



EUNOIA JUNIOR COLLEGE
JC2 Preliminary Examinations 2025
General Certificate of Education Advanced Level
Higher 2

CANDIDATE
NAME

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CIVICS
GROUP

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REGISTRATION
NUMBER

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H2 Biology

9744/03

Paper 3 Long Structured and Free-response Questions

17 September 2025

2 hours

Additional Materials: 12-page Answer Booklet

READ THESE INSTRUCTIONS FIRST

Write your name, civics group and registration number on all the work you hand in.

Write your answers in dark blue or black pen.

You may use an HB pencil for any diagrams or graphs.

Do not use paper clips, highlighters, glue, or correction fluid/tape.

Section A

Answer **all** questions on the **Question Paper**.

Section B

Answer **one** question on the **12-page Answer Booklet** provided.

Write your answer to each part of the question on a fresh sheet of paper.

The use of an approved scientific calculator is expected, where appropriate.

The number of marks is given in brackets [] at the end of each question or part question.

At the end of the examination, ensure that you submit both the Question Paper and Answer Booklet.

For Examiner's Use	
Section A	
1	
2	
3	
Section B	
4 OR 5	
Total	75

This document consists of **12** printed pages.

Section A

Answer **all** questions on the Question Paper.

- 1 Fig. 1.1 is a diagram showing the transcription of part of the *CALD1* gene that codes for a protein known as caldesmon. The part of the *CALD1* gene shown is a section of exon. Structure **A** represents an enzyme involved in transcription.

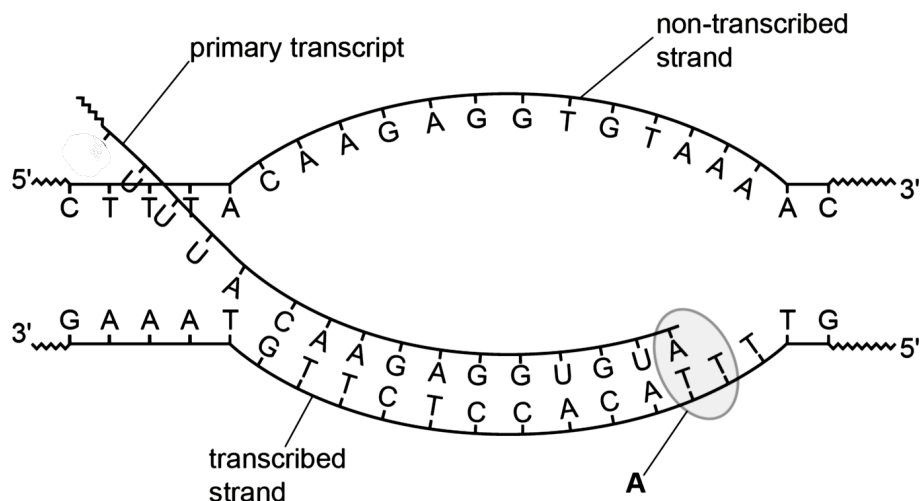


Fig. 1.1

- (a) (i) Name the enzyme labelled **A** in Fig. 1.1. [1]

..... [1]
[RNA polymerase](#);

- (ii) Name the bond that forms between the nucleotides in the primary transcript. [1]

..... [1]
[Phosphodiester \(bond\)](#);

Table 1.1 shows the codons that correspond to some amino acids.

Table 1.1

amino acid	codons
Phe	UUU UUC
Trp	UGG
Met	AUG
Thr	ACU ACC ACA ACG
Arg	AGA AGG
Val	GUU GUC GUA GUG
Gly	GGU GGC GGA GGG

- (iii) State the amino acid sequence that is coded for by the sequence of nucleotides on the primary transcript shown in Fig. 1.1. [1]

[starting from UUU] **Phe–Thr–Arg–Gly–Val**

R: starting from AUG: Met–Trp–Arg–Thr–Phe (wrong direction)

(iv) Explain why one of the strands of DNA is **not** transcribed. [3]

1. Non-transcribed strand is not the template strand / only the template strand is transcribed;
2. If non-template strand is transcribed, the mRNA sequence codes for a different sequence of amino acids (A: different sequence of codons / different primary transcript for RNA);
3. Thus resulting in a non-functional polypeptide (A: polypeptide with a different function / structure / 3D conformation);
4. Translation would be a waste of energy / **translation will not occur**;
5. AVP;
e.g. if non-template strand is transcribed as well, ds RNA will form which cannot be translated

Caldesmon is a large protein with a number of binding sites to attach to other proteins.

Caldesmon exists in two different forms, H-caldesmon and L-caldesmon.

H-caldesmon helps to regulate contraction and relaxation in smooth muscle cells.

L-caldesmon is found in some non-muscle cells, where it also acts as a regulatory protein.

- Caldesmon is coded for by a gene known as *CALD1*.
- *CALD1* has 17 exons.
- The primary structure of H-caldesmon has a repeating sequence in the middle of the amino acid chain that is **not** present in L-caldesmon.

(b) (i) Researchers have discovered that a gene mutation is **not** the cause of the two different forms of caldesmon.

