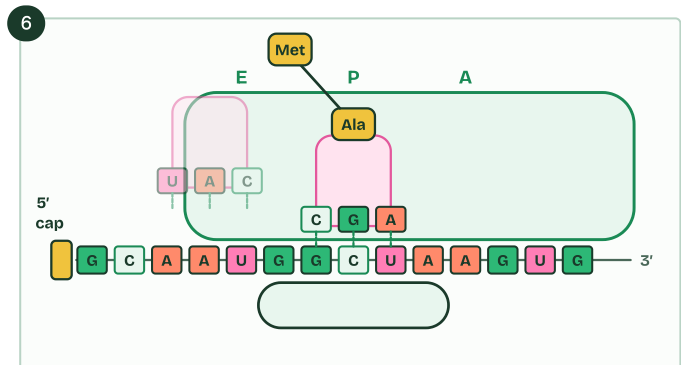
The **large subunit** joins: the initiator tRNA is in the **P site**.



The next tRNA arrives in the **A site**.

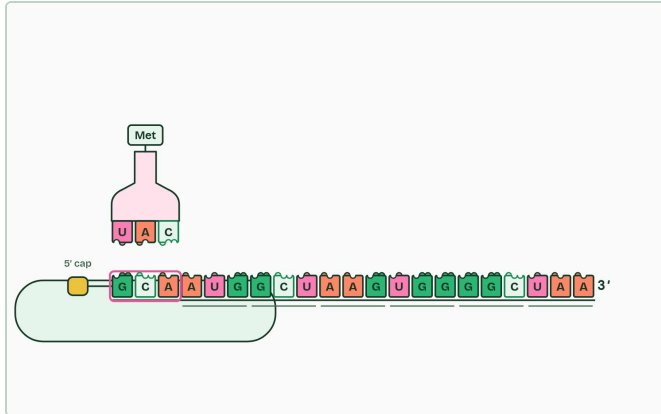


A peptide bond joins the two amino acids.

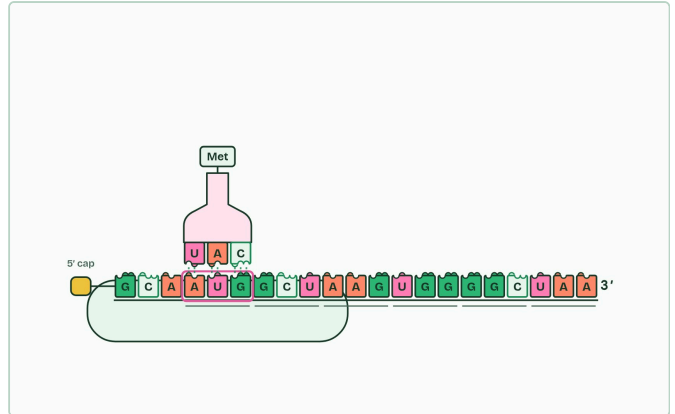


The ribosome moves one codon; the empty tRNA leaves from the **E site**.

1 SMALL SUBUNIT AT THE 5' END 2 UNDER THE SUBUNIT: AUG

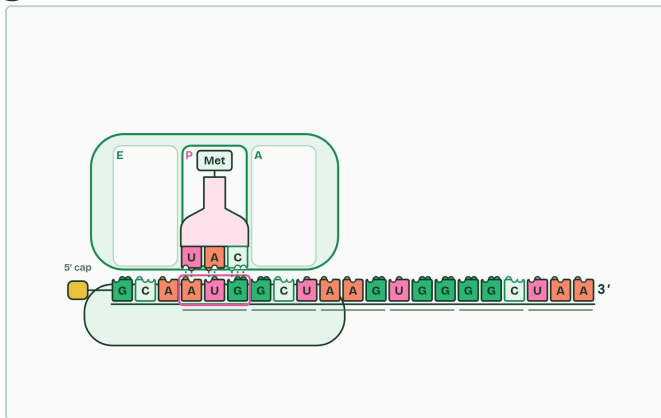


The small subunit attaches to the mRNA at its 5' end.

