DUNMAN HIGH SCHOOL
Promotional Examination
Year 5

H2 Biology Promo Exam 2022
Mark Scheme

Paper 1: Multiple Choice Question

1	B	6	C	11	C
2	C	7	D	12	A
3	A	8	D	13	D
4	A	9	D	14	B
5	B	10	B	15	A

Q **Explanation**

1 Region P refers to the nucleoid region and region Q the nucleolus.

Option A is incorrect because DNA in the bacterial nucleoid region (region P) is coiled around histone-like proteins, not histone proteins.

Option C is incorrect because ATP synthesis does not occur in the bacterial nucleoid region (region P). The nucleolus (region Q) is also not the site of protein synthesis.

Option D is incorrect because DNA is present in nucleolus (region Q).

2 The larger the organelle, the lower the centrifugal speed required for the organelle to sediment. Diagram shows the size of organelle.

Sediment 1 will be the largest organelle – nucleus
Sediment 2 – mitochondria
Sediment 3 – endoplasmic reticulum
Sediment 4 – ribosome

3 Statement 1 is correct: The reducing group is not bound in the first glucose.

Statement 2 is correct: The first glucose is beta glucose.

Statement 3 and 4 are false: The bond is a 1,2 glycosidic bond and this is not the bond in cellulose formation (1, 4 glycosidic bond).

4 The question is indirectly asking for the change in membrane structure that increases the membrane fluidity. More cholesterol and more C=C double bonds in the hydrocarbon chain (aka higher unsaturation level) will increase membrane fluidity.

5 Option A addition of lysine will increase inhibition of the enzyme that converts aspartate to aspartylphosphate. This will lead to decrease in all downstream process/product, including methionine.

Option B addition of aspartate semialdehyde will lead to increase in all downstream process/product, including methionine.

Option C addition of threonine will increase isoleucine production. But will also lead to inhibition of enzyme that converts aspartate to aspartylphosphate. This will lead to decrease in all downstream process/product, including methionine.

Option D addition of isoleucine inhibits the enzyme that converts threonine to α-oxobutyrate, which does not interfere with methionine synthesis pathway.

6 Change in quantity over time can be simplified as the rate of reaction. Especially change in product or substrate quantity over time.

As quantity of product should increase over time, the graph should be 1, where the rate of reaction increases with increasing temperature, until optimum temperature of the enzyme. Beyond optimum temperature, the rate decreases.

Graph 3 is the reflection of graph 1. It represents the quantity of substrate because substrate decreases over time, hence the change is negative. But the change in rate of reaction with changing temperature is the same as product (graph 1).

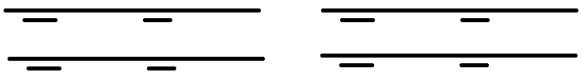
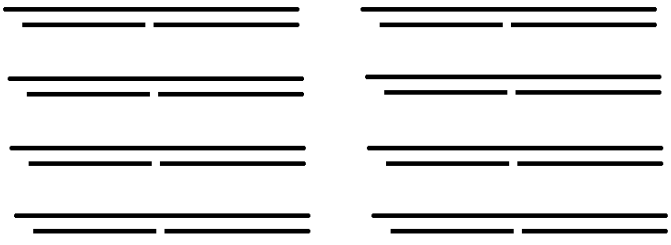
Graph 2 shows how enzyme quantity decreases with increasing temperature.

7 The strand on the left is running 5' to 3' from top to bottom.

The bases with 2 rings are either A or G, and those with one ring are either T or C.

A forms 2 hydrogen bonds (dotted lines) with T. G forms 3 hydrogen bonds with C.

8 The question stated that when all the molecules were mixed, the student successfully obtained many DNA molecules. This suggests that the set up is working.

Set up	**Result**	
1	A few DNA strands, with some short double stranded regions of DNA-RNA hybrid.	
2.	A few DNA molecules.	
3.	Many DNA strands with long stretches of double stranded DNA regions.	

