EUNOIA JUNIOR COLLEGE
JC1 Promotional Examination 2022
General Certificate of Education Advanced Level
Higher 2

CANDIDATE NAME	**ANSWER KEY**

CIVICS GROUP	2	2	-			REGISTRATION NUMBER		

H2 Biology **9744 / 02**

04 October 2022

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 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.

Section A
Answer **all** questions in the spaces provided on the Question Paper.

Section B
Answer **all** questions in the 12-page Answer Booklet.

The use of an approved scientific calculator is expected, where appropriate. You may lose marks if you do not show your working or if you do not use appropriate units.

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

At the end of the examination, submit the Question Booklet and the 12-page Answer Booklet separately.

For Examiner's Use	
Section A	
1	
2	
3	
4	
5	
Section B	
6	
Total	/80

This document consists of **22** printed pages.

Section A

Answer **all** questions in the spaces provided.

1 Fig. 1.1 shows the process of collagen synthesis in a fibroblast cell.

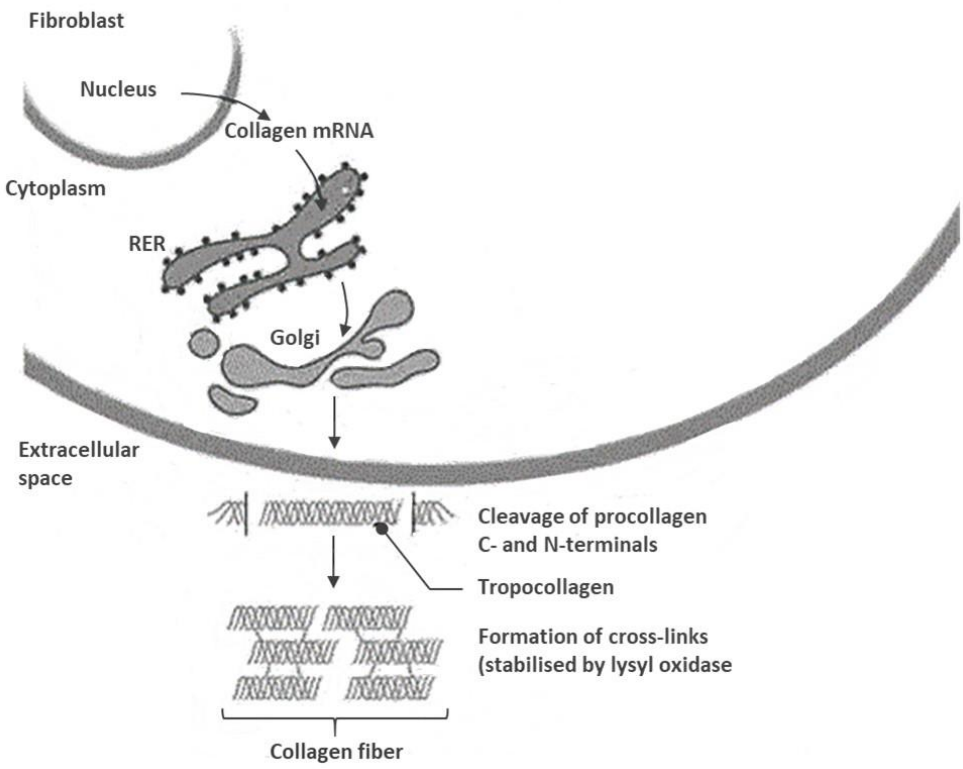


Fig. 1.1

(a) With reference to Fig. 1.1, describe how procollagen is transported out of the cell. [3]

1. **Secretory vesicle** containing procollagen **buds off** from the trans face of the **Golgi apparatus**;
2. Moves along **microtubules** towards **cell surface membrane**;
3. Membrane of the secretory vesicle **fuses** with the cell surface membrane by and procollagen is released out of the cell via **exocytosis**;

Comments

Majority of students did not read the question properly and wasted time writing about how procollagen was synthesised (i.e. details of transcription and translation). The question is only concerned with how procollagen is transported out of the cell, not how procollagen is made.

Also, students need to be careful in differentiating between procollagen and collagen. Question's focus is on procollagen, not collagen.

Point 1

- R: transport vesicle / Golgi vesicle
- R: pinch off. "Pinch off" does not have the same meaning as "bud off".
- It is incorrect to say that a protein/procollagen buds off from the Golgi apparatus. The term "buds off" is used to describe how a vesicle is formed, not the protein.
- Students need to be aware to use a capital "G" when spelling "Golgi".

Point 2
- Many students failed to earn a mark here due to the lack of mention of the involvement of microtubules.

Point 3
- A number of students failed to earn a mark here due to the lack of mention of "exocytosis" as the transport process.

(b) The primary structure of a collagen polypeptide has a repeating pattern of three amino acids.

Fig. 1.2 shows the two forms of this pattern.

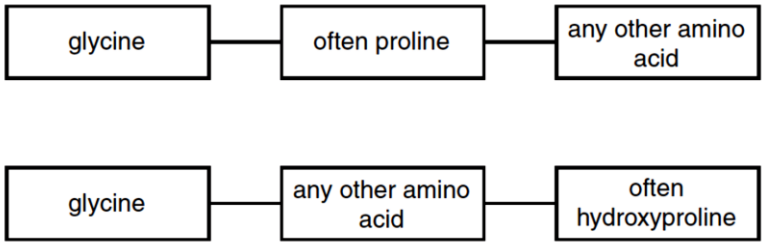


Fig. 1.2

Hydroxyproline is a proline molecule that has a hydroxyl (-OH) group added to its R-group. The hydroxyl groups are involved in hydrogen bonding in tropocollagen.

Glycine makes up approximately 30% of the total amino acid composition of collagen.

Explain how the structure of glycine plays an essential role in contributing to the high tensile strength of tropocollagen. [3]

1. Glycine is the amino acid with the **smallest R-group**;
2. This allows the formation of a **tight triple helix** / allow the three polypeptide to be closely associated;
3. This in turn allows for **hydrogen bonds** to be form between the 3 polypeptides in the triplex helix, contributing to high tensile strength;

Comments

Point 1
- A number of students did not seem to know the structure of glycine, and incorrectly mentioned that glycine has hydroxyl group.
- Students need to note that the R group of glycine is not involved in the formation of hydrogen bonds.
- A number of students incorrectly mentioned that glycine is "*one of the* smallest amino acids". This does not carry the same meaning as saying glycine is the smallest amino acids.

Point 2
- R: compact triple helix. "compact' and "tight" do not have the same meaning.
- A number of students did not seem to have a clear idea of how to use / how not to use the term "tropocollagen" or "collagen molecule". A collagen molecule is essentially termed as tropocollagen, an tropocollagen has 3 polypeptides chains wound around each other to form a triple helix. It is therefore incorrect to say that "glycine can fit in small spaces *between tropocollagen molecules*", or that "glycine allow tropocollagen ti be packed closely together".

Point 3
- It is incorrect to describe hydrogen bonds as strong.

(c) Many of the lysine amino acids in a collagen polypeptide also have a hydroxyl (-OH) group added to their R-group.

Fig. 1.3 shows hydroxylysine.

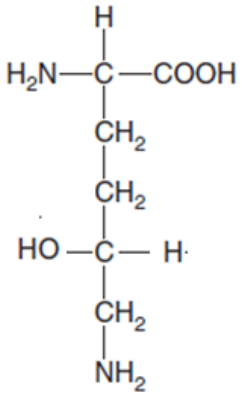


Fig. 1.3

(i) On Fig. 1.3, draw a box around the R group of hydroxylysine. [1]

Comments

A surprising number of students were not able to indicate the R group correctly.