Explain what is meant by a gene mutation. [2]

1. A gene mutation is a change in the sequence of base pairs in a DNA molecule;
(A: change in DNA/base/nucleotide sequence)
 2. Which codes for / results in an altered / different polypeptide;
(A: altered amino acid sequence / primary structure of polypeptide/protein)
- I: change in RNA base sequence, types of mutations

(ii) Researchers now know that the two different forms of caldesmon are the result of events occurring **directly after** transcription of DNA. Changes occur to the primary transcript that is formed by DNA transcription.

Explain how the smooth muscle cells and non-muscle cells can produce different forms of caldesmon from the same primary transcript. [2]

1. Different forms of caldesmon are produced via alternative splicing;
(R: DNA splicing, mutation occurring during gene/RNA splicing)
2. Which involves the removal of introns;
(R: introns described as bases/nucleotides/codons)
(R: different number of introns removed / some introns remain)
and joining of different combination of exons;

3. Thus, producing different types of mature messenger RNA (A: mRNA without “mature” as long as not referring to primary transcript);

(iii) Suggest how the two different forms of caldesmon can still have similar functions, even though they have a different primary structure. [1]

1. Despite having different primary structures, H-caldesmon and L-caldesmon may still have **similar** (R: **same**) **tertiary structure / 3D conformation/shape** OR

Binding sites of H-caldesmon and L-caldesmon still have **similar 3D conformation**;

2. Hence, binding sites (R: **active site**) are still complementary to attach to proteins;

3. Removed amino acids are not structural amino acids / not part of binding sites; (Note to marker: accept “non-essential amino acids”)

4. R-group interactions within caldesmon are still the same / similar;

5. AVP: e.g. caldesmon has more than one binding site and only one/few changed;

6. AVP: e.g. same type of binding site, but a different number

Caldesmon was recently reported in the scientific literature to be involved in gastric cancer progression, invasion, and migration.

Tumour cells can become invasive through increased mobility and decreased adhesion, which can lead to metastasis from the primary tumour site. This process is triggered through changes in gene expression mediated by signalling pathways, including the PI3K-AKT pathway.

Fig. 1.2 shows the PI3K-AKT signalling pathway, in which:

- KRAS and RHEB are G-proteins.
- PI3K, AKT, RAF, MEK, and ERK are all protein kinases.
- Sharp arrows ($\downarrow$) represent activation, while blunt arrows ($\perp$) represent inhibition.

