VCE Biology Units 3&4 Complete Study Guide

Complete study guide · Units 3&4 · AceGuides

This guide follows the VCAA VCE Biology Study Design that commenced in 2022 (originally accredited for 2022–2026; VCAA now lists it as "Accreditation period 2022" and it remains the design in force for 2026). It covers every key knowledge dot point in Unit 3 (How do cells maintain life?) and Unit 4 (How does life change and respond to challenges?), including the Unit 4 student-designed investigation and scientific poster.

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About this guide

How to use this guide

Each section matches one part of an Area of Study. Read the explanation, cover it up, then try to explain it aloud in your own words. Work through every worked example with a pencil before reading the answer. Finish each section with the "Check your understanding" questions and mark them against the worked solutions at the back. Questions you get wrong go into a "redo" list that you revisit one week later.

Words in **bold** are the terms examiners expect you to use. Blue boxes are exam tips; amber boxes are mistakes that regularly cost students marks.

Which study design?

VCE Biology currently runs on the study design that began in 2022. When VCAA reviewed accreditation periods, Biology was first listed as expiring on 31 December 2026; VCAA now shows it with an accreditation start year only. At the time of writing (October 2026) VCAA had not published a replacement Biology study design. If a new design is released for 2027 or later, most of this content will carry over: DNA structure, gene expression, enzymes, photosynthesis, cellular respiration, immunity, natural selection and evidence for evolution are core content in every VCE Biology design. Check the VCAA Biology study design page for your year before you rely on any dot point that is not core biology (for example, the named case studies such as

Howea palms or the *trp* operon).

How Units 3&4 are assessed

Component	What it is	Contribution to study score
Unit 3 School-assessed Coursework	Two SACs, one for each of Outcomes 1 and 2	20%
Unit 4 School-assessed Coursework	Two SACs (Outcomes 1 and 2) plus the scientific poster and logbook (Outcome 3)	30%
End-of-year examination	Written exam covering all of Units 3 and 4 and the key science skills	50%

The SACs for Unit 3 Outcomes 1 and 2 and Unit 4 Outcomes 1 and 2 are each chosen from four task types: analysis and evaluation of a biological case study; analysis and evaluation of generated primary and/or collated secondary data; comparison and evaluation of three student practical activities; or analysis and evaluation of a contemporary bioethical issue. Each task type can only be used once across Units 3 and 4. Written SAC tasks take about 50–70 minutes.

The Unit 4 Outcome 3 task is a scientific poster of no more than 600 words, supported by your logbook.

The examination

The end-of-year exam is 2 hours 30 minutes of writing plus 15 minutes reading time. In recent exams Section A has been 40 multiple-choice questions (1 mark each) and Section B has been short-answer and extended-response questions worth about 80 marks, for a total of about 120 marks. Section B always includes unfamiliar contexts, data analysis and at least one question on experimental design. Always check the current VCAA examination specifications for your year.

Ten-week revision plan

Week	Focus	Tasks
1	Nucleic acids, gene expression, *trp* operon, protein structure	Sections 1; draw transcription/translation from memory

2	DNA manipulation, PCR, gels, CRISPR, insulin, GMOs	Section 2; label a plasmid map; interpret 3 gels
3	Enzymes, coenzymes, inhibitors	Section 3; sketch rate graphs for each factor
4	Photosynthesis, respiration, biotech applications	Section 4; complete input/output tables blank
5	Barriers, innate and adaptive immunity	Section 5; flowchart from infection to antibody
6	Acquiring immunity, disease strategies, mAbs	Section 6; one case study summary per pathogen
7	Allele frequencies, selection, drift, resistance	Section 7; three allele-frequency calculations
8	Fossils, speciation, relatedness, phylogenetic trees	Section 8; build a tree from a sequence table
9	Human evolution and migration; key science skills	Sections 9 and 10
10	Full practice exam under timed conditions	Practice exam, mark it, redo weak areas