The hydroxyl group of hydroxylysine is important as a possible attachment site for a β-galactose molecule. The joining of β-galactose to hydroxylysine involves the formation of a glycosidic bond.

The molecular structure of β-galactose is shown in Fig. 1.4.

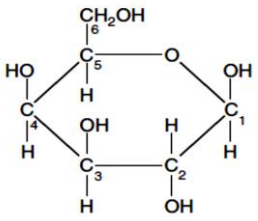


Fig. 1.4

(ii) Show how a glycosidic bond could be formed between carbon 1 of β-galactose and the R group of hydroxylysine. [3]

1. Show interacting parts of galactose and hydroxylysine (dotted box) + structure of galactose and hydroylysine drawn correctly (R: only R group drawn)
2. Condensation reaction + H_2O
3. Final product drawn correctly + correct labelling of glycosidic bond (R: alpha glycosidic bond)

Comments

Some students did not seem to understand the command word “show how”, and only drew the final product.

[Total: 10]

2 In human retinal photoreceptor cells, the *EGFLAM* gene codes for a protein known as Pikachurin.

The production of this protein is depicted in Fig. 2.1 below.

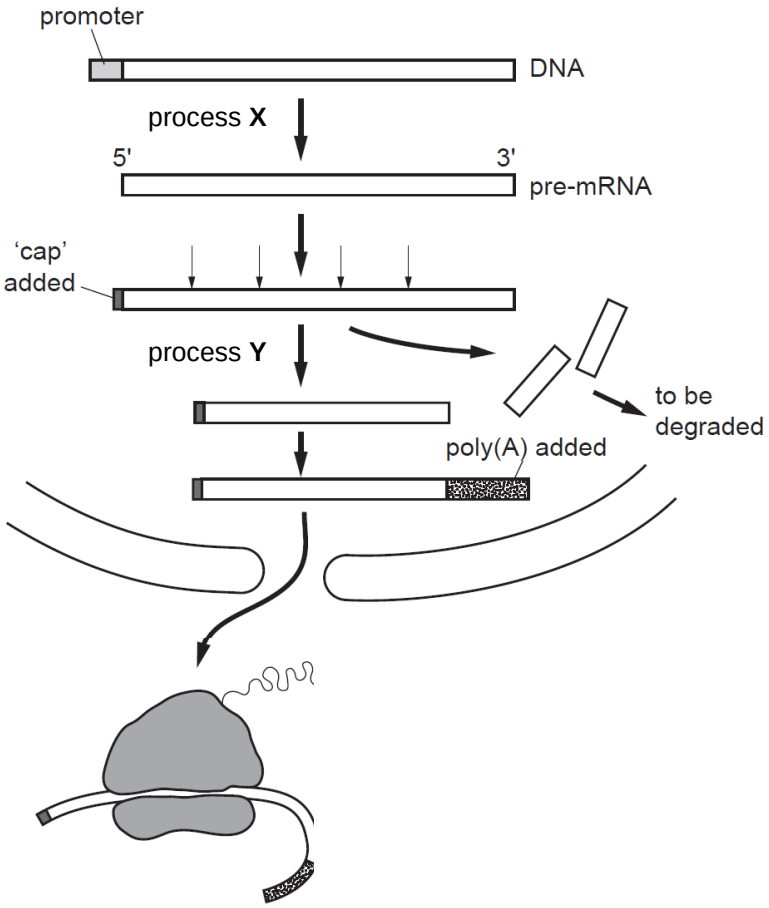


Fig. 2.1

(a) **(i)** Describe process **Y**. [3]

1. Process is **splicing**;
2. **Spliceosome** recognises and binds to **splice sites** at both ends of each intron;
3. **Introns** are then **cut out / excised** that will be degraded and **exons are spliced / joined together** by the spliceosome;

Comments:

- Most students correctly identified and described process **Y** in detail.
- A small number of students did not name process **Y**, or mistakenly identified it as alternative splicing even though it was not depicted in Fig. 2.1.
- Some students named process Y as “mRNA splicing” or “pre-mRNA splicing”; do take note that the proper term is RNA splicing.
- Some also failed to mention the involvement of the spliceosome, or its function in splicing.

(ii) Contrast DNA replication with process **X**. [4]

1. [Enzyme involved in synthesis of product] DNA replication is carried out by **DNA polymerase** while transcription is carried out by **RNA polymerase**;
2. [Monomer of nucleic acid strand formed] **Deoxyribonucleotides** are joined together in DNA replication while **ribonucleotides** are joined together in transcription;
3. [Identity of nucleic acid strand formed] Two (identical) **DNA molecules are produced** during DNA replication whereas a single **RNA molecule is produced** during transcription;
4. [Nature of nucleic acid strand formed] The product of DNA replication is **double-stranded** DNA while the product of transcription is **single-stranded** RNA;
5. [Process of nucleic acid strand formation] Daughter DNA strand **may not be synthesised continuously** (i.e., formation of Okazaki fragments on lagging strand) while RNA strand is **synthesised continuously**;
6. [Number of DNA template strands] **Each DNA strand serves as a template** in DNA replication whereas **only one DNA strand serves as a template** during transcription;
7. [Extent of DNA molecule involved] The **entire DNA molecule** is copied during DNA replication while **only part of the DNA molecule** (gene) is transcribed during transcription;
8. [Phase during cell cycle] DNA replication only occurs during **S phase of interphase** while transcription occurs **all throughout interphase**;
9. [Location of initiation along nucleic acid] DNA replication is initiated at **origin of replication** while transcription is initiated at **transcription start site / promoter region**;

Comments:
Majority of students made valid point-for-point comparisons with a single feature of comparison. The most common points of comparison were 1, 2, 3, and 6.

A small number of students misinterpreted the command word in the question as “Compare”, which requires both similarities and differences. However, “Contrast” simply refers to differences between the two processes.

Point 2
- Some students named the different nitrogenous bases present in DNA vs RNA (i.e., thymine instead of uracil); however, the identity of the nucleotide as a deoxyribonucleotide or ribonucleotide is a more important difference to name first.

Point 3
- Many students failed to mention that transcription does not only produce mRNA and did not include other forms of RNA (tRNA and rRNA) as products of transcription.

Misconceptions:
- Some students described the directionality of both processes (i.e., 5’ to 3’ vs 3’ to 5’) as a difference. However, **both DNA replication and transcription occur in the 5’ to 3’ direction** with respect to the growing DNA or RNA strand; this is necessary because both DNA polymerase and RNA polymerase can only add nucleotides to the 3’ end to elongate the strand. Hence, any comparisons involving directionality will be incorrect for this question.

- Some students also mentioned the requirement for **post-transcriptional modifications** to produce a mature mRNA strand, whereas DNA replication does not require any. However, by definition, these modifications occur **after** transcription is finished and thus, are not relevant.

Fig. 2.2 shows a section of the *EGFLAM* mRNA molecule.

