IB / A Level Exam Preparation Notes

D1.2 Protein Synthesis

D Continuity and Change - Molecules

Transcription, translation, the genetic code, mutations and HL gene expression control

How to use these notes

This PDF condenses the D1.2 Protein synthesis content into exam-focused notes for IB Biology and A level Biology. It keeps the key biology, adds HL extensions, and ends with exam-style practice and marking guidance.

Guiding questions

1. How does a cell produce a sequence of amino acids from a sequence of DNA bases?
2. How is the reliability of protein synthesis ensured?

Core idea: the base sequence in DNA is transcribed into RNA and then translated into an amino acid sequence at a ribosome. A protein is therefore indirectly controlled by DNA through the sequence of codons in mRNA.

Assessment map

Section	What you must be able to do
Transcription	Explain how RNA is synthesized from a DNA template; describe RNA polymerase, promoters, hydrogen bonding and complementary base pairing.
Translation	Explain how mRNA, tRNA, rRNA and ribosomes produce a polypeptide; use codons and anticodons accurately.
Genetic code	Use mRNA codon tables; explain triplet, degeneracy and universality.
Reliability and mutation	Explain how base pairing improves accuracy and how point mutations can change protein structure.
HL extensions	Explain directionality, promoters, transcription factors, RNA processing, alternative splicing, translation initiation, post-translational modification and proteasomes.

1. The central dogma and the need for RNA

DNA stores genetic information in the sequence of its bases. Ribosomes, where proteins are assembled, are located in the cytoplasm. In eukaryotic cells, DNA remains in the nucleus, so the cell uses RNA to carry information from DNA to ribosomes.

Central dogma

The central dogma describes the usual flow of genetic information: DNA is used to make RNA, and RNA is used to make protein. This flow is essential because the base sequence of DNA determines the amino acid sequence of a polypeptide.

Key terms

Gene: a specific base sequence in DNA that codes for a functional product, such as a polypeptide or an RNA molecule.
Gene expression: the process by which information in a gene is used to make a functional product.
Protein synthesis: transcription plus translation, followed by any required protein modification.

DNA does not need to leave the nucleus. Instead, a temporary RNA copy of a gene is made. This RNA copy then directs the formation of a protein at a ribosome.

2. Transcription: making RNA from DNA

Transcription is the synthesis of RNA using one DNA strand as a template. The DNA strand used is called the template strand. The RNA produced from a protein-coding gene is messenger RNA, or mRNA.

Sequence of events in transcription

- A region of DNA containing a gene opens so that the bases of the template strand are exposed.
- RNA polymerase binds near the start of the gene at a promoter sequence.
- RNA polymerase separates the DNA strands in the gene region and catalyses the formation of bonds between RNA nucleotides.
- Free RNA nucleotides pair with exposed bases on the DNA template strand by complementary base pairing.
- The growing RNA molecule separates from the DNA; the DNA double helix reforms behind RNA polymerase.

Important base pairing rule in transcription

DNA template base	RNA base added
Adenine (A)	Uracil (U)
Thymine (T)	Adenine (A)
Cytosine (C)	Guanine (G)
Guanine (G)	Cytosine (C)

Exam warning

In transcription, RNA uses **uracil (U)**, not thymine. If a sequence contains U, it is RNA. If a sequence contains T, it is DNA.

Hydrogen bonding and reliability in transcription

Hydrogen bonds form between complementary bases on the DNA template strand and the incoming RNA nucleotides. The shape and bonding patterns of the bases allow only specific pairing. This is one reason transcription is reliable.

RNA polymerase has two essential functions in transcription: it opens the DNA in the region being transcribed, and it catalyses the joining of RNA nucleotides into a growing RNA strand.

Important facts about transcription

- Only one of the two DNA strands is copied for a particular gene.
- The mRNA is shorter than the whole DNA molecule because it is a copy of a gene, not the whole chromosome.
- All types of RNA in the cell are produced by transcription.
- Transcription is the first stage of gene expression, so switching transcription on or off is a major way to regulate genes.
- DNA can be used repeatedly as a template without its base sequence changing.

3. DNA template stability and gene expression

DNA is relatively stable, so the same gene can be transcribed many times without the DNA sequence itself changing. This is especially important in long-lived somatic cells, such as nerve cells, which may not divide but still need to make RNA and proteins throughout life.