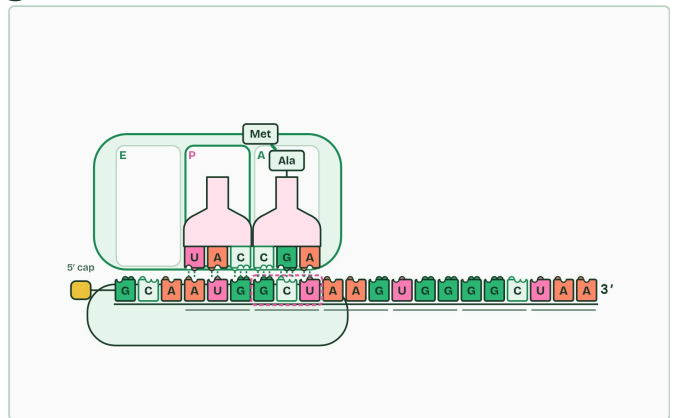


It moves towards the 3' end until it reaches the start codon, AUG. The initiator tRNA pairs with it.

3 CODON 1: AUG, MET, P SITE 4 CODON 2: GCU, ALA, A SITE

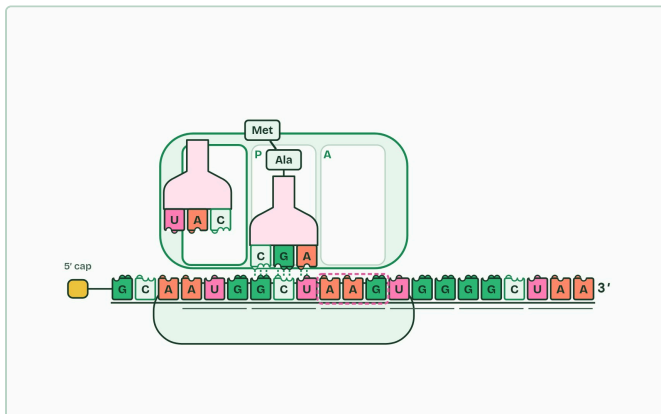


The large subunit joins. The initiator tRNA sits in the P site.

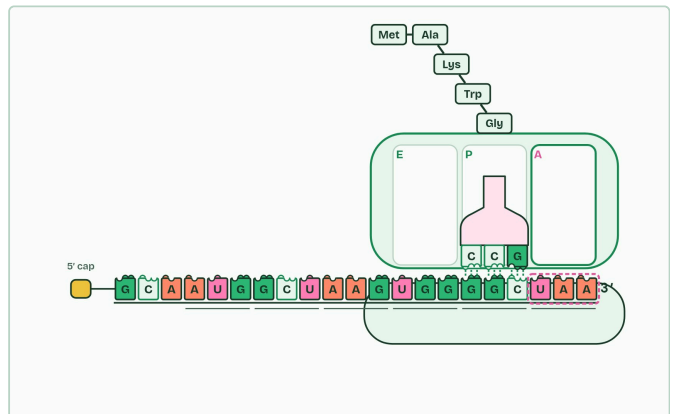


Another tRNA arrives in the A site. A peptide bond joins methionine to its amino acid.

5 CODON 3: AAG, LYS, A SITE 6 CODON 6: UAA, STOP, A SITE



The ribosome moves one codon. The empty tRNA leaves from the E site; the chain's tRNA is now in P.



At the stop codon the chain is released and the subunits come apart.

Watch it move, and change it as it runs: biologybybradford.com/guides/ib-biology-d1-2-protein-synthesis#initiation

REMEMBER IT

The three sites

A Arrive	P Pass	E Exit
A site a loaded tRNA arrives	P site holds the chain and passes it on	E site the empty tRNA leaves

WATCH OUT

The initiator tRNA starts in the P site, not the A site. Every other tRNA enters at the A site and reaches the P site only when the ribosome moves. And the small subunit binds the mRNA first, the large subunit after it.

PREDICT

The first peptide bond has just formed, joining methionine to the second amino acid. Before the ribosome moves, which site holds the tRNA carrying both amino acids?