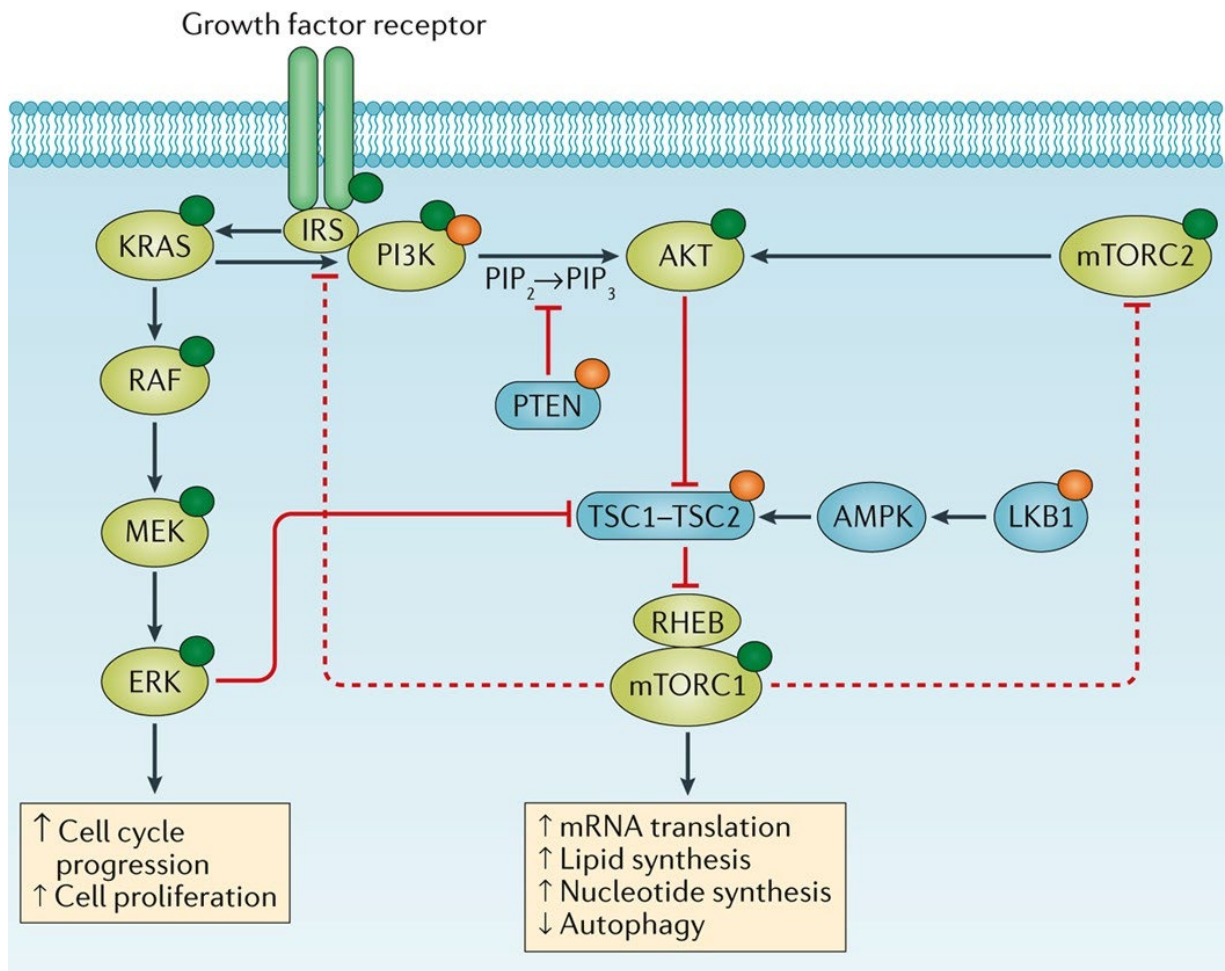


Fig. 1.2

- (c) (i) Other than signal amplification, describe **one** advantage of the PI3K-AKT signalling pathway using one example shown in Fig. 1.2. [2]

1. There are multiple checkpoints for regulation / several steps in the signalling pathway can be regulated/controlled;
2. For instance, inhibition by PTEN (A: other examples, MTORC1 / AKT etc)

OR

3. Ability of a signal molecule/ligand (growth factor) to elicit cellular responses such as gene expression (A: other examples of cellular response) upon binding to cell surface receptor;
4. **without the need to move into cell;**

- (ii) Using Fig. 1.2, describe a phosphorylation cascade that results in cell cycle progression. [2]

(RAF→MEK→ERK)

1. Phosphorylation cascade is the sequential activation of kinases within a signalling pathway;
2. Where RAF phosphorylates and activates MEK;
3. and then MEK phosphorylates and activates ERK;

(d) Describe the role of second messengers.

[2]

1. Second messengers bind to a downstream protein kinase/relay protein
2. This induces a conformational change in the downstream protein kinase/relay protein, thus activating it;
3. In this way, the 'signal' is passed on/relayed to the next protein kinase / relay protein during signal transduction;

I: water-soluble, non-protein molecules or ions

R: amplify the signal / elicit a large cellular response;

ERK induces the expression of two transcription factors, Jun and Fos. These are both reported in the scientific literature to be involved in the control of the mitotic cell cycle.

Cyclin-dependent kinases (CDKs) are enzymes involved in the control of the mitotic cycle. The gene *CDKB2* codes for one of these kinase enzymes.

Genes *KRP4* and *CycD6* code for proteins that regulate the activity of CDKs.

The scientists investigated the effect of Jun and Fos on gene expression. They measured the relative quantities of mRNA produced by transcription of the three genes, *CDKB2*, *KRP4*, and *CycD6*.

Fig. 1.3 shows the effects of Jun alone, Fos alone, as well as Jun and Fos combined on the expression of the three genes. Error bars show **standard deviation** ($n = 3$).