DNA can be damaged by free radicals, some chemicals, cigarette smoke and ultraviolet radiation. Cells have repair systems, but permanent DNA changes are mutations. Some mutations are harmful, some have no effect, and a few may be beneficial in particular environments.

Gene expression control

Not every gene in a cell is expressed at the same time. Different genes are expressed in different cell types, at different stages of development, and in response to different signals. Because transcription is the first stage of gene expression, controlling transcription is a key way to switch genes on or off.

4. Translation: making a polypeptide from mRNA

Translation is the synthesis of a polypeptide using the base sequence of mRNA. The mRNA sequence is read in codons, and each codon specifies an amino acid or a stop signal. Translation occurs at ribosomes in the cytoplasm.

The product of translation is a polypeptide: a chain of amino acids joined by peptide bonds. Many polypeptides later fold or combine with other molecules to become functional proteins.

The three major types of RNA

RNA type	Main role in protein synthesis	Exam detail
mRNA - messenger RNA	Carries a copied genetic message from DNA to the ribosome.	Contains codons. Binds to the small ribosomal subunit.
tRNA - transfer RNA	Carries a specific amino acid to the ribosome.	Contains an anticodon complementary to an mRNA codon. Two tRNAs can bind to the large subunit at the same time during elongation.
rRNA - ribosomal RNA	Combines with proteins to form ribosomes.	Forms a major structural and catalytic part of ribosomes.

5. Ribosomes, tRNA and peptide bonds

A ribosome has a small subunit and a large subunit. mRNA binds to the small subunit. tRNA molecules carrying amino acids bind to the large subunit. The ribosome positions mRNA codons and tRNA anticodons so that amino acids can be joined in the correct sequence.

Basic translation cycle

- mRNA binds to the small ribosomal subunit.
- A tRNA with a specific amino acid pairs its anticodon with a complementary mRNA codon.
- A second tRNA enters and pairs with the next codon.
- A peptide bond forms between the amino acids by a condensation reaction, releasing water.
- The first tRNA leaves without its amino acid and may be reused.
- The ribosome moves along the mRNA by one codon; another tRNA enters and the cycle repeats.
- The polypeptide grows until a stop codon is reached.

Peptide bond formation

A peptide bond is a covalent bond between amino acids. It forms by condensation, meaning water is released as the bond forms.

6. Codons, anticodons and the genetic code

A triplet is a sequence of three bases in DNA that corresponds to one amino acid. A codon is a sequence of three bases in mRNA. An anticodon is a sequence of three bases in tRNA that is complementary to a codon.

Term	Where found?	Function
Triplet	DNA	Three DNA bases that correspond to an amino acid.
Codon	mRNA	Three RNA bases read by the ribosome.
Anticodon	tRNA	Three RNA bases that pair with an mRNA codon.

Why the code is a triplet code

There are four RNA bases: A, U, C and G. One base gives only 4 possible codes. Two bases give 16 possible codes. Three bases give 64 possible codons, which is enough to code for the 20 amino acids plus start and stop signals.

Features of the genetic code

Feature	Meaning	Why it matters
Triplet	Three bases form one codon.	Provides enough combinations for all amino acids.
Degenerate	Most amino acids have more than one codon.	Some base changes do not alter the amino acid.
Universal	Almost all organisms use the same code.	Genes can be transferred between species; for example, bacteria can express the human insulin gene.
Unambiguous	A codon specifies only one amino acid or a stop signal.	The message is reliable; a codon does not have multiple meanings.
Start and stop signals	AUG is start and codes for methionine; UAA, UAG and UGA are stop codons.	Defines where translation begins and ends.

7. mRNA codon table for amino acid deduction

Use the table below for mRNA codons. Read the first base down the left, the second base across the top, and the third base inside the cell. Amino acid abbreviations are used to keep the table exam-friendly.