- ☐ A A site
☐ B P site
☐ C E site

Decide before you look. Answer on page 47.

12

D1.2.18 HL

D1.2.19 HL

MODIFICATION AND PROTEASOMES

Finished, then *recycled*

Many polypeptides cannot work as they come off the ribosome. They are modified first, which is called **post-translational modification**: they are cut, folded and bonded, or given extra groups such as sugars or phosphates. Insulin is the guide's example, and it is made in two stages.

It starts as **pre-proinsulin**, 110 amino acids long, which begins with a **signal peptide** of 24 amino acids. The signal peptide sends the ribosome to the rough ER, so the chain is threaded into the ER as it is made. In stage 1, in the rough ER, the signal peptide is cut off, leaving **proinsulin** (86 amino acids). Proinsulin folds, and three **disulfide bonds** form: two join what will become the B chain to the A chain, and one lies within the A chain. In stage 2, in the Golgi apparatus and the vesicles that bud from it, enzymes cut out the middle section, the C-peptide, leaving insulin: an A chain of 21 amino acids and a B chain of 30, held together by two disulfide bonds. Insulin is stored in vesicles until it is released (what it does is D3.3).

Cells break proteins down as well. A **proteasome** is a barrel-shaped complex of proteins, in the cytoplasm and the nucleus, that hydrolyses the peptide bonds of a protein into short pieces, which other enzymes then split into single amino acids for the cell to use again in building new proteins. A protein is marked for breakdown with a small protein tag. Damaged and misfolded proteins carry one, and so do healthy proteins the cell no longer needs. A protein's life may be minutes or months.

The **proteome** is all the proteins a cell makes. Keeping it working needs constant breakdown and synthesis: broken proteins are cleared away, and the amount of each protein can change quickly when the cell needs something new. The protein factory after chapter 7 has orders for this chapter too, when the page is at higher level.

KEY TERMS

post-translational modification

Changes made to a polypeptide after it has been translated, such as cutting, folding, bonding or adding groups, so that it can work.

pre-proinsulin

The first polypeptide made from the insulin gene, 110 amino acids long, with a signal peptide at its start.

signal peptide

A short stretch at the start of a polypeptide that sends the ribosome making it to the rough ER. It is cut off in the ER.

proinsulin

A single polypeptide of 86 amino acids made from pre-proinsulin. It folds, forms disulfide bonds and is cut again to make insulin.

disulfide bonds

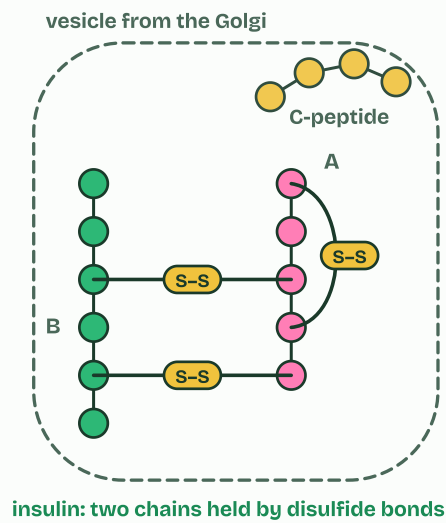
Strong covalent bonds between the sulfur atoms of two cysteines, which hold a folded protein, or two chains, together.

proteasome

A barrel-shaped complex of proteins in the cytoplasm and nucleus that breaks proteins down into short pieces, which are then split into amino acids.

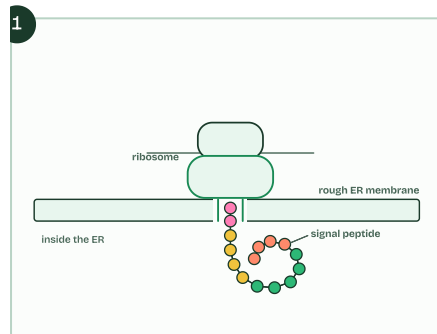
proteome

All the proteins that a cell, or an organism, makes.