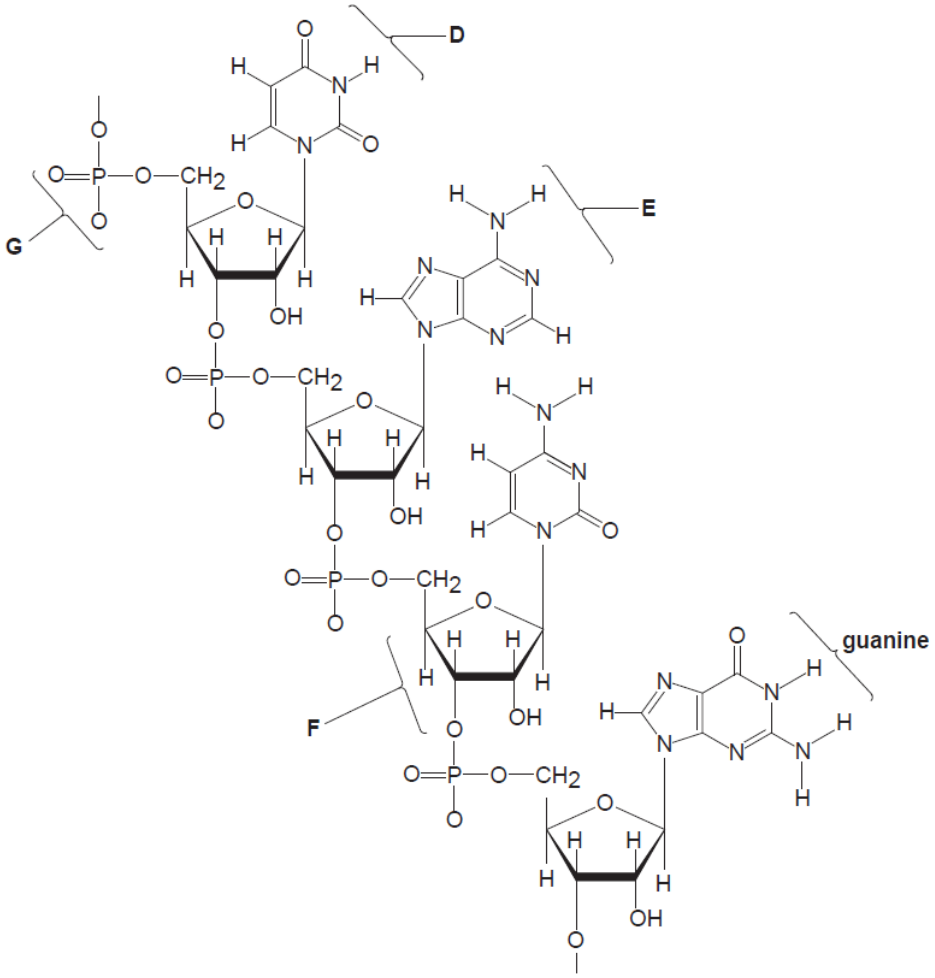


Fig. 2.2

(b) **(i)** It is known that **D** and **E** are complementary bases.

Name the parts of the mRNA molecule labelled **D**, **E**, **F**, and **G**. [2]

D: uracil
E: adenine
F: ribose (I: pentose, R: oxyribose)
G: phosphate (R: head / backbone)

Comments:

- To correctly deduce the identity of the nitrogenous bases, students should be aware that adenine and guanine are purine bases, which have two-ring structures, and since guanine is already labelled, the other two-ring base must hence be adenine.
- Many students did not use the given information that **D** and **E** are complementary bases to correctly deduce that **D** must be uracil.

Misconceptions:

- Many students were unable to identify the nitrogenous bases **D** and **E**; some even mistakenly identified either one as thymine, despite the question saying this is an mRNA molecule and not a DNA strand.
- Many students did not identify **F** as ribose; giving vague answers such as “pentose sugar” instead – this term applies to any 5-carbon carbohydrate.
- Some students incorrectly described the phosphate group as a phosphate **head**, which is a term only used in reference to phospholipids.

(ii) Explain why the ribosomal proteins that interact with the mRNA molecule are made of mostly positively charged amino acids. [2]

1. The mRNA sugar-phosphate backbone has **negatively charged phosphate groups**;
2. Hence, ribosomal proteins that contact the mRNA molecule must be positively charged to be **complementary** (in conformation and) **charge** / form **ionic bonds** with the mRNA to hold it in place within the ribosome; (R: electrostatic bonds)

Comments:

- Most students were able to infer that ionic bonds / electrostatic forces of attraction are formed between negatively charged mRNA and positively charged ribosomal proteins.
- However, many students gave vague answers such as "mRNA molecule is negatively charged" and failed to state exactly which part of the mRNA molecule.

Misconceptions:

- Again, some students incorrectly described the phosphate group as a phosphate **head**, which is a term only used in reference to phospholipids.
- A small number of students mistakenly said that hydrogen bonds are formed between oppositely charged groups. Similarly, some students mistakenly attributed the negative charge of mRNA to hydroxyl groups (OH^-), which is incorrect.

It was discovered that the protein Otx2 plays a large role in regulating the formation of the sensory organs, including the eye and optic nerve. This protein is encoded by the *OTX2* gene.

Fig. 2.3 shows the changes in mRNA levels of the *OTX2* and *EGFLAM* genes.

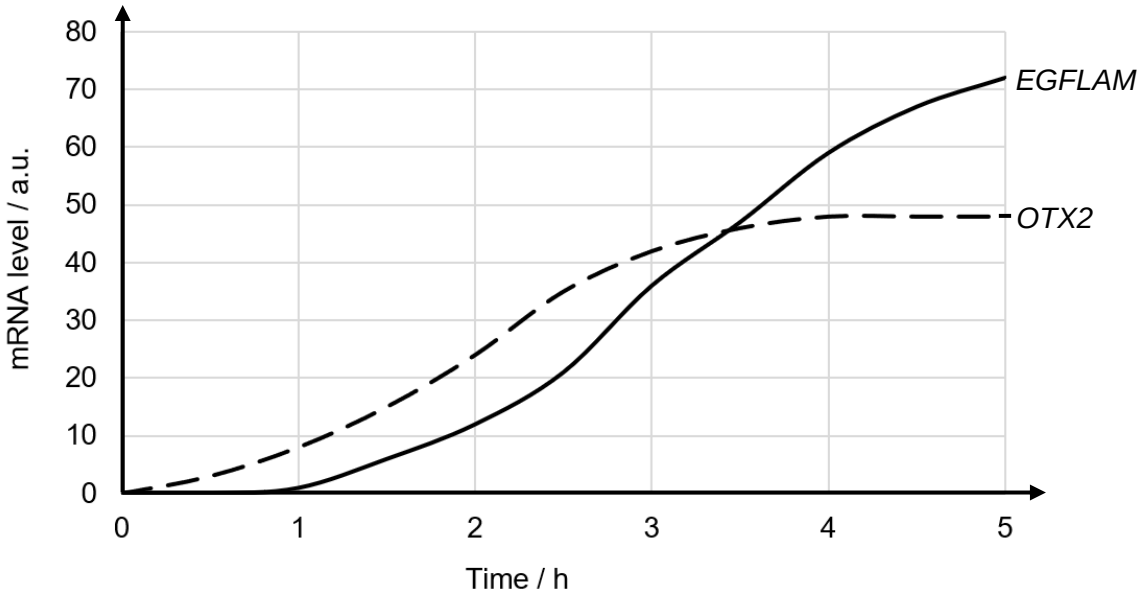


Fig. 2.3

(c) **(i)** Calculate the average rate of *OTX2* mRNA production over 5 hours. [1]

48 a.u. / 5 h = 9.6 a.u. / h (R: no / wrong units)
A: 47 to 49 a.u. (9.4 or 9.8 a.u. / h)

Comments:

- Most students were able to calculate the average rate of mRNA production over 5 hours.
- Some students took the mRNA level at each hour and divided by 5; this, however, would give an incorrect answer as the mRNA level is cumulative over the period of time.