First base	Second base U	Second base C	Second base A	Second base G
U	UUU Phe UUC Phe UUA Leu UUG Leu	UCU Ser UCC Ser UCA Ser UCG Ser	UAU Tyr UAC Tyr UAA Stop UAG Stop	UGU Cys UGC Cys UGA Stop UGG Trp
C	CUU Leu CUC Leu CUA Leu CUG Leu	CCU Pro CCC Pro CCA Pro CCG Pro	CAU His CAC His CAA Gln CAG Gln	CGU Arg CGC Arg CGA Arg CGG Arg
A	AUU Ile AUC Ile AUA Ile AUG Met/Start	ACU Thr ACC Thr ACA Thr ACG Thr	AAU Asn AAC Asn AAA Lys AAG Lys	AGU Ser AGC Ser AGA Arg AGG Arg
G	GUU Val GUC Val GUA Val GUG Val	GCU Ala GCC Ala GCA Ala GCG Ala	GAU Asp GAC Asp GAA Glu GAG Glu	GGU Gly GGC Gly GGA Gly GGG Gly

Amino acid abbreviations

Ala alanine, Arg arginine, Asn asparagine, Asp aspartic acid, Cys cysteine, Gln glutamine, Glu glutamic acid, Gly glycine, His histidine, Ile isoleucine, Leu leucine, Lys lysine, Met methionine, Phe phenylalanine, Pro proline, Ser serine, Thr threonine, Trp tryptophan, Tyr tyrosine, Val valine.

Worked example

DNA template strand: TAT GCC CCA CTA ATC
mRNA: AUA CGG GGU GAU UAG
Amino acid sequence: Ile - Arg - Gly - Asp - Stop

Remember: if the DNA sequence is explicitly called the **template strand**, use complementary base pairing to produce mRNA. If the question gives mRNA directly, translate it without changing it first.

8. Elongation: ribosome movement and growing polypeptides

During elongation, the ribosome moves along the mRNA one codon at a time in the 5' to 3' direction. tRNAs carrying amino acids enter sequentially, and each anticodon pairs with a complementary codon. The ribosome catalyses peptide bond formation, so the polypeptide chain lengthens in the correct amino acid order.

Elongation is often tested through labelled biological structures. Be ready to identify mRNA, codon, anticodon, ribosome small subunit, ribosome large subunit, tRNA, amino acid, growing polypeptide and peptide bond.

9. Mutations and protein structure

A mutation is a permanent change in the DNA base sequence. A point mutation changes one base in a gene. Because transcription and translation depend on base sequence, a point mutation can change an mRNA codon and may alter one amino acid in a polypeptide.

A point mutation can have different effects: it may be silent if the amino acid stays the same, missense if a different amino acid is inserted, or nonsense if a stop codon is produced early.

Example: sickle-cell disease

Sickle-cell disease is caused by a single base substitution in the gene coding for beta-globin, part of haemoglobin. This changes one amino acid in the haemoglobin polypeptide. The altered haemoglobin can form strands inside red blood cells, causing them to become sickle-shaped. These cells may block blood vessels and carry oxygen less effectively.

Exam link

Use sickle-cell disease as a clear example of how a point mutation can change primary structure, which can alter protein folding, protein function and cell phenotype.

HL extension 1: directionality of transcription and translation

RNA polymerase builds RNA in the 5' to 3' direction by adding the 5' end of each free RNA nucleotide to the 3' end of the growing RNA strand. Because the RNA is antiparallel to the DNA template strand, the template is read in the 3' to 5' direction.

Translation also proceeds in the 5' to 3' direction along the mRNA. The ribosome reads codons starting at the 5' end, moves toward the 3' end, and assembles the polypeptide in sequence.

Process	Direction	What this means
Transcription	RNA synthesized 5' to 3'	RNA polymerase adds nucleotides to the 3' end of the growing RNA.
DNA template reading	Template read 3' to 5'	Template and mRNA are complementary and antiparallel.
Translation	mRNA read 5' to 3'	Ribosome moves along codons from the 5 end toward the 3 end.

HL extension 2: promoters, transcription factors and terminators

A promoter is a DNA sequence near the beginning of a gene where RNA polymerase binds. The promoter helps determine which strand of DNA will be used as the template and where transcription will start. The promoter itself is not transcribed.

In eukaryotic cells, transcription factors bind to promoter regions and other DNA control sequences before RNA polymerase can initiate transcription. Some transcription factors activate transcription, while others repress it. A specific combination of transcription factors may be required for a gene to be expressed.