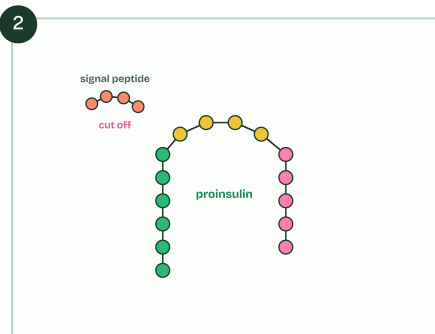


STEP BY STEP

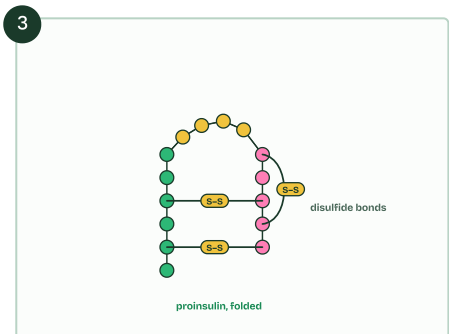
5 STEPS



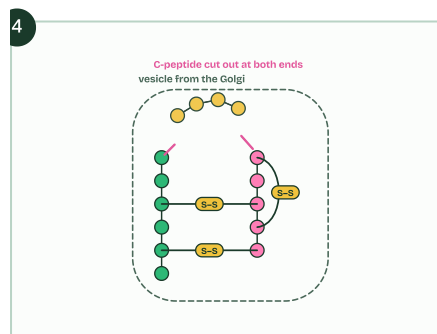
Pre-proinsulin: a **signal peptide** sends it into the rough ER.



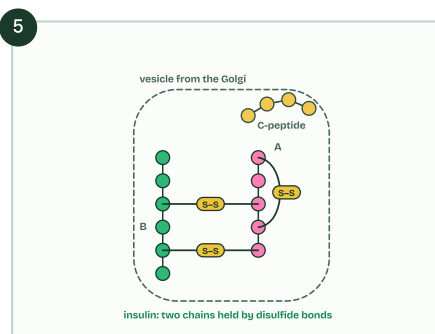
Stage 1: the signal peptide is cut off, leaving **proinsulin**.



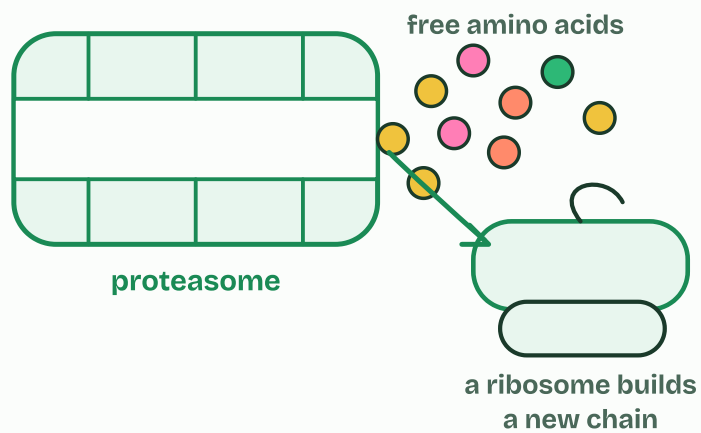
Proinsulin folds and **disulfide bonds** form.



Stage 2: the **C-peptide** is cut out.

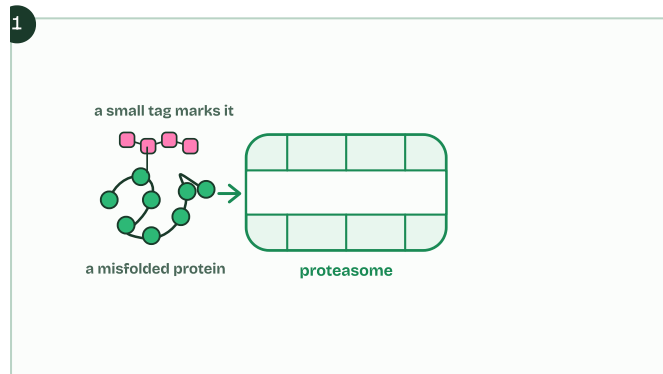


Insulin: two chains held by disulfide bonds.