When something is removed in set up 1, DNA are in strands, instead of molecules. This suggest that the double stranded DNA is separated (by helicase). There are short double stranded regions of DNA-RNA hybrids suggest that primase had synthesized RNA primers. But there is no synthesis of daughter DNA strand, implying that DNA polymerase is missing.

In set up 2, a few DNA molecules results. The DNA remains as double stranded DNA molecules, suggesting that helicase is absent to unwind the existing parental DNA molecules.

In set up 3, long stretches of double stranded DNA implies that DNA polymerases has elongated the daughter strands. But them being in stretches along DNA strands implies that ligase is absent to join up the Okazaki fragments.

9 A child gets half of their DNA from their father and half from their mother. So every band in son R and daughter S must correspond to a band of the same length in their father's or mother's electrophoresis result.

Band 4 matches son R to husband V. Band 8 matches daughter S to male X.

10 This is a factual question. Marker's comments: Most students chose option A, thinking that the semi-conservative replication of the F plasmid occurs before the transfer of the single-stranded copy into the recipient cell. However, this is *not* possible as the F plasmid is naturally double-stranded and it is not possible for replication to occur for a double-stranded molecule before the transfer. Thus, the transfer of one copy from donor to recipient has to occur first before the other copy in the donor acts as a template for semi-conservative replication of the F plasmid.

11 The arg operon is similar to that of the trp operon.

Statement 1 is correct as the operon is switched off since arginine acts as a co-repressor which activates the repressor.

Statement 2 is correct as the use of a repressor is an example of negative regulation.

Statement 4 is correct as the arg operon ultimately leads to the biosynthesis of arginine which is an example of an anabolic reaction.

12 A gamete has half the amount of DNA than that of a diploid cell. However, after the S phase, a diploid cell will have four times the amount of DNA due to DNA replication. Thus, among the options given, the diploid cell will only contain twice the amount of DNA before the S phase, which is the entire G1 phase.

13 Statement 1 is correct because the cell cycle would not progress past the G2 checkpoint where proteins check for correctly replicated DNA. This is before prophase where the nucleus is still intact.

Statements 2, 3 and 4 are incorrect because these processes would have been checked by proteins at the M checkpoint where the nuclear envelope has already disintegrated and the nucleolus has disappeared, leaving a nucleus that is no longer intact.

14 Template DNA strand: 3' ---------- GTA ACC GCA TCT CAG ATT ---------- 5'

Mutated DNA strand: 3' ---------- GTA AUU GUA TUT UAG ATT ---------- 5'

Complementary mRNA strand: 5' ---------- CAU <u>UAA</u> CAU AAA AUC <u>UAA</u> ---------- 3'

As 5'-<u>UAA</u>'-3' is a stop codon, translation would be terminated prematurely and a truncated polypeptide would be synthesised.

15 The combination XXY can be formed by these gametic combinations:

XY + X, where the abnormal sperm contains X and Y chromosomes → however, the only way that this can happen is through non-disjunction at meiosis I which is not provided in any of the options given.

XX + Y, where the abnormal egg contains two X chromosomes → this is a possible product of non-disjunction at meiosis I.

Options B and D are factually incorrect and do not happen in reality.

Paper 2
Section A: Structured Questions

Question 1

(a) (i) **glycine**; R!: proline [1]

(ii) **hydrogen** bond; [1]

Marker's comments: Many students did not understand that the procollagen chain is the same as the polypeptide chain that makes up a tropocollagen (termed procollagen trimer in Fig 1). Hence they did not identify that the procollagen chain has a Gly-Pro-X repeat. Some of those who understood this, identified 'proline' as the most common amino acid, this is rejected because glycine is needed every 3rd position to enable to tight coiling of the triple helix. Also, refer to TYS 2015 paper 1 Q4, where a similar understanding that glycine appears more frequently than other amino acids.

Upon understanding that the procollagen trimer is a triple helix, similar to tropocollagen, you should understand that the bond stabilising the procollagen trimer is hydrogen bond, between C=O of proline and N-H of glycine.