A terminator is a DNA sequence that signals the end of transcription. When this region is transcribed, RNA polymerase detaches, the RNA transcript is released, and transcription stops.

Region or molecule	Role
Promoter	RNA polymerase recognition and binding site; transcription begins here.
Transcription unit	Region of DNA that is transcribed into RNA.
Terminator	Sequence that causes RNA polymerase to stop and release the RNA transcript.
Transcription factor	Protein that regulates transcription by helping activate or repress gene expression.

HL extension 3: non-coding DNA

Only a small proportion of DNA codes directly for polypeptides. Non-coding DNA does not code for polypeptides, but much of it has important functions.

Non-coding DNA example	Function or importance
Regulators of gene expression	Promoters, enhancers, silencers and insulators help control transcription.
Genes for rRNA and tRNA	These genes produce RNA molecules used in translation, not polypeptides.
Telomeres	Repetitive sequences at chromosome ends that help protect chromosomes.
Introns	Non-coding sequences within genes; removed from pre-mRNA during RNA processing. Some have regulatory roles.

Exam warning

Do not describe all non-coding DNA as useless. Non-coding regions can regulate gene expression, produce functional RNA, protect chromosomes, or affect mRNA processing.

HL extension 4: post-transcriptional modification in eukaryotes

In eukaryotic cells, the first RNA transcript produced from a protein-coding gene is called pre-mRNA or the primary RNA transcript. It contains exons and introns. Before translation, it must be processed to form mature mRNA.

Main modifications

- Introns are removed by spliceosomes.
- Exons are spliced together to form a continuous coding sequence.
- A 5' cap is added to protect the mRNA and help it bind to the ribosome.
- A 3' polyA tail is added to stabilize the mRNA and reduce degradation in the cytoplasm.

Alternative splicing

Alternative splicing occurs when the same pre-mRNA is spliced in different ways, producing different mature mRNA molecules. This allows one gene to produce more than one protein variant.

Example: cardiac troponin T gene

In foetal heart muscle, one exon of the cardiac troponin T transcript is included in mature mRNA. In adult heart muscle, that exon is not included. This produces different protein variants and contributes to functional differences between foetal and adult cardiac muscle, including differences in calcium sensitivity.

HL extension 5: initiation of translation and ribosome sites

Initiation brings together mRNA, the small ribosomal subunit, the initiator tRNA and the large ribosomal subunit. The small ribosomal subunit attaches to the 5' end of mRNA and moves to the start codon, AUG. The initiator tRNA pairs with AUG and carries methionine. The large subunit then joins, forming a complete ribosome.

The ribosome has three tRNA binding sites: A, P and E.

Ribosome site	Name to remember	Function during elongation
A site	Aminoacyl / arrival site	Holds the tRNA carrying the next amino acid.
P site	Peptidyl site	Holds the tRNA carrying the growing polypeptide chain.
E site	Exit site	Releases the tRNA after it has lost its amino acid.

Sequence of tRNA movement

A site: next amino acid arrives. P site: growing chain is held. E site: empty tRNA exits.

HL extension 6: modifying polypeptides into functional proteins

Many polypeptides are not functional immediately after translation. They may need folding, cleavage, chemical modification or combination with other chains.

Example: insulin production

Stage	What happens
Pre-proinsulin	Initial polypeptide produced in pancreatic beta cells; contains a signal peptide that directs it into the endoplasmic reticulum.
Proinsulin	Signal peptide is removed. The molecule folds and forms disulfide bonds.
Insulin	C peptide is removed by enzymes. Mature insulin has two chains linked by disulfide bonds and is packaged by the Golgi apparatus for secretion.

Other modifications include chaperone-assisted folding, disulfide bond formation and glycosylation, where carbohydrate groups are added to proteins.

HL extension 7: proteasomes and amino acid recycling

The proteome is the full set of proteins expressed by a cell, tissue or organism. Cells must constantly synthesize new proteins and break down damaged, misfolded or unneeded proteins.

In eukaryotic cells, proteins marked with ubiquitin are directed to proteasomes. The proteasome breaks the protein into amino acids, which can be reused in protein synthesis.

Summary pathway

Damaged or unneeded protein -> ubiquitin tag -> proteasome -> amino acids -> reused for protein synthesis

Exam skills: converting sequences

Sequence questions are common in IB and A level assessments. Always identify which molecule is given before converting.