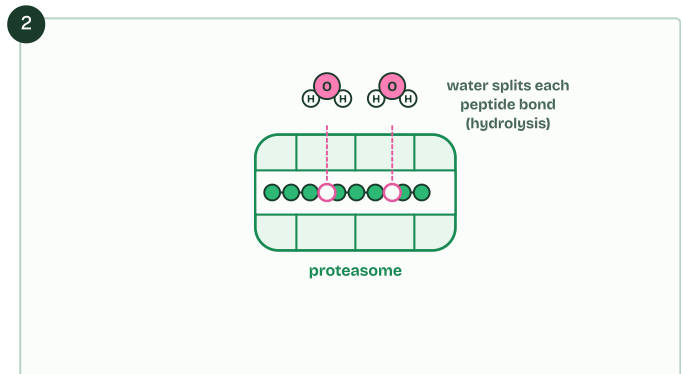


STEP BY STEP

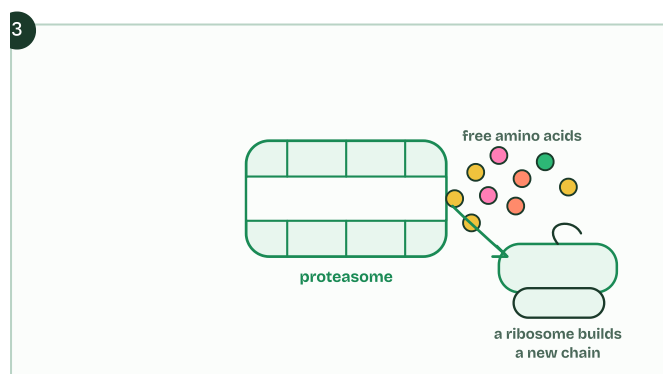
3 STEPS



A tagged protein reaches a **proteasome**.



Its peptide bonds are **hydrolysed**.



The amino acids are used again to build new proteins.

PREDICT

Insulin's two chains are 21 and 30 amino acids long, and pre-proinsulin is 110. How many amino acids are cut away in all?

- ☐ (A) 80
- ☐ (B) 59
- ☐ (C) 51

Decide before you look. Answer on page 47.

PREDICT

A cell makes a protein and breaks it down again within an hour. Is that wasteful?

- ☐ (A) No: the amino acids are reused, and levels can change fast
- ☐ (B) Yes: the amino acids from broken proteins cannot be used again
- ☐ (C) Yes: making and breaking proteins wastes amino acids

Decide before you look. Answer on page 47.

WATCH OUT

A polypeptide straight off the ribosome is not always a working protein. And proteasomes do not only destroy faulty proteins: they also clear healthy ones the cell no longer needs.

Key terms

Every term this guide defines, A to Z, with the chapter it is in. Cover the right-hand side and test yourself.

3' end 08

The end of a strand where the last nucleotide has a free OH on its carbon 3'.

5' cap 10

A modified guanine nucleotide added to the 5' end of an mRNA. It protects the mRNA and helps the ribosome find it.

5' end 08

The end of a strand where the last nucleotide has a free phosphate on its carbon 5'.

5' terminal 11

The 5' end of an mRNA, where its first nucleotide lies.

5' to 3' 08

The direction of a strand: from its 5' end to its 3' end. RNA is built this way, and mRNA is read this way.