(b) **Processes in cell (max 3)** [4]

i1. **Procollagen trimers** are **packaged into large transport carriers** that **bud out** from the **rough endoplasmic reticulum membrane**;

i2.The carrier **fuses** with at the **cis face of the Golgi apparatus**;

i3. Procollagen trimers are **chemically modified** + eg. hydroxylation of proline and lysine / cleaving of the ends;

i4. Modified timers are **packaged into secretory vesicles** which bud out from the trans face of the Golgi, and **fuse with the cell surface membrane**, releasing the trimers out of the cell via exocytosis;

Formation of fibril outside cell

o1. Arrangement of the modified trimers (tropocollagen) **parallel** to each other **in a staggered manner**;

o2. **Covalent cross linking** between hydroxylysines on adjacent trimers; **R!**: hydrogen bonds between hydroxyprolines

Marker's comments: Most students could understand the need for procollagen trimers to undergo chemical modification in the Golgi before being secreted via exocytosis. However, only a handful gave relevant example of the chemical modification, with most people providing a generic type - glycosylation / phosphorylation. Note the importance of being context specific. Some thought that the trimers will be covalently cross-linked in the Golgi as the form of chemical modification, without understanding that in the question, it was stated that the collagen fibrils are synthesized outside the cell. Quite a significant described hydrogen cross-links between the trimers' hydroxyproline residues, which is undeniably present, but when it comes to describing collagen fibril structure, the covalent cross links are the more significant ones. Reason being that this is the most important structural feature that gives collagen its high tensile strength, the main property for collagen function.

Question 2

(a) [4]

	Transcription (Synthesis of *PG* mRNA)	Translation (Synthesis of PG)
1. Location	occurs in nucleus	occurs at ribosomes in cytoplasm
2. Monomers used	polymerisation of ribonucleotides	polymerisation of amino acids
3. Template	reads DNA	reads mRNA
4. Reading of template	reads template from 3' to 5'	reads template from 5' to 3'
5. Enzymes responsible for formation of product / bond	Requires RNA polymerase for elongation of strand / formation of phosphodiester bond	Requires Peptidyl transferase for elongation of polypeptide chain / formation of peptide bond
6. AVP;		

max 4

Marker's comments:
[Misinterpretation] Many students confused the command word 'contrast' with 'compare' and wrote both similarities and differences. However, for a 4-mark 'Contrast' question, students should give 4 differences only.

[Misconception] Many students wrote that the synthesis of PG is related to the process of DNA replication, but PG (polygalacturonase) is a protein which is not involved in DNA replication at all.

[Phrasing] Most students did not phrase their answers in a way that directly answers the question. For instance, students phrased their answers as such:

"The monomers of PG mRNA are ribonucleotides but the monomers of PG are amino acids."

*However, the focus of this statement is on the differences between the **products**, rather than the **process** which was stated in the question itself. A better way to phrase this statement would be:*

"The monomers used to form the product are different for both processes, where the polymerisation of ribonucleotides occurs to produce PG mRNA but the polymerisation of amino acids occurs to produce PG."

*[Basis of comparison] Most students do not have a clear basis of comparison, stating that RNA polymerase is needed in the synthesis of PG mRNA while ribosomes are needed in the synthesis of PG. It is unclear why these molecules are selected when others such as aminoacyl-tRNA are also needed for translation. A clearer basis of comparison could include stating the **enzymes** that carry out a specific **process** in both examples, for instance, the catalysis of the bond between monomers (phosphodiester bonds between ribonucleotides vs. peptide bonds between amino acids).*

[Keyword] Some students wrote that nucleotides are used in the synthesis of PG mRNA instead of ribonucleotides. As the molecule in question is mRNA and simply writing 'nucleotides' could also include deoxyribonucleotides which is incorrect, students are reminded to be as specific in their answers as they can.

[Phrasing] Students are reminded to write answers in full sentences regardless of whether the answers are organised in tables or not.

