Protein synthesis

D1.2 · SL

The same gene can produce different amounts and forms of protein

Follow information, then follow the product

Full shared D1.2: transcription, stable DNA templates, gene expression, RNA/ribosome roles, codons, elongation and mutation effects.

Sequences and numerical examples are invented unless explicitly identified as named biology.

Name the template, product and purpose

Process	**Information and product**
Replication	DNA $\rightarrow$ DNA; copies for continuity
Transcription	DNA $\rightarrow$ RNA; supplies a transcript
Translation	mRNA $\rightarrow$ polypeptide sequence at a ribosome
Protein synthesis	Amino acids are assembled; DNA and RNA do not turn into amino acids

A polypeptide is not automatically a finished functional protein

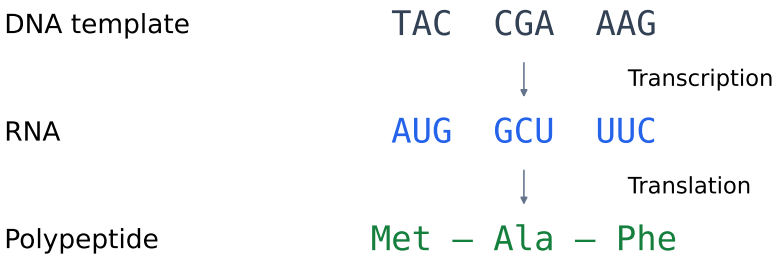
Keep cell type and gene product explicit

Some genes make functional RNAs, including rRNA and tRNA, rather than polypeptides.

Eukaryotic nuclear transcription and cytoplasmic translation are separated by a nuclear envelope; prokaryotes have no nucleus.

A new amino-acid chain may need folding, processing or assembly before functioning.

Follow complementarity before reading codon meanings



Invented aligned segment; complementary RNA, then codon meanings

DNA specifies RNA; RNA codons specify amino-acid order.

Construct the RNA segment from the template bases

1. **Invented template.** T–A–C–C–G–A–A–A–G.
2. **Pair DNA with RNA.** T→A; A→U; C→G; G→C.
3. **RNA product.** A–U–G–G–C–U–U–U–C. In the stated frame: AUG GCU UUC. Do not put thymine in RNA.

Explain polymerase and the two bonding relationships

Feature	Mechanism
Template exposure	A short DNA region opens; one strand is used for this transcript
Base pairing	Hydrogen bonding supports complementary nucleotide selection
RNA polymerase	Catalyses covalent joining into the new RNA backbone
After copying	RNA separates; DNA can pair again without losing its normal base sequence

A long-lived non-dividing cell still uses its stable templates

Transcription does not consume the gene

RNA nucleotides come from the available supply, not pieces removed from the DNA backbone.

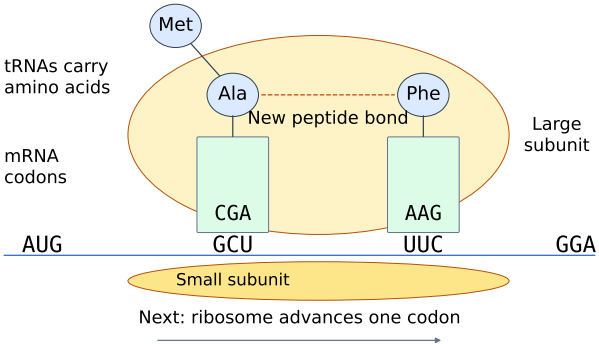
The same gene can be transcribed repeatedly. A cell can make proteins without copying its whole genome for cell division.

Maintained sequence does not mean DNA damage or mutation is impossible.

Do not infer gene loss from a missing product signal

1. **Invented observation.** Both cells contain an intact gene; only A has detectable transcript and protein at this sampling time.
2. **Explanation.** Different **transcription** activity can change mRNA availability and product abundance without different genes.
3. **Evaluate.** Check DNA, RNA and protein separately. Later regulation, detection sensitivity and timing also affect the result.

Two tRNAs connect neighbouring codons with chain transfer



Matching tRNAs position a growing chain and an amino acid.

Distinguish the message, adaptor and assembly machinery

Component	Role
mRNA	Ordered codons specify the sequence
tRNA	Anticodon pairs with a **codon**; a separate site carries an amino acid
Small subunit	Binds and positions mRNA
Large subunit	Supports peptide bonding; two tRNAs can participate together

A codon and its aligned anticodon are complementary

1. **Codon GCU.** Aligned anticodon CGA; the appropriate charged tRNA carries alanine.
2. **Codon UUC.** Aligned anticodon AAG; the appropriate charged tRNA carries phenylalanine.
3. **Accuracy.** Correct amino-acid charging matters. The anticodon is not the site to which the amino acid attaches.

Compare the numbers of possible base signals

1. **One base.** $4^1 = 4$ possible signals.
2. **Two bases.** $4^2 = 16$: too few for twenty standard amino acids.
3. **Three bases.** $4^3 = 64$: sufficient for amino acids and stop signals. Three bases form one **codon**.