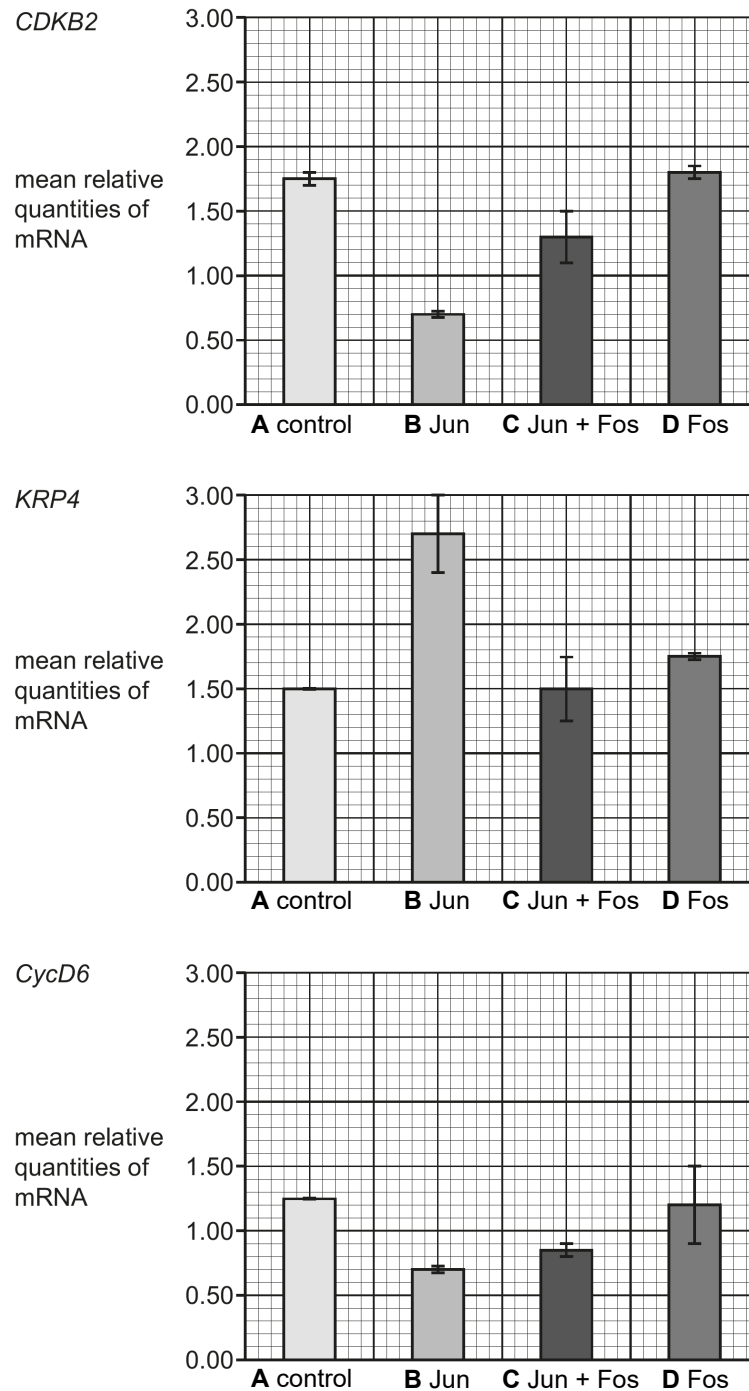


Fig. 1.3

- (e) (i) Complete Table 1.2 to show how the expression of the three genes is affected by the presence of Jun alone and Fos alone, shown in Fig. 1.3.

Use **only** these descriptions to complete the table:

large increase small increase no change small decrease large decrease

Table 1.2

gene	effect of gene expression	
	Jun only	Fos only
<i>CDKB2</i>	large decrease	no change / small increase;
<i>KRP4</i>	large increase	small increase;
<i>CycD6</i>	large decrease	no change / small decrease;

[3]

(one mark per row)

- (ii) Fig. 1.3 also shows the combined effect of Jun and Fos (**C**) on the expression of the three genes.

The scientists made two conclusions about the effects of the mixture of Jun and Fos (**C**) on the expression of the genes *KRP4* and *CycD6*.

Conclusion 1: Fos counteracts the stimulation of gene expression of *KRP4* by Jun.

Conclusion 2: Fos does not reverse the effect of Jun on gene expression of *CycD6*.

State **and** explain whether the evidence from Fig. 1.3 **fully supports**, **partially supports** or **does not support** each of these conclusions. [2]

conclusion 1

fully supports + quantity of mRNA for Jun + Fos (**C**) is **lower** than with Jun alone (**B**) (OWTTE);

conclusion 2

partially supports + quantity of mRNA for Jun + Fos (**C**) **higher** than with Jun alone (**B**) but **not as high** as control (**A**) / Fos alone (**D**);

OR

fully supports + quantity of mRNA for Jun + Fos (**C**) **is similar to** Jun alone (**B**)

or

fully supports + no statistical test carried out to show that there is a significant difference between the quantity of mRNA for Jun + Fos (**C**) and Jun alone (**B**)

The relative quantities of mRNA shown in Fig. 1.3 were derived using a modified form of PCR.

Fig. 1.4 shows how mRNA is first used to form complementary DNA (cDNA), which is subsequently amplified by PCR.

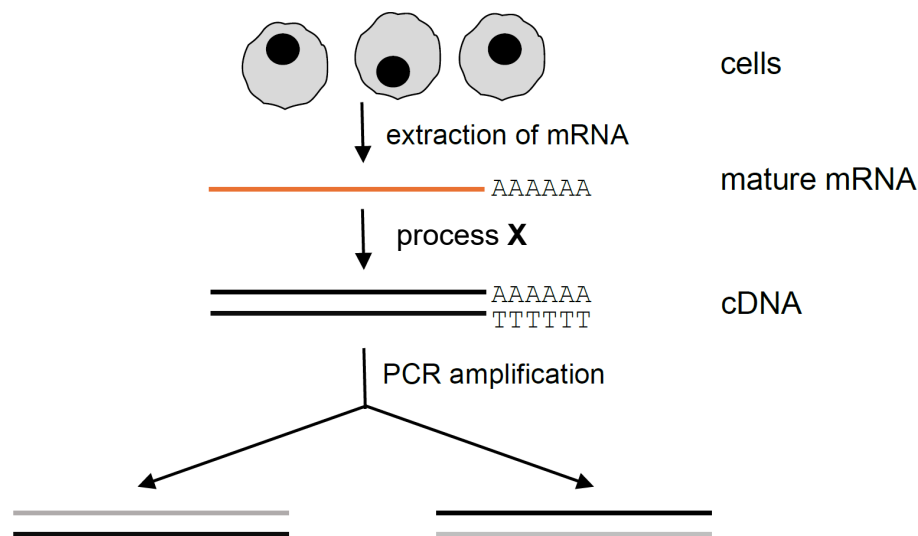


Fig. 1.4

- (f) (i) State the name of the enzyme that catalyses process X. [1]

Reverse transcriptase;

- (ii) Suggest why RNA cannot be used directly in PCR amplification without first undergoing process X. [1]

1. Tag polymerase active site can only recognise / only complementary to DNA but not RNA;
2. RNA is unstable and hence more prone to degradation;

mRNA produced from transcription of *Jun* was amplified using the process shown in Fig. 1.4.