Contents

1. Nucleic acids, proteins and gene expression (Unit 3 AoS 1)
2. DNA manipulation techniques and applications (Unit 3 AoS 1)
3. Enzymes and the regulation of biochemical pathways (Unit 3 AoS 2)
4. Photosynthesis, cellular respiration and biotechnology (Unit 3 AoS 2)
5. Responding to antigens and acquiring immunity (Unit 4 AoS 1)
6. Disease challenges and strategies (Unit 4 AoS 1)
7. Genetic changes in populations (Unit 4 AoS 2)
8. Evidence of evolution: fossils, speciation and relatedness (Unit 4 AoS 2)
9. Human change over time (Unit 4 AoS 2)
10. The scientific investigation and poster (Unit 4 AoS 3 and key science skills)
11. Exam technique
12. Practice exam
13. Worked solutions
14. Glossary
15. One-page summary

1. Nucleic acids, proteins and gene expression

Nucleic acids as information molecules

Nucleic acids (DNA and RNA) are information molecules: the sequence of their bases stores the instructions for making proteins. Their monomers are **nucleotides**. Each nucleotide has three parts: a **phosphate group**, a **five-carbon (pentose) sugar** and a **nitrogenous base**. Nucleotides join by **phosphodiester bonds** (between the phosphate of one nucleotide and the sugar of the next) to form a **sugar–phosphate backbone**.

DNA is a **double helix** of two antiparallel strands. One strand runs 5′ → 3′ and the other runs 3′ → 5′. The bases pair by **complementary base pairing** with **hydrogen bonds**: adenine (A) with thymine (T) using two hydrogen bonds, and cytosine (C) with guanine (G) using three hydrogen bonds. A and G are purines (double ring); C, T and U are pyrimidines (single ring).

There are three main forms of **RNA**, all single-stranded:

- **mRNA (messenger RNA)** carries a copy of a gene's code from the nucleus to a ribosome.
- **tRNA (transfer RNA)** folds into a cloverleaf shape, carries a specific amino acid and has an **anticodon** that pairs with an mRNA codon.
- **rRNA (ribosomal RNA)** combines with proteins to form ribosomes and catalyses peptide bond formation.

Feature	DNA nucleotide	RNA nucleotide
Sugar	Deoxyribose (no –OH on carbon 2)	Ribose (–OH on carbon 2)
Bases	A, T, C, G	A, U, C, G
Strands in molecule	Double-stranded helix	Single-stranded (tRNA and rRNA fold back on themselves)
Location (eukaryotes)	Nucleus, mitochondria, chloroplasts	Made in nucleus; works in cytosol and ribosomes
Stability	Very stable; long-term storage	Less stable; short-lived (especially mRNA)

Common mistake: writing that nucleotides are joined by hydrogen bonds. Hydrogen bonds join the two strands (base to base). Phosphodiester bonds join nucleotides along one strand.

The genetic code

The **genetic code** is the set of rules linking mRNA **codons** (three-base sequences) to amino acids. Learn its three properties:

- **Triplet**: each codon is three bases long, giving $4^3 = 64$ possible codons.
- **Degenerate (redundant)**: most amino acids are coded by more than one codon (for example, GGU, GGC, GGA and GGG all code for glycine). This means some point mutations in the third base are **silent**.
- **Universal**: almost all organisms use the same code, which is why a human gene can be expressed in a bacterium.

AUG is the **start codon** (it also codes for methionine). UAA, UAG and UGA are **stop codons**; they code for no amino acid and end translation.

Gene structure

A **gene** is a section of DNA that codes for a functional product (a polypeptide or functional RNA). Important regions:

- **Promoter**: a sequence upstream of the gene where **RNA polymerase** binds to start transcription.
- **Operator** (prokaryotes): a sequence next to or overlapping the promoter where a **repressor** protein can bind and block transcription.
- **Exons**: coding sequences that are kept in mature mRNA and are expressed.
- **Introns**: non-coding sequences within eukaryotic genes that are removed during RNA processing.
- **Termination sequence**: signals the end of transcription.

The **template (antisense) strand** is the DNA strand read by RNA polymerase. The **coding (sense) strand** has the same sequence as the mRNA, except with T instead of U.

Gene expression step 1: transcription

Transcription makes an RNA copy of a gene. In eukaryotes it happens in the **nucleus**.