A site 11

The place in the ribosome where each new tRNA arrives with its amino acid.

alternative splicing 10

Splicing the exons of one gene together in different combinations, so that one gene codes for more than one polypeptide.

amino acids 03

The monomers of polypeptides. Twenty kinds are used in cells, each with a different R group.

anticodon 04

The three exposed bases of a tRNA, complementary to an mRNA codon.

base substitution 07

A point mutation in which one base is swapped for another. It changes one codon.

coding strand 01

The DNA strand that is not read. Its base sequence matches the RNA, with T in place of U.

codon 04

A group of three bases on an mRNA that codes for one amino acid (or a stop).

complementary base pairing 01

The rule that each base pairs with one particular other base: A with T (or U), and C with G.

condensation 06

A reaction that joins two molecules and releases a molecule of water.

conserved 02

Kept unchanged over a long time, for the whole life of a cell or through many generations.

degenerate 05

Having more than one codon for most amino acids. A codon never stands for two amino acids.

disulfide bonds 12

Strong covalent bonds between the sulfur atoms of two cysteines, which hold a folded protein, or two chains, together.

E site 11

The place in the ribosome where an empty tRNA goes after the ribosome moves one codon, and from where it leaves.

elongation 06

The stage of translation in which the polypeptide grows by one amino acid for each codon read.

exons 10

Parts of a gene that stay in the mature mRNA and code for the polypeptide.

gene 01

A length of DNA whose base sequence codes for a polypeptide, or for an RNA that does a job of its own.

gene expression 02

The use of the information in a gene to make its product, starting with transcription.

genetic code 05

The rules that say which amino acid each codon stands for.

genome 02

All the DNA of a cell or organism, with all its genes.

haemoglobin 07

The protein in red blood cells that carries oxygen.

hydrogen bonds 01

Weak attractions between a slightly positive hydrogen atom on one molecule and a slightly negative atom on another.

initiation 11

The first stage of translation: the ribosome assembles on the mRNA at the start codon, with the initiator tRNA in place.

initiator tRNA 11

The tRNA that starts translation. Its anticodon is UAC, it carries methionine, and it pairs with the start codon AUG.

introns 09

Stretches inside a gene that are transcribed but cut out of the RNA before it is used.

large subunit 03

The larger part of a ribosome. It can hold two tRNAs at once and joins their amino acids.

mature mRNA 10

The finished mRNA, capped, tailed and spliced, that leaves the nucleus to be translated.

messenger RNA 01

RNA copied from a gene. It carries the gene's base sequence to a ribosome, where it is read.

missense 07

A substitution that changes one amino acid in the polypeptide.

mutation 07

A change in the base sequence of a gene.

Non-coding sequences 09

DNA that codes for no polypeptide, such as promoters, introns, telomeres and genes for rRNA and tRNA.

nonsense 07

A substitution that makes a stop codon, so the chain ends early.

P site 11

The place in the ribosome that holds the tRNA carrying the growing chain.

peptide bond 06

The covalent bond between the carbon of one amino acid and the nitrogen of the next. It holds a polypeptide together.

point mutation 07

A mutation that changes a single base.

poly-A tail 10

A long run of adenine nucleotides added to the 3' end of an mRNA, to protect it.

polypeptide 03

A chain of amino acids joined by peptide bonds.

post-transcriptional modification 10

Changes made to an RNA after it is transcribed, such as capping, tailing and splicing.

post-translational modification 12

Changes made to a polypeptide after it has been translated, such as cutting, folding, bonding or adding groups, so that it can work.

pre-mRNA 10

The first RNA made from a eukaryotic gene, with its introns still in. It is processed in the nucleus.

pre-proinsulin 12

The first polypeptide made from the insulin gene, 110 amino acids long, with a signal peptide at its start.

proinsulin 12

A single polypeptide of 86 amino acids made from pre-proinsulin. It folds, forms disulfide bonds and is cut again to make insulin.

promoter 09

A region of DNA just before a gene, where transcription factors and RNA polymerase bind to start transcription. It is not itself transcribed.

proteasome 12

A barrel-shaped complex of proteins in the cytoplasm and nucleus that breaks proteins down into short pieces, which are then split into amino acids.

proteome 12

All the proteins that a cell, or an organism, makes.

reading frame 05

The way the bases of an mRNA are grouped into codons. A different start gives different codons.

regulators of gene expression 09

Sequences where transcription factors bind, such as promoters, that control how often a gene is transcribed.

ribosomal RNA (rRNA) 03

RNA that, with protein, makes up the two subunits of a ribosome.

ribosomes 03

Structures in the cytoplasm that read mRNA and join amino acids into polypeptides. Each is made of rRNA and protein, in two subunits.