Amplified *Jun* cDNA fragments from two different individuals were subjected to gel electrophoresis and nucleic acid hybridisation.

Fig. 1.5 shows the results of a healthy individual and a cancer patient.

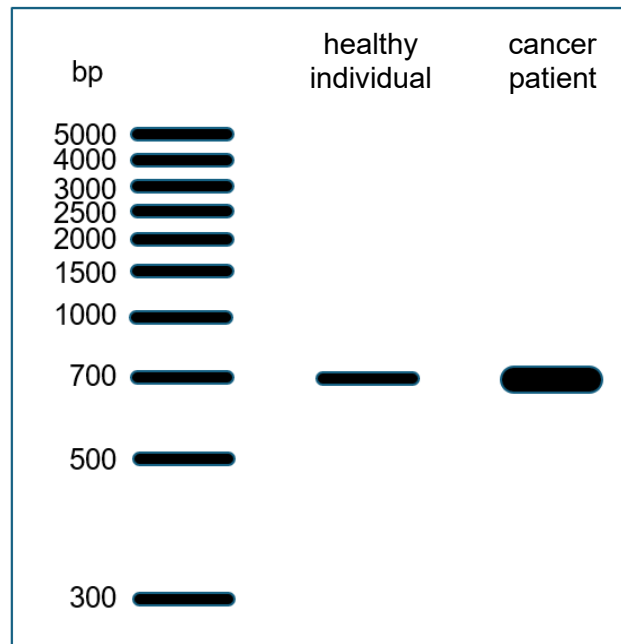


Fig. 1.5

- (g) (i) With reference to Fig. 1.5, describe the difference in relative quantities of *Jun* cDNA, and explain how nucleic acid hybridisation was used to investigate this. [4]

1. Thicker band (as compared to healthy individual) indicates higher quantity of *Jun* cDNA for the cancer patient (or vice versa);
2. Using NaOH/alkaline solution, double stranded cDNA is made single stranded and transferred to nitrocellulose membrane;
3. Single stranded radioactive probes that are complementary to *Jun* cDNA are then used and will bind/hybridise to the single stranded *Jun* cDNA;
4. Autoradiography is carried out next and the relative amounts of *Jun* cDNA fragments can be visualised;

- (ii) Genes that are typically involved in cancer development are classified as either proto-oncogenes or tumour suppressor genes.

Suggest and explain which type of gene *Jun* may be. [2]

1. *Jun* is a proto-oncogene;
2. Because it is overexpressed in the cancer patient;

[Total: 30]

2 One of the proteins found in milk is β -casein.

A molecule of β -casein consists of a single polypeptide of approximately 200 amino acids.

Molecules of β -casein have a **high** proportion of the amino acids proline and leucine. These amino acids have hydrophobic R groups.

Fig. 2.1 compares the structure of proline with the general structure of an amino acid. Proline is an unusual amino acid because it has a cyclic R group and the nitrogen atom is attached to only one hydrogen atom.

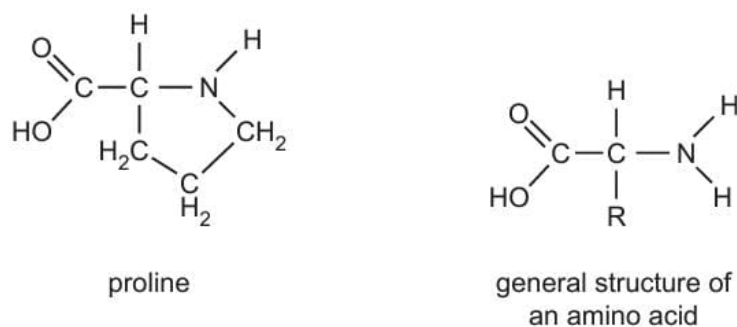


Fig. 2.1

(a) Using the general structure of an amino acid shown in Fig. 2.1, show how two amino acids are joined together. [3]

1. 2 amino acids to form a dipeptide
2. Condensation reaction + loss of one water molecule
3. Peptide bond correctly drawn + labelled correctly

(b) When a molecule of proline becomes part of a polypeptide, the hydrogen atom is lost from the nitrogen atom and is therefore **not** available for the formation of hydrogen bonds.

Compared to other protein molecules with a similar number of amino acids, β -casein molecules have a much less organised secondary structure.

Suggest why is this so.

[4]

1. β -casein has high proportion of proline;
2. Hence less formation of hydrogen bonds between NH and C=O along the polypeptide backbone;
3. Lesser occurrence / formation of α helix and/or β -pleated sheets;
4. Greater proportion of random coiling;

Molecules of β -casein have a relatively **low** proportion of amino acids cysteine and serine. Table 2.1 shows the R groups of cysteine and serine.