Given in the question	What to do
DNA template strand	Use complementary base pairing to make mRNA, replacing A on DNA with U in RNA.
DNA coding/sense strand	mRNA has the same base sequence except U replaces T.
mRNA strand	Split into codons and translate directly using the codon table.
tRNA anticodons	Use complementary base pairing to find mRNA codons, then translate.

Worked sequence example

Question: From the DNA template sequence TAC CGT CAT AGA AAA ATC, determine the amino acid sequence.

Step	Sequence
DNA template	TAC CGT CAT AGA AAA ATC
mRNA codons	AUG GCA GUA UCU UUU UAG
Amino acids	Met - Ala - Val - Ser - Phe - Stop

Common mistakes to avoid

Do not translate the DNA template directly. Do not use T in mRNA. Do not include stop as an amino acid in the final polypeptide. Do not forget that AUG codes for methionine and also acts as the start codon.

High-yield comparisons

Comparison	Transcription	Translation
Main purpose	Makes RNA from DNA.	Makes a polypeptide from mRNA.
Location in eukaryotes	Nucleus.	Cytoplasm at ribosomes.
Template/read molecule	DNA template strand.	mRNA codons.
Key molecule/enzyme	RNA polymerase.	Ribosome, tRNA and enzymes/rRNA activity.
Base pairing	DNA template with RNA nucleotides.	mRNA codons with tRNA anticodons.
Product	RNA, including mRNA.	Polypeptide/protein.

Practice questions

Use these questions for active recall. Suggested marks are included to support exam-style revision.

1. Define transcription and state where it occurs in a eukaryotic cell. **[2]**

2. Explain the role of RNA polymerase in transcription. **[3]**

3. A DNA template strand contains the sequence TAC GGA TTT ACT. Deduce the mRNA sequence. **[2]**

4. State two differences between DNA and RNA that are relevant to transcription. **[2]**

5. Describe the roles of mRNA, tRNA and rRNA in protein synthesis. **[6]**

6. Explain how complementary base pairing contributes to the reliability of protein synthesis. **[4]**

7. The mRNA sequence AUG GCU UAC UGA is translated. Deduce the amino acid sequence. **[2]**

8. Distinguish between a codon and an anticodon. **[2]**

9. Explain why the genetic code must be a triplet code. **[3]**

10. Describe what is meant by the genetic code being degenerate and universal. **[4]**

11. Explain how a point mutation can affect protein structure, using sickle-cell disease as an example. **[5]**

12. Outline how a peptide bond forms during translation. **[3]**

HL practice questions

13. Explain what is meant by 5' to 3' transcription and 5' to 3' translation. **[4]**

14. Describe the roles of promoters, transcription factors and terminators in transcription. **[6]**

15. Explain post-transcriptional modification of pre-mRNA in eukaryotes. **[5]**

16. Use cardiac troponin T as an example to explain alternative splicing. **[4]**

17. Describe the roles of the A, P and E sites during translation elongation. **[3]**

18. Explain how pre-proinsulin is modified to form functional insulin. **[5]**

19. Explain the role of ubiquitin and proteasomes in maintaining a functional proteome. **[4]**

20. Multiple choice: In eukaryotes, gene expression can be regulated at which stage? A only transcription, B only translation, C transcription, post-transcription, translation and post-translation, D only post-transcription. **[1]**

Answer key and marking guidance

1. Transcription is the synthesis of RNA using a DNA template. In eukaryotes it occurs in the nucleus.

2. RNA polymerase binds to the promoter, opens the DNA in the gene region, moves along the template strand, and catalyses the joining of RNA nucleotides into an RNA strand.

3. AUG CCU AAA UGA.

4. RNA contains ribose while DNA contains deoxyribose; RNA contains uracil while DNA contains thymine; RNA is usually single-stranded while DNA is double-stranded.

5. mRNA carries codons copied from DNA to ribosomes. tRNA carries specific amino acids and has anticodons that pair with mRNA codons. rRNA forms part of ribosomes and helps position/catalyse translation.

6. Specific base pairing ensures correct RNA nucleotides are added during transcription and correct tRNA anticodons pair with mRNA codons during translation. Hydrogen bonding between complementary bases supports specificity. This helps maintain the correct amino acid sequence.