(ii) With reference to Fig. 2.3, describe the changes in *EGFLAM* mRNA level. [2]

1. *EGFLAM* mRNA level **remains / is constant at 0 a.u.** for the **first hour**;
2. After which it **increases steeply/rapidly from 0 to 72 a.u.** over the **next four hours**;

OR

1. *EGFLAM* mRNA level **increases at an increasing rate from 0 a.u. to 36 a.u.** for the **first three hours**;
2. After which it **increases at a decreasing rate from 36 to 72 a.u.** over the **next two hours**;

Comments:

- Most students were able to give accurate descriptions of the graph using precise data.
- Some students did not quote data at all, or quoted imprecise data (e.g., 70 a.u. at 5h).
- A small number also gave inaccurate descriptions, such as the mRNA level increasing "steeply" for the first three hours, then increasing "gradually" for the next two hours; this is inaccurate as the actual change in mRNA level is the same at about 36 a.u.
- A small number of students also quoted data from the *OTX2* mRNA level, even though this was not asked for.
- Some students included explanations for the increasing trend, which is not relevant for this "Describe" question.

(iii) OTX2 protein was found to bind to a DNA sequence far away from the *EGFLAM* gene.

Explain how the Otx2 protein regulates *EGFLAM* gene expression. [3]

1. Otx2 acts as a transcriptional **activator** which **binds** to **enhancer** region;
2. Spacer DNA will bend and bring the activator in close proximity to the promoter;
3. To promote/stabilise the **formation** of the **transcription initiation complex**, which **increases** the **frequency of transcription** / gene expression;

Comments:

- Most students were able to infer from Fig. 2.3 that the Otx2 protein has a **positive regulatory** role for *EGFLAM* gene expression; since *EGFLAM* mRNA production only begins 1 hour after *OTX2* mRNA is produced.
- Many students missed out point 2 on how exactly the activator promotes the formation of the transcription initiation complex. Some also included other details that were not necessary, including recruiting other chromatin modifiers (e.g., histone acetylase and chromatin remodelling complexes) – these are additional ways in which activators may increase the frequency of gene expression.
- Many students also failed to make the link in point 3 to state what effect Otx2 protein ultimately has on the expression of the *EGFLAM* gene.

Misconceptions

- Many students identified *Otx2* protein as the distal control element, which is incorrect. The control elements refer to specific DNA sequences (i.e., enhancer or silencer) that are bound by specific transcription factors (i.e., activator or repressor respectively).
- Some students stated that the *Otx2* protein would bind to the promoter region, but this directly contradicts the information given in the question preamble.
- Moreover, some students confused eukaryotic gene regulation with prokaryotic, and stated that the *Otx2* protein would bind to the allosteric site of the repressor protein, likely drawing from their knowledge of operons (associated mainly with prokaryotes).

Upon translation of *EGFLAM* mRNA, the polypeptide produced must first be processed before it is folded into metabolically active Pikachurin protein.

Fig. 2.4 shows the production of active Pikachurin protein from a Pikachurin polypeptide.

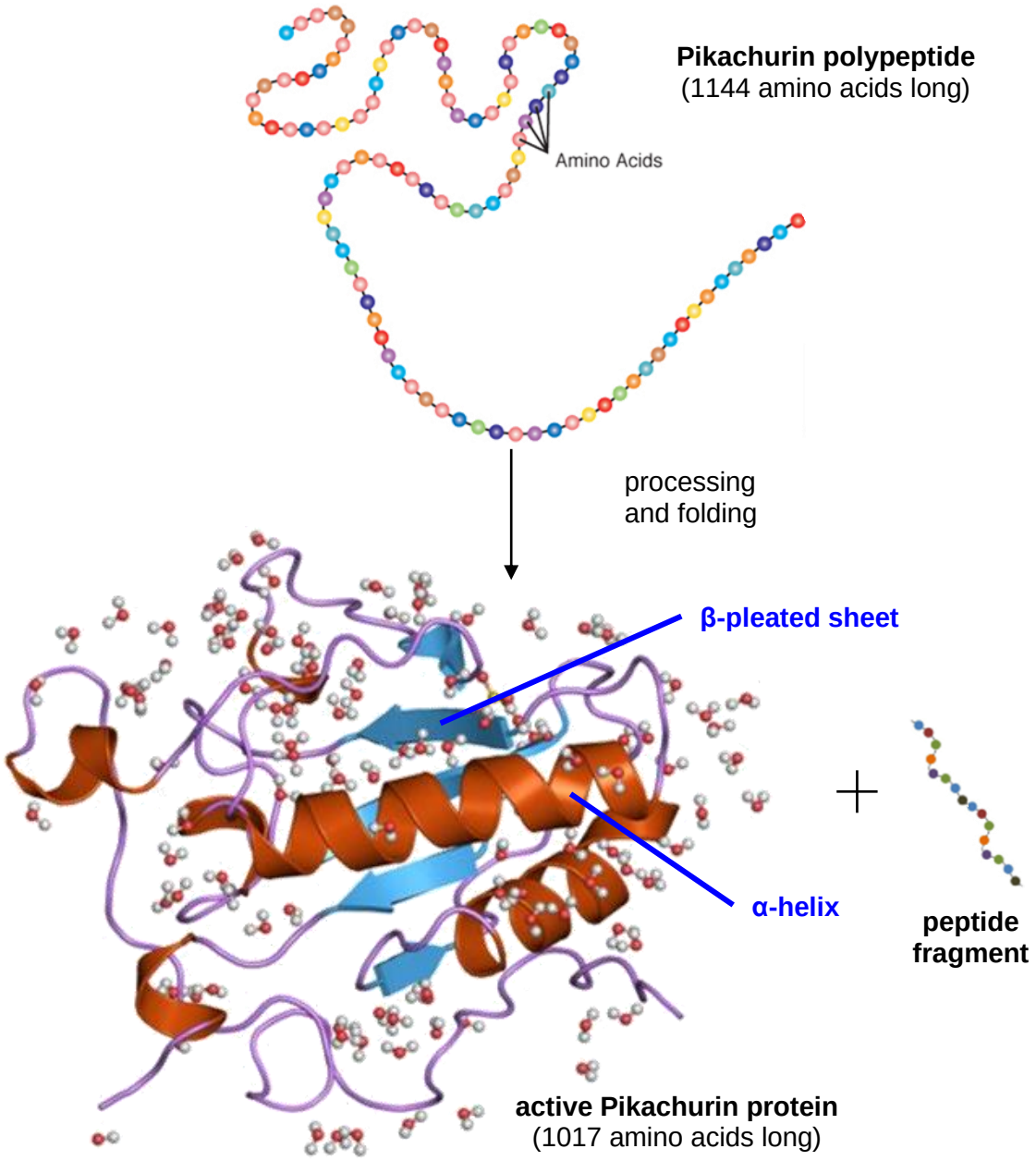


Fig. 2.4

(d) **(i)** Using separate label lines, label on Fig. 2.4 **two** types of secondary structures. [1]

Comments:
This question was void and all students were awarded one mark.

(ii) Describe the processing that the Pikachurin polypeptide undergoes to form the active Pikachurin protein. [2]

1. The polypeptide must undergo **proteolytic cleavage**;
2. Whereby a **peptide fragment** **127 amino acids long** is cleaved/cut out from the Pikachurin polypeptide;

Comments:
This question required students to use Fig. 2.4 to make the necessary inferences.