1. RNA polymerase binds to the promoter and unwinds the DNA, breaking hydrogen bonds between bases.
2. RNA polymerase moves along the template strand (reading it 3′ → 5′) and adds free RNA nucleotides that are complementary to it, building the RNA 5′ → 3′.
3. At the termination sequence, RNA polymerase detaches and the **pre-mRNA** is released.

The DNA re-forms its double helix.

Gene expression step 2: RNA processing (eukaryotes only)

Pre-mRNA is modified into **mature mRNA** before it leaves the nucleus:

- **5′ methyl-G cap** added: protects mRNA from degradation and helps ribosome attachment.
- **Poly-A tail** (a chain of adenine nucleotides) added to the 3′ end: increases stability and helps export from the nucleus.
- **Splicing**: introns are removed by a spliceosome and exons are joined. **Alternative splicing** joins exons in different combinations, so one gene can code for several different proteins. This is one reason the human proteome is much larger than the number of genes (roughly 20,000 protein-coding genes).

Exam tip: if a question says "prokaryote", there is no RNA processing and no splicing; transcription and translation can even happen at the same time in the cytoplasm.

Gene expression step 3: translation

Translation turns the mRNA base sequence into an amino acid sequence at a **ribosome** (free in the cytosol or attached to rough ER).

1. **Initiation**: the small ribosomal subunit attaches to the mRNA near the 5′ end and moves to the start codon AUG. A tRNA carrying methionine with the anticodon UAC pairs with AUG. The large subunit joins.
2. **Elongation**: tRNAs bring amino acids in the order set by the codons. Each anticodon pairs with its complementary codon. Peptide bonds form between adjacent amino acids (a **condensation reaction**, releasing water). The ribosome moves along the mRNA one codon at a time and the empty tRNA leaves to collect another amino acid.
3. **Termination**: when the ribosome reaches a stop codon, no tRNA matches it. A release factor binds and the polypeptide is released.

Worked example: from DNA to polypeptide

Template strand: 3′–TAC GGA TTC ACT–5′

Step 1, mRNA (complementary to template, U instead of T): 5′–AUG CCU AAG UGA–3′

Step 2, tRNA anticodons (complementary to codons): UAC, GGA, UUC (no tRNA for UGA)

Step 3, amino acids from a codon table: AUG = Met, CCU = Pro, AAG = Lys, UGA = stop

Answer: Met–Pro–Lys. The polypeptide has three amino acids.

Common mistake: using the anticodon to read the codon table. Codon tables are written for mRNA codons.

Gene regulation: the trp operon

An **operon** is a group of prokaryotic genes under the control of one promoter and one operator, transcribed together as one mRNA. The *trp* operon in *Escherichia coli* contains five **structural genes** (*trpE, trpD, trpC, trpB, trpA*) that code for the enzymes that make the amino acid **tryptophan**. Making tryptophan costs energy, so the bacterium switches the operon off when tryptophan is plentiful. **Regulatory genes** code for products (such as repressor proteins) that control the expression of other genes. There are two control mechanisms.

Repression

- The regulatory gene *trpR* (located elsewhere in the genome) codes for a **repressor protein** that is inactive on its own.
- When tryptophan levels are **high**, tryptophan acts as a **co-repressor**: it binds the repressor, changing its shape so that it binds to the **operator**. RNA polymerase is blocked, so the structural genes are not transcribed.
- When tryptophan levels are **low**, the repressor is inactive, it does not bind the operator, and RNA polymerase transcribes the structural genes.

Attenuation

The operon has a **leader sequence** (*trpL*) between the operator and *trpE*. It contains two tryptophan codons side by side and four regions that can pair to form hairpin loops. Because transcription and translation are coupled in prokaryotes, a ribosome starts translating the leader while it is still being transcribed.

- **High tryptophan**: there is plenty of tRNA carrying tryptophan, so the ribosome moves quickly through the trp codons and covers region 2. Regions 3 and 4 pair to form a **terminator hairpin** and RNA polymerase detaches. Transcription stops early.
- **Low tryptophan**: the ribosome **stalls** at the trp codons in region 1. Region 2 pairs with region 3 to form an **anti-terminator** hairpin, so the 3–4 terminator cannot form and transcription continues into the structural genes.