7. Met - Ala - Tyr - Stop. The polypeptide sequence is Met - Ala - Tyr; stop is not an amino acid.

8. A codon is a three-base sequence on mRNA. An anticodon is a complementary three-base sequence on tRNA.

9. There are 4 RNA bases. A one-base code gives 4 possibilities and a two-base code gives 16, which is not enough for 20 amino acids. A three-base code gives 64 possibilities, enough for all amino acids plus start/stop signals.

10. Degenerate means most amino acids are coded for by more than one codon. Universal means almost all organisms use the same codons for the same amino acids, allowing genes to be expressed across species.

11. A point mutation changes one base in a gene. This may alter an mRNA codon and change one amino acid in the polypeptide. In sickle-cell disease, a base substitution changes beta-globin, altering haemoglobin structure; haemoglobin forms strands and red blood cells become sickle-shaped.

12. Two tRNAs hold amino acids close together at the ribosome. A condensation reaction joins the amino acids with a peptide bond and releases water. The growing chain is transferred to the next tRNA.

13. In transcription, RNA is synthesized 5' to 3' because RNA polymerase adds nucleotides to the 3' end of the growing RNA. The DNA template is read 3' to 5'. In translation, the ribosome reads mRNA codons from the 5' end toward the 3' end.

14. The promoter is the DNA site where transcription begins and where RNA polymerase binds. In eukaryotes, transcription factors bind promoters or other regulatory sequences and help activate or repress transcription. The terminator sequence signals RNA polymerase to stop and release the RNA transcript.

15. Pre-mRNA contains introns and exons. Spliceosomes remove introns and join exons. A 5' cap and 3' polyA tail are added to stabilize the mRNA, help export/translation, and protect it from degradation.

16. Alternative splicing means the same pre-mRNA can be spliced in different ways to include different exons. In cardiac troponin T, an exon included in foetal heart mRNA is excluded in adult heart mRNA, producing protein variants with different calcium sensitivity.

17. A site holds the incoming tRNA with the next amino acid. P site holds the tRNA carrying the growing polypeptide. E site releases the tRNA that has lost its amino acid.

18. Pre-proinsulin is produced with a signal peptide that directs it into the endoplasmic reticulum. The signal peptide is removed to form proinsulin. Proinsulin folds and forms disulfide bonds. Enzymes remove the C peptide, producing mature insulin with two chains linked by disulfide bonds, which is packaged for secretion.

19. Proteins that are damaged or no longer needed are tagged with ubiquitin. Ubiquitin directs them to proteasomes. Proteasomes break proteins into amino acids, which can be reused to synthesize new proteins. This helps maintain a functional proteome.

20. C. In eukaryotes gene expression can be regulated at transcriptional, post-transcriptional, translational and post-translational stages.

Final one-page recall checklist

- DNA base sequence determines amino acid sequence through transcription and translation.
- Transcription produces RNA from a DNA template; RNA polymerase binds at a promoter.
- RNA uses uracil instead of thymine: A on DNA pairs with U in RNA.
- Only one DNA strand is used as the template for a specific gene.
- Translation uses mRNA codons and tRNA anticodons at ribosomes.
- mRNA binds to the small ribosomal subunit; tRNAs bind to the large subunit.
- A peptide bond forms by condensation between amino acids.
- AUG is the start codon and codes for methionine; UAA, UAG and UGA are stop codons.
- The genetic code is triplet, degenerate, universal and unambiguous.
- A point mutation changes one base and can change protein structure, as in sickle-cell disease.
- HL: transcription and translation both proceed using 5 to 3 directionality rules.
- HL: eukaryotic pre-mRNA is processed by splicing, 5 cap addition and 3 polyA tail addition.
- HL: alternative splicing allows one gene to produce multiple protein variants.
- HL: A site accepts new tRNA, P site holds the polypeptide, E site releases tRNA.
- HL: pre-proinsulin is modified into insulin; damaged proteins can be recycled by proteasomes.

Extended-response structure

For a long answer on protein synthesis, organize your response as: **DNA/gene -> transcription -> mRNA processing if eukaryotic -> translation at ribosome -> codon/anticodon pairing -> peptide bonds -> polypeptide modification -> reliability mechanisms**.