(b) 1. **Less** single-stranded mRNA bound to probe in ripe transformed fruit at **7%** (A! 5-8%) vs 100% in ripe untransformed fruit; [4]
2. In ripe transformed fruit, both PG mRNA and antisense RNA are synthesised and some of them bind via complementary base pairing, forming several **double-stranded** RNA molecules;
3. Ribosomes cannot bind to double-stranded RNA molecules, hence **less translation / PG synthesised** (from existing single-stranded PG mRNA);
   R! zero translation as there is still 7% PG mRNA detected;
4. Hence, fruit takes **longer to ripen**;

Marker's comments:
*[Data] Most students did not quote data from the graph. For students who did, many did not quote the correct figure, stating that there is 10% of PG mRNA in ripe transformed fruit. Students are reminded to use a ruler to see the correct level rather than 'eyeballing' the graph. Some students also did not write that there is **less** PG mRNA in ripe transformed fruit, only stating the percentages without any adjectives.*

[Scope] Many students correctly wrote that the antisense RNA will form complementary base pairs with the normal mRNA but did not continue to mention that a double-stranded RNA molecule will be formed.

[Phrasing] Many students wrote that the antisense RNA technology can prevent translation from occurring, hence PG cannot be formed. However, this is not true as there is still 7% of PG mRNA detected. Answers need to be carefully phrased such that the content brought across is factually correct - refer to point 3 in the answer scheme.

[Misconception] Some students wrote that the antisense RNA acts as a 'competitive inhibitor' of the normal mRNA, and an incorrectly translated polypeptide would be produced by ribosomes instead. However, this is not the reason why translation will be halted.

[Phrasing] Some students did not phrase their answers correctly, writing that 'PG mRNA is transcribed to give rise to PG'. The correct process should be 'translated', and only DNA (PG gene) can be transcribed to give rise to mRNA.

[Scope] Some students did not mention the overall impact on the ripening process which is delayed.

(c) **1.** A plant produces different PGIPs **specific to the 3D conformation** of **different pathogenic PGs**; [2]

2. Different plant produces different **PGIPs with different binding affinity** to the **same pathogenic PG**;

Marker's comments:
*[Misinterpretation] Some students did not utilise the hints in the bullet points at all, writing answers that do not address the two different phenomena observed. Some students also wrote about differences in cell wall composition but the question already requested reasons **other** than this.*

[Scope] Most wrote about how the same plant produces different PGIPs, but not the other point about how the same PGIP can have different affinity to the same PGs in different plants.

*[Misconception] Some wrote about how different quantities/**concentrations** of the PGIPs are formed but the variable response is linked to **type** of PGIP, not amount.*

[Scope] Many students wrote that different PGIPs can bind to different plants but they did not mention in what way these PGIPs are different. (In terms of 3D conformation? Binding affinity? Answers were too vague to be interpreted.)

[Misconception] Some students wrote that different plants have different levels of immunity - do not be misled by the keyword 'pathogens' in the preamble. Note: plants do not produce antibodies but they still have an immune system which functions differently from that in humans.

Question 3

(a) Permease **transport lactose into** the cell; [2]
With **symport** / transported in the same direction **of protons** + ref to **protons transported down concentration gradient**;

Marker's comments: A significant number of students misunderstood the question as 'explain', rather than 'describe'. Hence they explained the need for permease in lactose transport - lactose being large and polar, hence unable to pass through the hydrophobic core of the membrane.

Students who did not realise that E. coli are prokaryotes with an lac operon had a tendency to be too vague in their description, simply stating that permease transports lactose and protons across / in or out of the membrane, without specifying the direction of transport. Most did not effectively describe the transport of protons down its concentration gradient.

A handful understood that this is a co-transport system of which permease makes use of the proton motive force (when protons diffuse across) to transport lactose. These students described lactose transport as active transport, against concentration gradient. This is conceptually similar to the sucrose-proton co-transport system in plants (eg. in the lecture notes). However, in this case, because unlike plants that takes up sucrose for transport, prokaryotes takes up lactose for hydrolysis and respiration, it is unclear of the lactose concentration in the cell for such a conclusion. A more likely understanding is that the prokaryotes take up lactose with the use of proton motive force, regardless of lactose concentration in the cell (high or low).