RNA polymerase 01

The enzyme that makes RNA. It parts the two DNA strands over a short stretch, pairs free RNA nucleotides with one strand and joins them with covalent bonds.

sickle cell anaemia 07

An inherited disease in which a changed haemoglobin forms fibres that bend red blood cells into sickles, block small vessels and are destroyed early.

signal peptide 12

A short stretch at the start of a polypeptide that sends the ribosome making it to the rough ER. It is cut off in the ER.

silent 07

A substitution that does not change the amino acid, because the new codon codes for the same one.

small subunit 03

The smaller part of a ribosome. The mRNA binds to it.

somatic cells 02

Body cells: any cell of an organism except the cells that make eggs or sperm.

splicing 10

Cutting the introns out of pre-mRNA and joining the exons end to end.

start codon 05

The codon AUG, where translation begins. It codes for methionine.

stop codons 05

Codons that code for no amino acid and end translation: UAA, UAG and UGA.

switched off 02

Not being transcribed, so that its product is not made.

switched on 02

Being transcribed, so that its product is made.

telomeres 09

Repeats of a short sequence at the ends of a chromosome. They protect the genes near the ends from being lost each time the DNA is copied.

template strand 01

The DNA strand that RNA polymerase reads. The RNA is built complementary to it.

transcription 01

Making an RNA copy of a gene, using one strand of the DNA as a template.

transcription factors 09

Proteins that bind to DNA at a promoter, or other regulatory sequences, and control whether a gene is transcribed.

Transfer RNA (tRNA) 03

Small RNA molecules that each carry one particular amino acid and have three exposed bases, the anticodon, that pair with an mRNA codon.

translation 03

Making a polypeptide by reading the codons of an mRNA: the base sequence sets the amino acid sequence.

triplet code 05

A code in which each codon is three bases long.

universal 05

Shared by almost all living things: a codon means the same amino acid in nearly every organism.

uracil 01

The base U, found in RNA in place of thymine. It pairs with adenine.



Check yourself

The check for this guide is online: a fresh paper of past-paper style questions from the exam bank on D1.2 each time, marked as you go, and saved to your Exam practice progress when you are signed in. Scan the code, or type the link.

[biologybybradford.com/exam-maker/sit?
topics=D1.2&level=HL&paper=quiz&marks=15&src=ep](https://biologybybradford.com/exam-maker/sit?topics=D1.2&level=HL&paper=quiz&marks=15&src=ep)

Answers

PREDICTIONS IN THE CHAPTERS

- 01 A gene's template strand reads T A C C T G. Which RNA does RNA polymerase make from it?

B AUGGAC

Each RNA base pairs with the template base opposite it: T takes A, A takes U, C takes G and G takes C. So T A C C T G gives A U G G A C. "A T G G A C" has the right pairs but uses T, which RNA never has (it is the coding strand, written as DNA). "U A C C U G" copies the template with U for T instead of pairing with it.

- 02 A nerve cell in your brain is 60 years old and has never divided. Its genes have been transcribed all that time. What has happened to their base sequences?

C Read many times, and still the same

Transcription only opens the hydrogen bonds for a moment; it never breaks the backbone or changes a base. So a template can be read thousands of times and stay the same, which is just as well in a cell that must last a lifetime. (Damage from other causes does happen, and cells repair it: D1.3.)

- 03 The large subunit holds two tRNAs at the same moment. Why two, and not one?

B So one amino acid can be joined to the next

A peptide bond joins two amino acids, so both have to be held side by side: the growing chain on one tRNA and the newly arrived amino acid on the other. Codons are on the mRNA, not on a tRNA, and tRNAs do not check each other: each one pairs with its own codon.

- 04 A codon reads U G G. Which anticodon pairs with it?