Table 2.1

amino acid	R group
cysteine	- CH ₂ SH
serine	- CH ₂ OH

(c) Using Table 2.1,

- (i) state the level of protein structure that the R group of serine helps to maintain; [1]

Tertiary structure;

- (ii) explain how serine contributes to the level of protein structure specified in your answer to (c)(i). [2]

1. R group of serine contains a polar -OH group;
2. which can form hydrogen bond with the polar R group of another amino acid;
3. This allows the protein to fold into a specific 3D conformation;

[Total: 10]

3 *Spea multiplicata* is one of several species of American spadefoot toad.

Young spadefoot toads are called tadpoles and live in water in ponds.

S. multiplicata tadpoles show three different phenotypes due to genetic variation. The three phenotypes are: detritus feeder, intermediate and carnivore.

Detritus feeders are small, and carnivores are large. Intermediates vary in size between the two extremes.

A detritus feeder and a carnivore are shown in Fig. 3.1.



Fig. 3.1

Detritus feeders:

- eat detritus (small pieces of dead organic matter) and algae
- have smooth mouthparts, small jaw muscles and long intestines.

Intermediates:

- can eat all available food (detritus, algae and fairy shrimps)
- have teeth-like mouthparts, medium-sized jaw muscles and medium-sized intestines.

Carnivores:

- eat fairy shrimps and other small animals
- have teeth-like mouthparts, large jaw muscles and short intestines.

Scientists counted the number of each type of tadpole in two different ponds: pond 1 and pond 2.

(a) (i) In pond 1, the scientists observed:

- a high density of tadpoles
- a low abundance of food
- that most of the tadpoles they counted were either detritus feeders or carnivores, with very few intermediates present.

Describe **and** suggest explanations for the type of natural selection that appears to be acting in pond 1. [3]

1. Disruptive selection; (name of type of natural selection)
2. Extreme phenotypes / e.g. given carnivore and detritus feeders are selected for and intermediates are selected against; (description of disruptive selection)

Explanation (any one):

3. **Intense competition for food** between intermediates and carnivore / detritus feeders; (A: **Food is selection pressure** / food is limited, hence there is **intense competition between intermediates and extreme phenotypes** in pond 1)
4. Intermediates are **outcompeted for food / don't get enough of detritus, algae and fairy shrimps**;
5. **AVP**;

(ii) In pond 2, the scientists observed:

- a low density of tadpoles
- sufficient food availability for all tadpoles
- that most of the tadpoles they counted were intermediates, with fewer detritus feeders or carnivores.

Describe **and** suggest explanations for the type of natural selection that appears to be acting in pond 2. [3]

1. Stabilising selection; (name of type of natural selection)
2. Intermediate phenotype is selected for and extreme phenotypes / e.g. given carnivore and detritus feeders are selected against; (description of stabilising selection)

Explanation (any one):

3. **Less intense competition for food** faced by **intermediates over extreme phenotypes**;
4. As intermediates can **eat all types of food** given above / **wider range of food compared to either of the extreme phenotypes**; (A: **greater range** / variety of diet improves growth and development of intermediates)
5. **AVP**;

- (iii) A student suggested that the variation in *S. multiplicata* tadpoles could lead to sympatric speciation in some populations.

Outline the features of sympatric speciation.

[2]

1. Species forming in the **same geographical** region / area;
2. **Disruption of gene flow** is due to **behavioural / habitat / ecological differences / isolation**;

- (b) Fig. 3.2 shows the evolutionary relationships between three species of the American spadefoot toad.

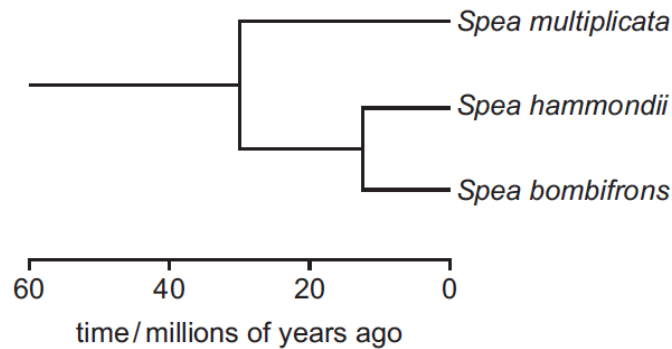


Fig. 3.2

Explain how analysis of DNA allowed the evolutionary relationships shown in Fig. 3.2 to be determined.

[2]

1. Use **same gene** present in **all** three species to **compare DNA sequences**;
2. **Count nucleotide / base differences**;
3. **More differences** means, **less closely related** e.g. *S. hammondi* and *S. bombifrons* / **less differences** means **less time for divergence from common ancestor (OWTTE)**;
4. **AVP**;

[Total: 10]

Section B

Answer **one** question in this section.

Write your answers on the Answer Booklet provided.

Your answers should be illustrated by large, clearly labelled diagrams, where appropriate.

Your answers must be in continuous prose, where appropriate.

Your answers must be set out in parts **(a)** and **(b)**, as indicated in the question.