- First, the diagram shows that the inactive polypeptide must undergo both “processing and folding” to become the active Pikachurin protein. Hence, the “processing” component that this question asks about does not include the folding of the polypeptide into its secondary and tertiary structure.
- Many answers named irrelevant processes, including glycosylation and ubiquitination, which is not alluded to in the diagram or in the question information.
- Of the students that recognised the “processing” had to do with the removal of a peptide fragment, most failed to name this process as proteolytic cleavage.
- Some students also did not make full use of the information given in the diagram to state that the peptide fragment removed was 127 amino acids long.

[Total: 20]

3 A student investigated growth in the roots of broad bean, *Vicia faba*. The student cut sections of the root tip of this plant and viewed them with a light microscope.

Fig. 3.1 is a photomicrograph of one of the sections. The cells labelled A to C illustrate certain stages of a type of nuclear division.

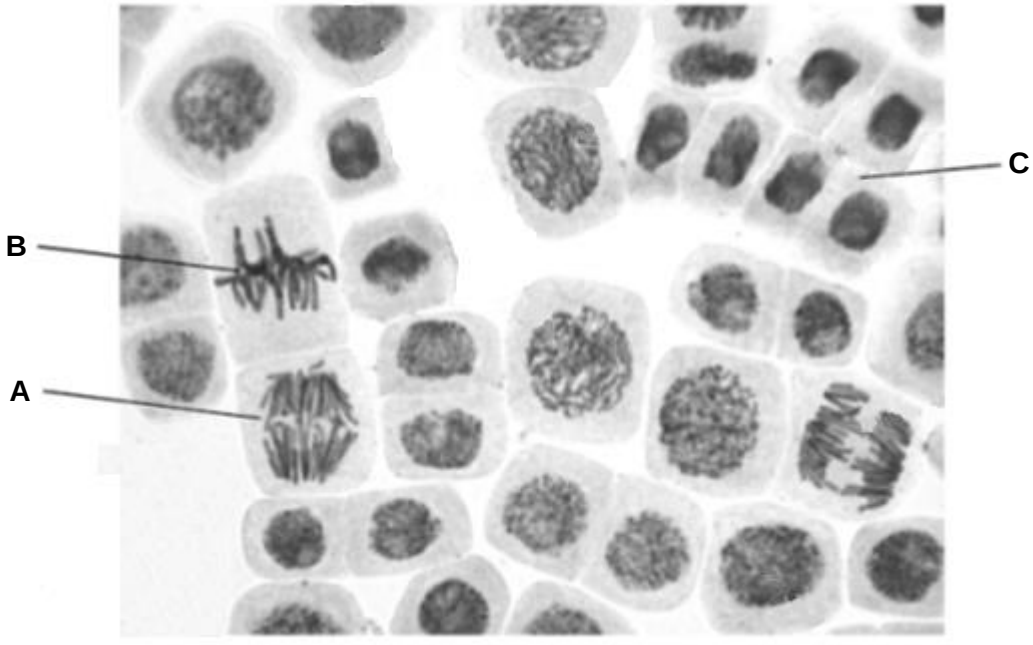


Fig. 3.1

(a) With respect to Fig. 3.1, identify the

(i) type of nuclear division, [1]

mitosis;

Comments:
Most students were able to answer this question correctly. Only a small handful of students identified it incorrectly as meiosis.

(ii) following stages of the nuclear division in cells B and C. [1]

Stage B **metaphase**

Stage C **telophase**

Comments
While most students were able to identify stage B correctly, a significant proportion of students were not able to do the same for stage C.

Stage C was incorrectly identified as anaphase / interphase / cytokinesis / prophase. Students who identified stage C incorrectly as interphase/cytokinesis either did not read the question properly or did not have a clear idea of what the stages in a nuclear division / mitosis are. Mitosis is only composed of prophase, metaphase, anaphase and telophase. It does not include interphase or cytokinesis.

(b) The diploid number of the broad bean plant is 12.

(i) State a difference between chromosome 8 in cell A and cell B. [1]

1. [amount of DNA] Chromosome 8 in cell B has **double the amount of DNA** than that of chromosome 8 in cell A;
2. [number of copies of genes / alleles of a gene] Chromosome 8 in cell B has **double the copies of genes / alleles of a gene** than that of chromosome 8 in cell A;

Comments:
Not a well done question generally. Ideally, students should focus more on structural differences between the chromosome 8 in cell a versus cell B, instead of behavioural differences. This is so as to avoid repetition of answers with subsequent part of the question.

A number of students who failed to gain the mark here showed lack of clarity of the terms "sister chromatid", "haploid", "diploid".

R:
- Cell A has one more chromosome 8 than cell B
- Chromosome 8 in cell A has one sister chromatid. (The use of the word "sister chromatid" is only applicable when two chromatids are joined at the centromere.)
- Chromosome 8 in cell A and cell B have different alleles. (This is not acceptable because cell A and B are found within the same plant organism, and therefore would carry the same type of alleles.
- Chromosome 8 in cell B is diploid, while that in cell A is haploid.

(ii) Explain if cell A has the same number of chromosomes as cell B. [3]

1. The number of chromosomes in cells A and B are **different** / cell A has double the chromosomes of cell B;
2. Cell A has **24 chromosomes** while cell B has **12 chromosomes**;
3. In cell A, centromeres have divided and sister chromatids of 12 chromosomes have separated. **Each of the 24 chromatids is now a chromosome**;

Comments

Point 1
- A small number of students failed to realise that the number of chromosomes in cell A and cell B are different.

Point 2
- A significant proportion of students did not provide data as according to the question context.

Point 3
- Many students rationalised the number of chromosomes by counting the number of centromere. Whilst this is a possible technique to employ to count the number of chromosomes, students should instead use **chromosome behaviour** to rationalise the number of chromosomes obtained.
- Note: it is incorrect to use the word "split", e.g " centromeres split" or "sister chromatids are split".
- Students need to be careful not to describe the shortening of the microtubules as the reason for the division of centromeres. This is incorrect.

The chemical, vincristine, is known to affect the polymerisation of tubulin to form microtubules.

The effect of vincristine is illustrated in Fig. 3.2.

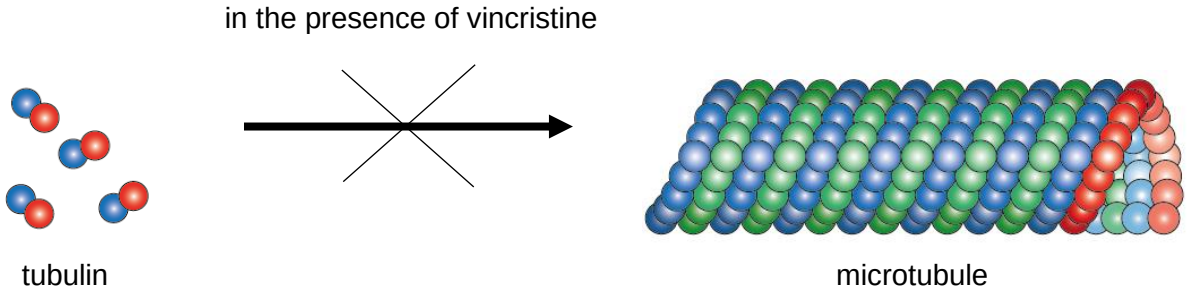


Fig. 3.2

(c) The student decided to investigate the effect of vincristine on dividing root tip cells of the broad bean.

Explain the effect of vincristine on the genetic material found in the daughter cells. [4]

1. Vincristine **prevents/inhibits** the polymerisation of tubulin to form microtubules; (A: prevents formation of microtubules)
2. **No microtubules attach** to the **kinetochore** proteins on the **centromeres of chromosomes** during prophase;
3. **Non-disjunction** occurs and **chromosomes are not separated to opposite poles** during **anaphase**;
4. This results in daughter cells having double the amount of DNA / double the number of chromosomes as compared to the parent cell;

Comments

Some students failed to read the information provided ("root tip cells") and incorrectly mentioned details of meiosis in their answer.