(b) 1. Increase in conversion / isomerisation of **lactose to allolactose** by β-galactosidase; [5]

2. Binding of **allolactose to** lacI **repressor** protein, changing its 3D conformation and **inactivating** it;

3. Lesser active repressor protein **binding to operator**;

4. More **RNA pol able to bind promoter + increase rate of transcription** of lac operon;

   Note: Penalise one mark (-1), from 5m full credit, for answering question in perspective of "presence of lactose" instead. eg. binding of RNA pol to the promoter allows transcription to take place.

5. Increase synthesis of permease hence **increase number of permease embedded in the cell surface membrane**;

Marker's comments: Large majority did well for this question, scoring full credits or close to because they missed out some descriptive terms. Many regurgitated from their lecture notes (phrased in terms of presence / absence of lactose), instead of answering the question (in terms of increasing concentration of lactose). Cambridge markers had commented before about students not answering the question in the right perspective. So it's important to rephrase the concepts to answer specifically to the question.

Some other poor expressions include 'RNA polymerase bind promoter and code for lac Y'; 'allolactose binds to active site of repressor proteins'; 'with repressor unbound from the operator, the RNA polymerase has higher affinity for the promoter region'.

There seems to be some confusion with the eukaryotic transcription process, with many stating that general transcription factors binds to the promoter, with RNA polymerase, to form the transcription initiation complex. Note that prokaryotes do not have transcription factors. The prokaryotic RNA polymerase comprise of core enzyme and sigma factors.

(c) Permease is embedded within the membrane with many **transmembrane regions**. The amino acid residues within these regions are **non-polar / hydrophobic**; [2]

In prokaryotes, there is a **lack of internal membranous system** / organelles **to provide optimal condition** for permease to fold and be embedded in membrane of secretory vesicle for exocytosis;

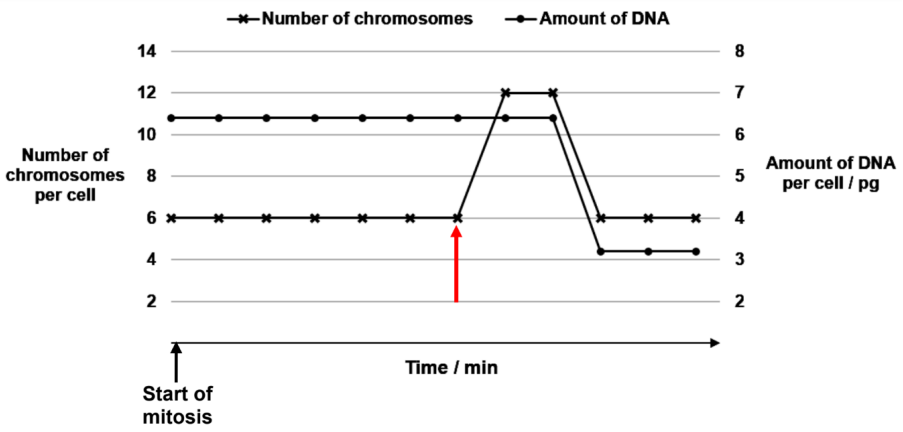
The chaperones provides an environment within the membrane, **protecting permease from the aqueous environment**, allowing it to fold and be embedded at the same time;

Max 2

Marker's comments: This is a high order thinking question that requires synthesis of conceptual understanding from multiple topics. First, there is a need to understand that a membrane protein like permease must have hydrophobic regions in order for it to be embedded in the membrane. Next, there is a need to understand that prokaryotes do not have membrane bound organelles. Lastly, there is a need to understand that amino acids are soluble (regardless of the R groups, because of the -NH_2 and COOH groups), and polypeptides are soluble (because of the polar C=O and N-H groups), but a protein's property is determined by the folding of the polypeptide. With all these understanding, students are then required to synthesize the answer. There were only a handful of students who managed to derive the answer and attain full credits.