- 4 (a) Explain the importance of non-coding sequences in eukaryotes. [14]

1. Centromeres (max 3)

- Centromeres are the constricted regions on chromosomes made up of non-coding tandem repeats;
- Centromeres are where two sister chromatids are attached during nuclear division;
- Centromeres allow attachment of spindle fibres/microtubules via kinetochore proteins;
- This enables the separation of sister chromatids during anaphase of mitosis/ anaphase II of meiosis to opposite poles of the cell during nuclear division;
- This enables the separation homologous chromosomes during anaphase I meiosis;

2. Telomeres (max 2)

- Telomeres are non coding tandem repeats found at the ends of chromosomes;
- Due to end-replication problem, the 5' end of the DNA strands will be eroded;
- Telomeres prevent the erosion of genes;
- Telomeres prevent fusion of the ends of different chromosomes;
- When telomeres reach a critical length, apoptosis results thus preventing unlimited cell proliferation in adult tissue;

3. Introns (max 3)

- Introns are non-coding sequences interspersed between exons in genes;
- After transcription, introns are excised through RNA splicing;
- Introns allow alternative splicing to occur, whereby introns are removed and different combinations of exons are joined together;
- producing different mRNAs (mature) which give rise to different proteins, using a single gene;

4. Promoters (max 2)

- Promoters are found upstream of the transcription start site of genes;
 - Promoters serve as recognition sites for the binding of general transcription factors and RNA polymerase;
 - forming the transcription initiation complex;
 - to initiate transcription;
- (either (c) or (d), not both will be credited)

5. Enhancers and Silencers (max 3)

- Enhancers and silencers are distal control elements/ regulatory elements, usually found distal from the promoter,;
- Enhancers can be bound by activators which increases the rate of transcription;
- (how) stabilise the transcription initiation complex/ help to recruit RNA polymerase;
- Silencers can be bound by repressors which decreases the rate of transcription;
- (how) prevent the formation of the transcription initiation complex/ prevent binding of RNA polymerase to promoter;

QWC: Clear, organised flow without ambiguity with each example clearly named and its importance clearly described and to include at least 4 different types of non-coding sequences and their importance.

Max 13 marks + 1 mark for QWC

- (b) Dinosaurs are now extinct but there are approximately 10,000 species of living birds. It is thought that birds evolved from small dinosaurs and that being small helped their survival during a time of rapid environmental change when species of large dinosaurs went extinct.

Suggest and explain why, in a rapidly changing environment, small animals may possess evolutionary advantages compared to large animals. [11]

- Small animals include insects, birds, small fishes, amphibians, reptiles and mammals; **(Give at least one example).**
- Rapidly changing environment means that selection pressures are **more intense and varied across time; (reference to this idea for full credit)***

Smaller animals can have shorter generation time → more mutations → more variation for adaptation to changing environment (max 3)

- These animals tend to have **shorter generation times** as compared to larger animals;
- Mutations** giving rise to favourable alleles which would be selected for in a given environment can **accumulate quickly** in the population with a short period of time;
- Changes in allele frequencies** would also then occur more quickly due to **natural selection** and **genetic drift** events;
- Allowing for the populations to **adapt more quickly** to the rapidly changing environment;
- AVP;

Smaller animals can produce a larger number of offspring → (i) more variation for natural selection to operate and also (ii) buffered from detrimental effects of genetic drift (max 3)

- Small animals tend to also have **larger number of offspring (large reproductive output)** and;
- Greater variation** is also seen in populations of smaller animals;
- With the struggle of existence and selection pressures, there is a **greater percentage chance of offspring from each generation surviving to reach sexual maturity** as compared to larger animals;
- Smaller animals also **reach sexual maturity faster and produce more offspring in their lifetimes** as compared to larger animals;

12. As populations of small animals tend to be larger, they are also **buffered better against random, chance occurrence such as genetic drift events** (Founder's effect/Bottleneck effect) which can cause affect the survivability of the populations;
13. AVP;

Smaller animals have smaller size → (i) larger variety of ecological niches to exploit + (ii) escape from predators (max 3)

14. Smaller animals can also **exploit more niches/habitats easily** due to **their small size and metabolic requirements**;
15. Smaller animals tend **to also spread their offspring more widely away from the areas** they live in, hence increasing their survivability;
16. Small animals can also **escape better from predators** as they can take **advantage of small crevices/spaces despite the changes in the environment**;
17. AVP;

QWC: Clear and logical flow of arguments with ideas **from each of the three highlighted sections** showing advantages that smaller animals may have and these advantages are clearly explained.

Max 10 marks + 1 mark for QWC

- 5 (a) Many enzymes are proteins, but not all proteins are enzymes.

Using examples, explain the importance of non-enzymatic proteins that are found embedded in membranes. [14]

1. **Receptors** (max 5m)

- a. **Receptors** are embedded on **cell surface membrane** of **cells**;
- b. Idea of allowing the **extracellular signal/ligand** to be **detected** and then **stimulating changes within the cell**;

Examples:

- c. **Glucagon receptor** embedded on cell surface membrane of **liver cells**; (R: RTK)
- d. Has an **extracellular ligand-binding site** that is **complementary in conformation** to **glucagon**;
- e. **Binds** to **glucagon** and results in e.g. **glycogen breakdown / inhibition of glycogen synthase** (name one effect) in **liver cells** ("liver cells" mark for once);
- f. **Fc receptor** embedded on cell surface membrane of **macrophages**;
- g. **Binds** to **Fc region** of **antibodies**;
- h. Allows **pathogen/toxin** opsonised by antibodies to be **phagocytosed more efficiently** by **macrophages** ("macrophage" mark for once);
- i. **T cell receptor** embedded on **cell surface membrane** of **naïve T cells**;
- j. Have binding site **complementary in conformation** to **peptide-MHC complex** presented on cell surface membrane of **antigen-presenting cells/macrophages**;
- k. Upon binding to specific peptide-MHC complex, **naïve T cell** is **activated** to become **effector T cells**, such as **cytotoxic T cells** and **T helper cells**;
- l. **B cell receptor** embedded on **cell surface membrane** of **naïve B cells**;
- m. This allows naïve B cells to take up antigen via receptor-mediated endocytosis and subsequently activated by T helper cells to become **antibody-producing plasma cells**.