Point 1
- Most students were able to deduce the effect of vincristine on the formation of microtubules correctly.

Point 2
- R: no microtubules to attach to centromere.

Point 3
- R: "chromatids not *pulled apart*". This has a different meaning than "chromatids are not pulled to opposite poles".
- R: "kinetochore microtubules cannot split centromeres". Firstly, it is incorrect to use the word "split". Also, it is incorrect to describe the shortening of the microtubules as the reason for the division of centromeres.

Point 4
- R: polyploidy.
- R: mention of aneuploidy

[Total: 10]

4 The *ara* operon is an inducible operon involved in the breakdown of a pentose sugar, arabinose. Fig. 4.1 shows the organisation of the *ara* operon in a bacterium.

The *ara* operon encodes three structural genes (*araB*, *araA* and *araD*) and is regulated by the regulatory gene *araC*.

The arrows in Fig 4.1 represent the directions of transcription of the respective genes.

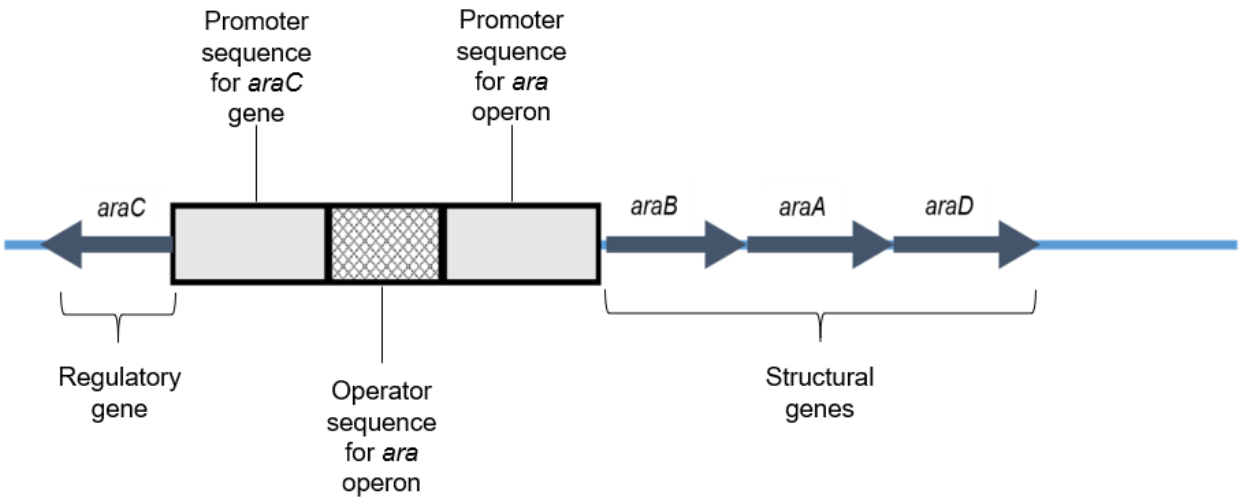


Fig. 4.1

(a) With reference to Fig. 4.1, explain what is meant by the term operon and its significance. [3]

1. Multiple structural genes such as ***ara B, ara A, ara D*** in the ara operon are grouped together/clustered together; [must quote the names of structural genes]
2. under the control of the **same promoter**;
3. This allows for **functionally related proteins / proteins involved in same metabolic pathway** to be synthesised together;

Comments:

Most students were able to show a certain degree of understanding of what an operon constitutes of. However, many lost marks when failing to relate this to the ara operon and making reference to Fig. 4.1 (Point 1).

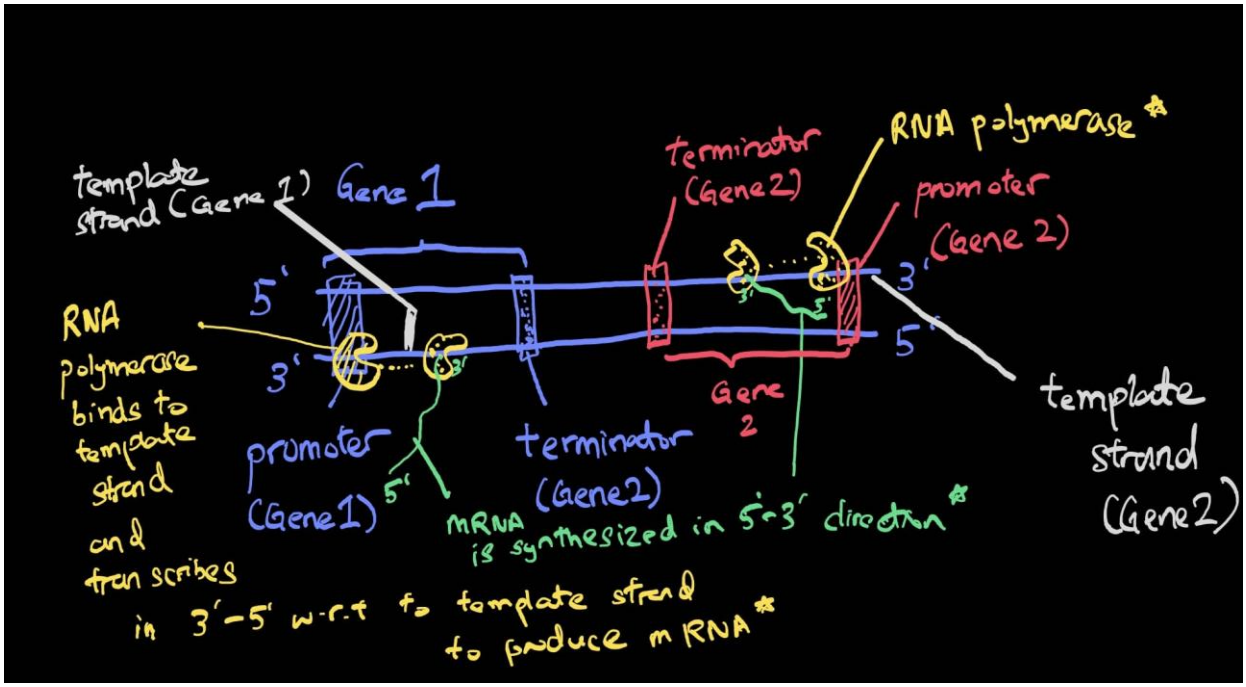
Many students also loosely mentioned 'functionally related genes' instead of stating 'genes which code for functionally related proteins' (Point 3). Credit was only given when this point was clear.

(b) Explain why the transcription of the structural genes (*araB*, *araA* and *araD*) proceeds in a different direction from the regulatory gene (*araC*). [2]

1. **Template strands** of structural genes and regulatory gene are **found on different DNA strands**;
2. Both strands are **antiparallel** and read from **3' to 5' direction by RNA polymerase**;

Comments:

Very poorly done question. To appreciate this question, one needs to be clear on the concept of genes and template strands. A gene is made up of two strands – template strand & non-template strand. However, only the template strand is used for transcription. The direction of the transcription of the template strand is in 3'-5' direction.



Some students loosely mentioned 'left to right' direction or vice-versa. This was not accepted.

(c) State another operon which is inducible in nature. [1]

lac operon

Comments:

Most students gained credit for this question.

(d) X-gal and IPTG are chemical molecules. These molecules are commonly used to study the activity of the enzyme β-galactosidase which is synthesised by the *lac* operon in *Escherichia coli*.