Question 4

(a) (i) [1]



(ii) [3]

1. Prior to anaphase, each chromosome comprises **two sister chromatids held at the centromere**;
2. During anaphase, the **centromere divides** and spindle fibres **pull sister chromatids apart** to opposite poles of the cell;
3. Separated chromatids are now regarded as individual chromosomes;
4. Hence, **number of chromosomes** per cell doubles from **6 to 12**;

max 3

Marker's comments:
*[Phrasing] Many students did not write about the centromere **dividing** before sister chromatids are pulled apart. Students should refrain from using the phrase 'centromere splits'.*

[Data] Some students only mentioned that chromosome number is doubled but did not go on to quote the relevant data (doubling from 6 to 12 chromosomes).

[Scope] Some students did not explain the stages of anaphase to justify their answer, but merely wrote that anaphase is in between the stages of DNA replication and telophase which is not meaningful in answering the question.

(iii) [3]

1. **Number of chromosomes** per daughter cell would be further halved to **3**;
2. **Amount of DNA** per daughter cell would be further halved to **1.6 pg**;
3. Meiosis results in the **halving of ploidy** OR meiosis leads to formation of haploid gametes with half the number of **sets** of chromosomes OR appropriate explanation (e.g., separation of homologous chromosomes in anaphase I, followed by separation of sister chromatids in anaphase II)

Marker's comments:
[Data] Though many students remembered to quote the data in the previous question part, they did not do so for this part and provided vague answers such as halving of chromosome number and amount of DNA only. Some students even misquoted the amount of DNA and wrote that the gamete will contain 1.5 pg of DNA, but the graph showed around 3.2 pg of DNA on the y-axis. Some students also misread the axes and divided 4 by 2 instead to get the amount of DNA. A few students did not write the unit for the amount of DNA (pg).

[Scope] Some students did not write that the amount of DNA will be halved and only focused on the halving of the number of chromosomes only. Some students also did not give an appropriate explanation of why the number of chromosomes and amount of DNA are halved in gametes.

(b) 1. **Crossing over** between non-sister chromatids of **homologous chromosomes** in **prophase I;** [3]
2. Results in new combination of **alleles** in the daughter cells;
3. **Independent assortment** of homologous chromosomes in **metaphase I** / random orientation of chromatids in metaphase II;
4. Results in new combination of **paternal and maternal chromosomes**;

max 3

Marker's comments:
[Keyword] Some students omitted the term 'non-sister chromatids' when describing where alleles are exchanged between homologous chromosomes during crossing over. Some students also did not state the keywords 'independent assortment' and used 'random assortment' instead, which is not sufficient. Some students also omitted the term 'homologous chromosomes' and only used 'chromosomes' when describing independent assortment.

*[Misconception] Some students wrote that **new alleles** are formed instead of **new combinations of alleles** as an outcome of crossing over. However, these terms are very different; new alleles can only be formed via **mutations** where there is a change in the genetic sequence. However, during crossing over, there is only a swap in alleles between non-sister chromatids between homologous chromosomes and there is no change in the genetic sequence at all. Hence, the correct outcome of crossing over is the production of 'new combinations of alleles'.*

*[Misconception] Many students wrote that independent assortment of homologous chromosomes occurs in both metaphase I and metaphase II. However, the **random orientation of chromosomes in metaphase II is not the same as independent assortment in metaphase I**. During meiosis II, each of the 23 chromosomes is either paternal or maternal in origin, so there is no 'assortment' of any kind during metaphase II.*

*[Scope] Many students did not elaborate what the genetic variation was as a result of crossing over and independent assortment, especially for the latter. Many students simply stated that genetic variation will be created without writing that it results in a new combination of **paternal and maternal** chromosomes. Students should be clear of the differences in outcomes of crossing over and independent assortment.*

[Misconception] Some students wrote that random fusion of gametes also gives rise to genetic variation; however, this process is not part of meiosis which has been already stated in the question.

[Scope] Some students did not state the phases when crossing over and independent assortment occurred.