2. **Transport proteins** (max 5m)

- a. **Transport proteins** are also found embedded in **cell surface membrane** of **cells**;
- b. Transport proteins allow **facilitated diffusion** / **active transport** to occur;
- c. Facilitated diffusion is carried out by transport proteins such as **channel proteins** / **carrier proteins**
OR
Active transport is carried out by transport proteins called **pumps**.
- d. e.g. of channel proteins: **aquaporins** / **ion channels**;
- e. Water is **polar** / Ions are **charged**
and will be **repelled by** the **hydrophobic core** of the **phospholipid bilayer**;
- f. Channel proteins provide a **hydrophilic pore** for water / ions to **move down concentration gradient** across the cell surface membrane / **pass from one side of the cell surface membrane to the other side**.

- g. e.g. of carrier proteins: glucose transporters; (R: GLUT4 / glucose transporters are channel proteins)
- h. Glucose is large, therefore unable to pass through transient pores
OR
Glucose is polar, therefore will be repelled by the hydrophobic core of the phospholipid bilayer;
- i. Glucose binds to glucose transporter, which will then change conformation and glucose is released on other side of the cell surface membrane.

3. Photosystems (max 5m)

- a. Photosystems are embedded in thylakoid membrane in chloroplasts
- b. Photosystems are protein complex made up of light harvesting complexes and a reaction centre.
- c. Photosynthetic pigments within photosystem help to absorb photons / light energy;
- d. Thereby allowing light-dependent stage of photosynthesis to occur to produce ATP and NADPH;
- e. ATP and NADPH produced allows Calvin cycle to occur to produce glucose;

4. Electron transport chain

- a. Electron transport chain (ETC) is embedded on thylakoid membrane in chloroplasts / cristae in mitochondria.
- b. ETC is made up of electron carriers arranged in decreasing energy levels.
- c. High energy electrons move down the ETC and energy is released.
- d. Energy released is used to create a proton motive force.
- e. The proton motive force is used by ATP synthase to produce ATP via chemiosmosis.

5. Others

- a. Glycoproteins found embedded on cell surface membrane of cells allows for cell-cell adhesion or cell-cell recognition;
- b. Peptide-MHC complexes embedded on cell surface membrane of antigen-presenting cells.
- c. T cell receptor of naïve T cells can bind and become activated to become T helper cells and cytotoxic T cells.
- d. AVP

QWC: Clear, organised flow without ambiguity with each example clearly named and its importance clearly described and to include at least 3 different types of non-enzymatic proteins and their importance.

Max 13 marks + 1 mark for QWC

- (b) Immunity can be described as passive, active, naturally acquired or artificially acquired.

Discuss how antibodies illustrate these forms of immunity, and explain why antibodies are considered part of the specific immune system. [11]

How antibodies illustrate passive, active, naturally acquired and artificially acquired immunity

1. Passive immunity refers to the **acquiring of antibodies from another source**.
2. Active immunity occurs when our **own body's** immune system **produce antibodies**
3. **Passive and active immunity** can be **naturally acquired or artificially acquired**.
4. **Passive and naturally acquired immunity:**
 - a) e.g. **placental transfer of antibodies from mother to fetus** during pregnancy
 - b) e.g. transfer of antibodies found in human colostrum and **milk to babies** who are **breastfed**.
5. **Passive and artificially acquired immunity:**
e.g. injection of antibody-containing serum / antibody, from another person or animal.
6. **Active and naturally acquired immunity:**
 - a) e.g. **natural exposure** to an infectious agent or other antigen by the body.
 - b) The body responds by making its own antibodies.
7. **Active and artificially acquired immunity:**
 - a) e.g. vaccination
 - b) whereby person vaccinated will be exposed to **antigens / attenuated microbes / fragmented microorganisms / toxins**, and this will result in **production of antibodies** and memory cells in the vaccinated individual

Why antibodies are considered part of the specific immune system

8. Each antibody **has 2 antigen-binding sites**.
9. **Each** antigen-binding site is made up of the **variable region of a heavy chain** and **variable region of a light chain**.
10. Each antigen-binding site **has a specific conformation**.
11. Whereby, the antigen-binding site is **complementary in conformation** and charge to a **specific antigen**;
12. **Different antibodies** have **different antigen-binding sites**;
13. Therefore, **different antibodies** can **bind** to **different antigens**;

QWC: Clear, organised flow without ambiguity with **both parts of question** tackled.

Max 10 marks + 1 mark for QWC