X-gal is a lactose analog that turns blue when metabolised by β-galactosidase, but it does not induce the *lac* operon.

IPTG is an inducer of the *lac* operon but is not metabolised by β-galactosidase.

Based on your knowledge on the *lac* operon and the given information,

(i) place a tick in the box beside the molecule(s) that you would expect to bind to β-galactosidase. [1]

molecule	binds to β-galactosidase (✓)
allolactose	✓
X-gal	✓
IPTG	

(ii) place a tick in the box beside the molecule(s) that you would expect to bind to the Lac repressor. [1]

molecules	binds to Lac repressor (✓)
allolactose	✓
X-gal	
IPTG	✓

Comments:
Students need to know the mechanism of the lac operon as well as understand the properties of X-gal and IPTG as shared in the question stem.

For (i), it is straightforward. Allolactose binds in β-galactosidase in E.coli cells. (this is knowledge you know from the lectures on the lac operon). X-gal is cleaved by β-galactosidase as well. (Question stems states – "X-gal is a lactose analog that turns blue when metabolised by β-galactosidase")

For (ii), Allolactose binds in Lac repressor in E.coli cells. (this is knowledge you know from the lectures on the lac operon). The question stem states that "IPTG is an inducer of the lac operon". This means IPTG binds to the Lac repressor to inactivate it so that the lac operon is induced ("switched on" for transcription)

(iii) Suggest why operons are necessary in bacteria. [2]

1. The genes in an operon can be **expressed or not expressed according to certain changes/conditions** of the environment; [must have]
2. Allowing the bacteria to make **economical use of energy and resources** i.e. relevant genes are expressed only when necessary;
   OR
   Especially since bacteria are **able to use a variety of metabolites** e.g. glucose is metabolised preferentially over lactose, thus not economical to produce lac genes in the presence of glucose;

OR

3. Operons allow for **functionally related proteins to be synthesised as a unit**;
4. Thereby enabling the bacteria to **respond rapidly and appropriately to changes** in the environment;

Comments:
For students who did not gain full credit, their answers were mostly incomplete and did not fully suggest why operons are necessary in bacteria.

[Total: 10]

5 Fig 5.1 shows a lentivirus, which can bind to cells lining the airways of the lungs. The lentivirus is a form of retrovirus. The general structure of this virus is similar to that of HIV.

The lentivirus is commonly used as a vector (vehicle to transport external copies of RNA coding for specific proteins into cells).

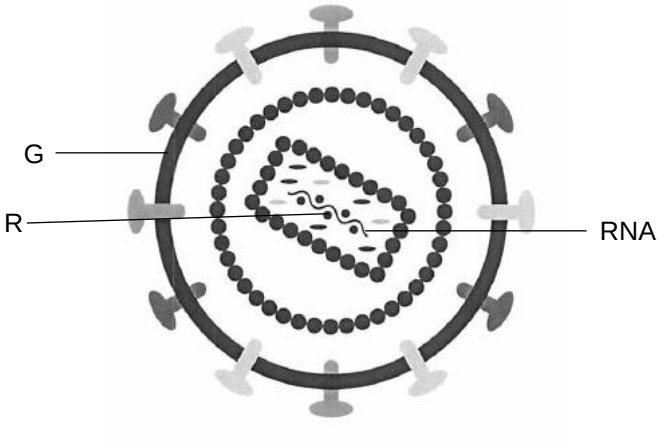


Fig. 5.1

(a) Suggest the identities of the following viral structures. [1]

G: Viral envelope;
R: Reverse Transcriptase/Protease/Integrase
Comments:
All or nothing. R is an enzyme in the lentivirus. As structure is similar to HIV, this enzyme should be one of the key enzymes in HIV.

(b) Explain why external copies of RNA intended to be introduced into cells cannot pass through the membrane of cells directly. [2]

1. RNA is **charged** (due to phosphate backbone) and is **hydrophilic**;
2. It will be repelled by the **hydrophobic core** of phospholipid bilayer and enter the cell directly;
3. AVP (large size + cannot pass through transient pores)

Comments:

Charged molecules are different from polar molecules. Some students mentioned that RNA is both charged and polar. This is incorrect.

For students who wrote about the large size of RNA being a factor, the point must be accompanied with the explanation that it is too large to be passed through the transient pores which appear in the phospholipid bilayer of cell membranes.

(c) RNA introduced into the host cell by the lentiviral vector does not persist in the host cell for long. However, the proteins encoded by the introduced RNA can be detected in host cells even in the absence of such RNA.

Using your knowledge on retroviruses, explain how the long-term expression of these proteins can occur in host cells.
[3]

1. Introduced RNA is **reverse transcribed** into to form **double stranded DNA** by viral **reverse transcriptase**
2. the resulting double stranded DNA is then **integrated / inserted** into host cell DNA using viral **integrase**;
3. This allows for **continual expression** as the DNA is stable and is **not degraded by nucleases**.

OR

4. This allows for long-term expression of proteins coded by the introduced RNA by host cell machinery e.g., **RNA polymerase and host cell ribosomes**.

Comments:

Most answers were missing keywords. A handful of students did not mention the correct enzymes/organelles which are meant for the processes of reverse transcription, integration of viral genome and viral gene expression.

Inaccurate descriptions of 'prophage', 'lysogenic cycle' were also seen. These are terms associated with replication of temperate bacteriophages – not animal viruses such as the lentivirus.

(d) Lentiviruses are enveloped viruses in nature.

Describe how the virus acquires the envelope as part of its reproductive cycle in the host cell. [4]

1. **Viral mRNA is translated into viral proteins** by **ribosomes at the rough endoplasmic reticulum** and embedded into the membrane of the rough endoplasmic reticulum;
2. **Glycosylation** of the viral proteins occurs at the **rough endoplasmic reticulum/Golgi apparatus;**
3. **Transport vesicles** with the embedded glycoproteins **fuse with the cell surface membrane** and are now part of the cell surface membrane;
4. The nucleocapsid will then be assembled near the cell surface, and it will **bud off from the host cell membrane** that is studded with the viral glycoproteins to form the viral envelope.

Comments:
Most answers were missing keywords. A common mistake was incorrectly detailing secretory vesicles instead of transport vesicles (Point 3).
Some students also mistook viral entry to be via exocytosis instead of budding. These are two different processes.

[Total: 10]

Section B

Answer **all** questions in the 12-page Answer Booklet.

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.

6 (a) Distinguish between the structure of cellulose and amylopectin, and relate these to their function. [10]

(b) Other than mutation, outline the other processes that result in genetic variation in nature. [10]

6 (a) Distinguish between the structure of cellulose and amylopectin, and relate these to their function. [10]

Differences between structure of cellulose and amylose (max 3)

	Feature of comparison	Cellulose	Amylopectin
D1	Monomer	• Consists of **β glucose** monomers held together	• Consists of **α glucose** monomers held together
D2	Bond between monomers	• **β -1, 4 glycosidic bond**	• **α-1, 4 glycosidic bond** and **α-1, 6 glycosidic bond at branch points**
D3	Orientation of monomer	• **Alternate β glucose residues are rotated 180^0**	• All α glucose monomers are in the **same orientation** (R: not rotated)
D4	Shape	• A cellulose molecule is a **straight** chain **without any branching**	• An amylopectin molecule is **helical** and **branched** in shape