Section B: Long Structured and Free-Response Questions

Question 1

(a) DNA methylation takes place in the **nucleus**, while protein chemical modification takes place in the **Golgi apparatus**; [1]

DNA methylation is the addition of a chemical group (methyl group) to **nitrogenous bases**, usually cytosine. But protein chemical modification is the addition of chemical groups (eg. Phosphate / hydroxyl / glycans) to **R groups** of amino acid residues;

AVP: Other than methylation, protein chemical modification can include phosphorylation, glycosylation, hydroxylation, cleaving etc (state at least 2).;

Max 1

R: DNA methylation involves addition of chemical group to DNA, while protein chemical modification involves addition of chemical groups to proteins.;

Marker's comments: This is a general comparison between DNA methylation and protein chemical modification. Vague responses, such as 'one occurs on DNA while the other occurs on protein', are rejected, especially when it can be lifted from the name of the process without value-adding. Examples of modification for each process can be compared (refer to AVP), however, at least two examples of protein chemical modification are required, since the process is much more general and broader as compared to DNA methylation. A small number of students directly compared DNA methylation and histone modification. Such narrow responses were rejected since the question is referring to protein chemical modification in general.

(b) 1. DNA methylation leads to **chromatin condensation** in eukaryotes; [4]

2. Methylation of DNA results in the **recruitment of histone deacetylase** (HDAC) which **deacetylates the lysine residues on histone proteins, making them more positively charged**;

3. This results in the **decrease in gene expression**;

4. As transcription factors and **RNA polymerase cannot bind to promoter**;

Marker's comments: Quite a number of students did not make reference to the recruitment of histone deacetylase and its effect (point 2). A handful described the role of DNA methylation incorrectly, by writing the exact opposite of the expected answer. Some students missed out important ideas / keywords e.g. making reference to RNA polymerase and transcription factors without mentioning the exact binding site on DNA (promoter).

(c) 1. **Lack of sufficient condensation** of centromeric region; [3]

2. Spindle fibres **cannot attach properly** / **kinetochore cannot bind** to centromeric region for homologous chromosomes / sister chromatids to separate properly during meiosis;

3. **Egg cell / ovum** has **2 copies of chromosome <u>21</u>** (n+1), and upon fertilisation, the embryo hence infant has an extra copy of chromosome 21 (2n+1);

Marker's comments: Responses were often incomplete - Most answers did not make reference to the lack of condensation of centromere (point 1), which is the direct consequence of the lack of methyl groups on centromere. Some answers did not make reference to the presence of extra chromosome 21 in the ovum, before linking back to the presence of extra chromosome 21 in infants as well. A handful did not make reference to the effect on the ovum (point 3) mentioning the presence of extra chromosome 21 in infants. Some students did not realise that centromere is a non-coding DNA and went on to explain that 'more genes in centromere are expressed', which is incorrect. In the question context, it was mentioned that the single base pair substitution in DNMT3B is found in some mothers. However, many students did not make reference to the presence of extra chromosome 21 in the ovum, but only mentioned gametes in general. Some students used 'diploid' to describe the gamete, without realising that 'diploid' refers to having 2 sets of chromosomes, instead of just one extra chromsome (aneuploidy).

(d) **(i)** **Prevents the degradation of the mRNA** by ribonucleases; [2]

Enables the binding of cap binding proteins, which are required for the **export of mRNA** to the cytoplasm for translation;

Helps to **initiate translation / attach to ribosome** for protein synthesis to take place;

Max 2

Marker's comments: Most students did well for this question. A handful did not realise that the question was asking for more than 1 functions of the 5' CAP.

(ii) Any answer with reference to the function of 5' end of mRNA; [1]

Eg. Further stabilises the mRNA by preventing degradation of the 5' mRNA end by ribonucleases
OR Regulates translation by preventing / facilitating binding of the small ribosomal subunit to the 5' end of the mRNA

Marker's comments: Many students who attempted this question managed to correctly infer and suggest the role of m6Am with reference to the function of the 5' end of mRNA, which is similar to the 5' CAP. However, quite a number of students left this question blank. Some students suggested that the role is to form bonds with 7-methylguanosine cap, but without m6Am, bonds can still be present between the 5' cap and the next adjacent nucleotide.