A ACC

Pair each base: U with A, G with C, G with C, so the anticodon is A C C. "T C C" uses T, which no RNA has, and "U G G" is the codon itself, and identical bases do not pair. (At higher level you write the ends: codon 5'-UGG-3', anticodon 3'-ACC-5'.)

- 05 Why can the code not use pairs of bases for each amino acid?

C Pairs give only 16 codons for 20 amino acids

With four bases, pairs make $4 \times 4 = 16$ different codons, and there are 20 amino acids to code for (and a stop signal as well). Triplets make 64: enough, with plenty over, which is why most amino acids have several codons.

- 06 A polypeptide is 150 amino acids long. How many codons did the ribosome read to make it, counting the codon that ended it?

B 151

One codon for each amino acid, 150, plus the stop codon that ended the chain: 151. That is 453 bases of mRNA. 450 is the number of bases for the 150 amino acids alone, not the number of codons.

- 07 In a gene, one base changes so that an mRNA codon GAA becomes GAG. What happens to the polypeptide?

C No change: GAG also codes for Glu

GAA and GAG both code for glutamic acid (the code is degenerate), so the polypeptide is the same: a silent mutation. Compare the sickle cell change, GAG to GUG, where the second base changes and Glu becomes Val.

- 08 A template strand reads 3'-TACAAGCGT-5'. Written 5' to 3', what is the mRNA?

B 5'-AUGUUCGCA-3'

Pair each base, keeping the template's order: T A C A A G C G T gives A U G U U C G C A. The template runs 3' to 5', so the mRNA opposite it runs 5' to 3': 5'-AUGUUCGCA-3' (it starts with the start codon). "5'-ACGCUUGUA-3'" has the right bases written backwards, and "5'-UACAAGCGU-3'" copies the template instead of pairing with it.

- 09 A gene for a tRNA is transcribed in every cell, but its RNA is never translated. Is it coding or non-coding DNA?

A Non-coding: its RNA is the product

"Coding" here means coding for a polypeptide. A tRNA gene is transcribed, and the tRNA itself does the job: no polypeptide is ever made from it. So it is non-coding DNA, even though it is a gene and is transcribed. The same is true of rRNA genes.

- 10 A gene has four exons. Exons 1 and 4 are always kept, and exons 2 and 3 can each be kept or left out. How many different mature mRNAs can it make?

C 4

1-2-3-4, 1-2-4, 1-3-4 and 1-4: each of the two optional exons is in or out, so $2 \times 2 = 4$. That is four polypeptides from one gene, without a single change to the DNA.

- 11 The first peptide bond has just formed, joining methionine to the second amino acid. Before the ribosome moves, which site holds the tRNA carrying both amino acids?

A A site

The bond joins methionine to the amino acid on the tRNA in the A site, so the two-amino-acid chain now hangs from that tRNA, still in the A site. The tRNA in the P site is empty. Only when the ribosome moves one codon does the chain's tRNA shift into the P site and the empty one into the E site.

- 12 Insulin's two chains are 21 and 30 amino acids long, and pre-proinsulin is 110. How many amino acids are cut away in all?

B 59

$21 + 30 = 51$ amino acids stay in insulin, so $110 - 51 = 59$ are cut away: the signal peptide (24) in the ER, then the C-peptide (31) and four more at its ends in the Golgi vesicles. (51 is what is kept, and 80 is $110 - 30$, forgetting the A chain.)

- 12 A cell makes a protein and breaks it down again within an hour. Is that wasteful?

A No: the amino acids are reused, and levels can change fast

The proteasome's amino acids go straight back into new proteins. Making and breaking costs some energy, but it buys control: a protein that is no longer wanted can be cleared in minutes, and damaged ones never build up. A working proteome depends on it.

How this was made. The course structure, the activities and the teaching choices come from my own classroom, my presentations and my years of teaching IB and AP Biology. I use Claude, an AI, to help write and build the interactive guides, lesson plans, slides and practice questions, and to draw the diagrams and code the interactives. I direct the work and review it against the IB and AP specifications before it goes live.

Written and drawn for Biology by Bradford, biologybybradford.com. Free to print and share with a class.