Comments

- A number of students did not manage to gain full credit for this first portion of their answer due to their answering technique (i.e. lack of a point-for-point comparison).
- Should students present this part of their answer in the form of a table, they need to include a "feature of comparison" column in the table drawn.
- Some students confused cellulose with collagen/protein. Such students incorrectly mentioned the terms "R groups", "triple helix", "α helix", "β-pleated sheet", "staggered arrangement", "polypeptide", "protein" in their answer

Relating structure → property → function of cellulose (max 3)

1. **Straight** chains of cellulose molecules can **lie parallel/adjacent to each other** to form **microfibrils**, which in turn bundle together to form **macrofibrils** and then **fibres**.
2. This gives rise to **high tensile strength** of cellulose; Therefore, cellulose can serve as component of cell wall to provide **structural support** for plant cells;

3. Cellulose is made up of **many β glucose** joined together to form a **large** molecule / **lack of available hydroxyl groups to form hydrogen bonds with water** due to hydroxyl groups involved in inter-chain hydrogen bonding;
4. This makes cellulose **insoluble in water**. Therefore, cellulose can serve as component of cell wall to provide **structural support** for plant cells;

Comments

Point 1

- Some students were incorrect in their terminology, e.g. “microfiber”, “macrofiber”.
- It is important to mention that because cellulose molecules are straight, they are then able to **lie parallel or adjacent to one another** to be bundled together.

Point 3

- Many students stop short in their answer by only making mention of the “hydroxyl groups are involved in extensive intermolecular hydrogen bonding”, and did not proceed to explain explicitly how does this then cause cellulose to be insoluble in water.

Point 4

- A number of students incorrectly mention that cellulose’s insolubility in water will then result in cellulose not being able to affect the water potential of the cells. Cellulose is not even located within the cell, it therefore will not have any impact on the water potential of cells!

Relating structure → property → function of amylopectin (max 3)

5. **Helical** structure of amylopectin makes it a **compact energy storage** molecule;

6. Amylopectin is made up of **many α-glucose** joined together to form a **large** molecule / **lack of available hydroxyl groups to form hydrogen bonds with water** due to most of the hydroxyl groups being projected into the interior of the helices;
7. This makes amylopectin **insoluble in water** and it **will not affect the water potential of cells**, making it a good energy storage molecule;

8. **Many branch points**, allows for **quick hydrolysis** of amylopectin (R: glucose);

Comments

- Some students imprecisely mention the role of amylopectin as an “energy *source*”. The word “source” does not have the same meaning as the word “storage”.
- A few students incorrectly referenced amylopectin as an energy storage molecule in animals.
- R: β-1,4 glycosidic bonds are harder to hydrolyse.(Note: answer should relate structure -> property -> function)

Point 8

- R: easily hydrolysed
- R: amylopectin is hydrolysed to release energy in the form of ATP. (Note: the hydrolysis of amylopectin does not give rise to ATP directly!)

QWC (1m)

- differences in structure of cellulose and amylopectin done via a **point-for-point comparison**
- **structure → property → function** made for **both** cellulose and amylopectin

6 (b) Other than mutation, outline the processes that result in genetic variation in nature. [10]

IN EUKARYOTES

Meiosis – max 4m

1. **Crossing over** occurs between **non-sister chromatids** **of a pair of homologous chromosomes** during **prophase I**;
2. Resulting in **different combinations of alleles** in **gametes**;

3. **Independent assortment** of **homologous chromosomes** during **metaphase I** and the subsequent separation of homologous chromosomes **anaphase I** to opposite poles of the cell;
4. Resulting in **different combinations of paternal and maternal chromosomes** in **gametes** (mark for "gametes' once only);

5. **Random arrangement** of **chromosomes** along the **metaphase plate** during **metaphase II** and **random separation** of **sister chromatids / chromosomes** to opposite poles during **anaphase II**;
6. This results in **different combination of alleles** in **gametes** (mark for "gametes' once only);

Fertilisation

7. During **fertilisation**, the **random fusion of gametes** results in genetic variation in the population;

Comments/misconceptions

- Some incorrectly stated that crossing over occurs between non-identical sister chromatids, but this term refers to the chromatids of a single chromosome **after crossing over** has occurred, and hence are no longer genetically identical. The correct term should be non-sister chromatids, which refers to chromatids of different chromosomes in the same homologous pair.
- Many students stated that **crossing over** occurs during metaphase I after homologous chromosomes line up in pairs along the metaphase plate; this is incorrect as homologous chromosomes pair up in prophase I and crossing over occurs then.
- Similarly, many students stated that **independent assortment** occurs during metaphase II, or even during anaphase I / II. This is incorrect as the term strictly refers to how pairs of homologous chromosomes align themselves at the metaphase plate in a random order, independent of all other pairs of homologous chromosomes – hence, it occurs during metaphase I.
- Some students also mentioned that new alleles will be generated through meiosis, but this is not true; only **new combinations of alleles** are generated – new alleles (i.e., new variants of a gene) are only generated during mutation.

IN PROKARYOTES

Horizontal gene transfer – max 4m

8. **Transformation** can occur whereby a competent bacterium cell takes up **naked, foreign DNA fragments** from the environment;
9. Following which, **homologous recombination** may occur with the recipient cell's chromosome / DNA, and it now expresses the **new allele**;

10. During **conjugation**, **F^+ bacteria** **attaches** to a **F^- bacteria** through its **sex pilus**;
11. A **mating bridge** is formed and subsequently, the **F plasmid is transferred** to the F^- bacteria;

12. **Generalised transduction** can occur, whereby a **lytic phage** may **incorrectly package a bacterial chromosome fragment** in its capsid head;
    OR
    Specialised transduction can occur, whereby a **temperate phage** may incorporate its genome into the host cell chromosome and upon **induction**, **improper excision of the prophage** results in a **bacterial chromosome fragment** being excised together with the phage DNA;

13. This bacterial DNA fragment is then **injected into another bacterial cell** by the bacteriophage and subsequently incorporated into the recipient cell DNA/chromosome via **homologous recombination**;

Comments/misconceptions

- Several students failed to specify which type of transduction they were describing (generalised or specialised).
- A few students confused the different processes, saying that transduction was the uptake of foreign naked DNA fragments.

IN VIRUSES

Antigenic shift

14. **Two different strains** of influenza virus can infect the **same host cell**;
15. **Antigenic shift** may then occur, whereby **genetic reassortments of RNA segments** from both strains may recombine to give rise to new combination of glycoproteins (H and N);

Comments/misconceptions

- Several students described antigenic drift in their essay, but this is defined as an **accumulation of mutations** in a virus, and hence is not an acceptable answer.
- Some students elaborated on viruses being able to cross the species barrier, which is also a consequence of antigenic shift – however, this does not explain how genetic variation arises.

QWC – 1m

- Covers processes from at least two groups: eukaryotes, prokaryotes, and viruses
- Well-structured essay with organised and cohesive flow of points

Overall comments:

- Many students were able to identify that meiosis and fertilisation in eukaryotes, as well as horizontal gene transfer in prokaryotesss, were all key processes that introduce genetic variation.
- However, not all students could describe the process in sufficient detail to obtain the mark.

- Note that the essay question only asks for an “outline” of each process, meaning there is no need for a detailed account of every single process, but simply how they result in genetic variation. For example, some students went into great detail about each and every phase of meiosis, but failed to make the link to answer the question about genetic variation.
- Other students named chromosomal aberrations as a way of generating genetic variation, but this falls under the wide umbrella of mutation and hence, not accepted in this question.

Misconceptions:

- Some students mentioned alternative splicing, but this process occurs during differential gene expression and does not generate genetic variation. The DNA sequence that produced the RNA transcript remains unchanged, and only the pre-mRNA is spliced to produce different mRNAs.