Tryptophan level	Repressor	Attenuation	Result
High	Active, bound to operator	3–4 terminator forms	Operon off; little or no tryptophan enzyme made

Low	Inactive, not bound	2–3 anti-terminator forms	Operon on; enzymes made

Exam tip: repression controls whether transcription starts; attenuation controls whether transcription that has started continues. Using both gives fine control and saves energy and resources.

Protein structure

Amino acids are the monomers of **polypeptides**. Each has a central carbon bonded to an amino group ($–NH_2$), a carboxyl group (–COOH), a hydrogen and a variable **R group**. There are 20 amino acids used in proteins and they differ only in their R groups, which may be polar, non-polar, acidic or basic. Amino acids join by **peptide bonds** in condensation reactions.

Level	What it is	Bonds that hold it
Primary	The sequence of amino acids in a polypeptide	Peptide bonds
Secondary	Local folding into α-helices and β-pleated sheets (and random coils)	Hydrogen bonds between backbone atoms
Tertiary	The overall 3D shape of one polypeptide	Interactions between R groups: hydrogen bonds, ionic bonds, disulfide bridges, hydrophobic interactions
Quaternary	Two or more polypeptides joined into one functional protein (e.g. haemoglobin has four; insulin has two)	Same as tertiary, between chains

The primary structure determines how the chain folds, and the final 3D shape determines the protein's **function**. A change in one amino acid can change the shape and stop the protein working (for example, sickle-cell haemoglobin, where glutamic acid at position 6 of the β chain is replaced by valine).

Denaturation is a change in the 3D shape of a protein (loss of secondary, tertiary and quaternary structure) caused by high temperature, extreme pH or some chemicals. Peptide bonds are not broken, but function is lost.

The proteome

The **proteome** is the complete set of proteins expressed by a cell, tissue or organism at a given time. It changes with cell type, age and conditions, whereas the genome is (almost) the same in every cell. Proteins are a very diverse group of molecules: **enzymes** (catalysts in biochemical pathways), structural proteins (collagen, keratin), hormones (insulin), transport proteins (haemoglobin, channel proteins), receptors, antibodies and contractile proteins (actin and myosin).

The protein secretory pathway

Proteins made for export (for example, insulin, antibodies and digestive enzymes) follow the **protein secretory pathway**:

1. Translation begins on a free ribosome; a signal sequence directs the ribosome to the **rough endoplasmic reticulum (RER)**.
2. The polypeptide enters the RER lumen, where it folds and may be modified.
3. It is packaged into a **transport vesicle** that buds off the RER and fuses with the **Golgi apparatus**.
4. In the Golgi, the protein is further modified (for example, adding carbohydrate to make a glycoprotein), sorted and packaged into **secretory vesicles**.
5. Secretory vesicles move to the plasma membrane, fuse with it and release the protein by **exocytosis**.

> **Common mistake:** saying proteins are "made in the Golgi". Proteins are made by ribosomes; the Golgi modifies, sorts and packages them.

Check your understanding: Section 1

Q1.1 (2 marks) Compare the nucleotides of DNA and RNA, giving two differences.

Q1.2 (3 marks) The coding strand of a short gene is 5′–ATG GCA TTT GAA TAA–3′. Write the mRNA sequence and the amino acid sequence. (Use: GCA = Ala, UUU = Phe, GAA = Glu.)

Q1.3 (2 marks) Explain why a substitution in the third base of a codon often has no effect on a protein.

Q1.4 (4 marks) A mutation in *trpR* produces a repressor that cannot bind tryptophan. Predict and explain the effect on the transcription of the *trp* structural genes when tryptophan is abundant. Refer to attenuation in your answer.

Q1.5 (3 marks) Describe the role of the RER, Golgi apparatus and vesicles in the export of an antibody from a plasma cell.

Q1.6 (2 marks) Explain how one human gene can produce more than one protein.

End of free sample

This is 10 of 71 pages.

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