Keep degeneracy, universality and stopping distinct

Property	**Meaning**
Degeneracy	Several codons can specify one amino acid; GCU and GCC both Ala
Standard meaning	A **codon** does not arbitrarily choose several amino acids
Near universality	Broad shared code with known exceptions, including some mitochondrial codes
Start/stop	AUG commonly starts in appropriate context; UAA/UAG/UGA add no amino acid

Read this excerpt as mRNA codons

Codon(s)	Amino acid or signal
AUG; GCU/GCC	Met; Ala
UUU/UUC; UAU/UAC	Phe; Tyr
GAA/GAG; GUG	Glu; Val
GGA; UAA/UAG/UGA	Gly; Stop

Read the specified frame from start to stop

1. **Invented coding region.** AUG GCU UUC GGA UAA.
2. **Use the mRNA table.** Met–Ala–Phe–Gly, then stop.
3. **Count.** Five codons, four residues. A stop is not an amino acid; an anticodon is not the message to look up.

Check what the nucleotide count includes

1. **Model.** 63 coding nucleotides, one terminal stop, no untranslated sequence or introns.
2. **Codons and residues.** Codons $= 63/3 = 21$; residues $= 21 - 1 = 20$.
3. **Peptide bonds.** One linear 20-residue chain has $20 - 1 = 19$ peptide bonds before processing.

Whole-gene length is not a ready-made peptide calculation

Use only the stated translated coding-region model

The relation $L = B/3 - 1$ assumes B includes one terminal stop and no other included sequence.

Genes may contain regulatory, untranslated and intron regions; full mRNA also contains untranslated sequence.

Mature proteins can differ from their initial chains after processing. A 90-nucleotide coding region under the stated model gives 29 residues.

Explain the repeating cycle in its causal order

1. **Match.** Incoming charged tRNA pairs with the next **codon**; another tRNA holds the chain.
2. **Transfer.** Peptide bonding attaches the chain to the incoming amino acid and its tRNA.
3. **Move.** The ribosome advances by one codon, repositions the tRNAs and permits uncharged tRNA exit. mRNA is not consumed as chain material.

One added amino acid creates one more peptide bond

1. **Existing chain.** Met–Ala–Phe–Gly: four residues joined by three peptide bonds.
2. **Add one residue.** Five residues joined by four peptide bonds.
3. **Interpretation.** Count the links within the stated linear chain; processing and multiple-chain proteins require their actual structures.

A base substitution can have different coding effects

Change	**Effect under the standard code**
GCU $\rightarrow$ GCC	Ala remains Ala; synonymous
UUC $\rightarrow$ UAC	Phe changes to Tyr
UAU $\rightarrow$ UAA	Creates a stop signal
Interpretation	Position and sequence determine the effect; one base change does not always destroy a protein

Connect the sickle-cell substitution to protein behaviour

1. **Coding DNA.** GAG → GTG; corresponding mRNA GAG → GUG.
2. **Residue.** Glu → Val, commonly numbered beta 6 in the mature chain.
3. **Consequence.** Changed side-chain properties favour deoxygenated haemoglobin S polymerization and can distort red cells. This is a named biological example, not invented data.

Regroup the sequence after deleting coding base 4

1. **Original.** AUG GCU UUC GGA UAA.
2. **Delete the G.** AUG CUU CGG AUA A: Met–Leu–Ser–Asp, plus an incomplete final group.
3. **Limit.** No complete stop is displayed in the regrouped segment. More downstream sequence is needed to infer the full product.

A shifted frame does not prove every later amino acid must differ

Predict the grouping, then inspect the actual code and sequence

A one-base insertion/deletion changes downstream triplet grouping. Degeneracy or chance agreement can preserve some amino acids.

A stop may arise later, but need not appear immediately. Do not invent the unseen downstream sequence.

A three-base deletion preserves the downstream frame; a boundary-crossing deletion can also change the joined codon. Frame preservation does not guarantee function.

Attempt the complete handout practice before checking

Name the strand, frame, count and processing step

Construct an RNA complement; explain template stability, expression, ribosome/tRNA roles, code properties and elongation.

Translate the given coding sequence, count residues/bonds, and evaluate synonymous, amino-acid-changing, stop and frameshift changes.

Check the shared sequence and chain calculations

1. **RNA complement.** TAC CCG AAA $\rightarrow$ AUG GGC UUU. Practice **translation** AUG GCC UAC GAG UGA gives Met–Ala–Tyr–Glu, then stop.
2. **Coding length.** $156/3 = 52$ codons; $52 - 1 = 51$ residues; $51 - 1 = 50$ peptide bonds in the initial single chain.
3. **Elongation.** Six residues/five bonds become seven/six after one amino acid is added. A stop adds no residue.

Check yourself

Move from the identified molecule to a justified inference

Read mRNA codons in the stated frame; distinguish template, coding DNA, message and anticodon.

State which length includes a stop and which includes untranslated sequence. Do not equate a changed frame with every downstream amino acid changing.