(e) 1. In the absence of a restriction enzyme, the **phage genome**, that is inserted into the cytoplasm of the prokaryotic cell, is **not hydrolysed** / digested; [4]

2. As a result, the phage genome can be **replicated and transcribed**;

3. **New phage particles can be produced** as newly synthesized phage structural proteins assemble around the newly replicated phage genome;

4. Eventually, **phage-coded lysozyme lyses** the peptidoglycan cell wall of the prokaryotic cell for the release of the new phage particles;

Marker's comments: This question is generally well done for students who revised the content for bacteriophage. However, some students did not phrase their responses accurately to mention that the phage genome remained intact / was not digested, hence marks were not awarded for point 1. A common example of an inaccurate response include, 'phage genome can be injected in the absence of restriction enzyme'. Note that the phage genome can be injected into the bacterial host cell as long as there is recognition and viral attachment, and this happens regardless of the presence of the restriction enzyme. What matters here is whether digestion of the phage genome occurs. Quite a number of students incorrectly mentioned that the phage genome will be integrated into the host bacterial genome at the methylated recognition site. Note that T4 is a lytic phage and integration of the phage genome to form a prophage does not occur here. The purpose of methylating the recognition site on the bacterial chromosome is so that the restriction enzyme is not complementary to the methylated recognition site and will not recognise and digest the bacterial genome. Since the phage genome is normally not methylated, the bacterial restriction enzyme, if present, will only digest the phage genome.

Question 2
Describe how the genome of influenza and HIV are replicated within their host cells and explain why the end replication problem does not exist in both cases. [15]

Influenza genome replication

1. Influenza has **8 segments of negative sense (-) single stranded (ss) RNA**;
2. Transported **into the nucleus**;
3. Viral **RNA dependent RNA polymerase**;
4. **synthesises** complementary **positive sense (+) ssRNA**
5. which serves as the **template for translation** and also to synthesize (-) ssRNA **genome**;

HIV genome replication

6. HIV has **2 identical (+) ssRNA**;
7. Viral **reverse transcriptase** synthesizes **dsDNA from ssRNA**;
8. dsDNA transported **into the nucleus**;
9. dsDNA **integrated** into the host chromosomal DNA with the aid of viral **integrase**;
10. Viral DNA **remains dormant as a provirus** within the host cell;
11. Upon **activation**, the **host RNA polymerase transcribes the viral DNA** into (+) ssRNA
12. which serves as the genome and as the **template for translation** of viral protein;

Why end replication problem does not exist

13. End replication problem arises because **gaps at the ends of the linear DNA** after **removal of RNA primers**,;
14. were **unable to be filled up by DNA polymerase I**;
15. Due to a **lack of upstream 3'OH group**;

16. HIV and influenza genome are **not replicated by DNA polymerase** / are replicated by **RNA polymerase which do not require upstream 3'OH group** for addition of nucleotides / AW;
17. HIV and influenza **do not have linear DNA** as their genome / AW;

Max 14

Note: no ECF in the event that influenza and HIV genome replication processes got confused.

QWC: 1m per segment;

Marker's comments:
Let's analyze this question.
*This Q asks to describe genome replication of influenza virus and HIV. So you need to zoom in from the whole life cycle (consisting of adsorption, entry, uncoating & **biosynthesis, maturation**, release) to only biosynthesis and maturation.*
In addition, Q also asks why there is no end replication problem in influenza virus and HIV. You should explain what the end replication problem is and then explain why influenza virus and HIV don't have it. Next, this Q is 15 marks. There are 3 sections so about 5 marks each for each section.

Some students actually analyze the question correctly. But these students are still spamming the whole life cycle. You all need to move away from the O Level way of spamming content; you are wasting precious time; and it is not exactly answering the question so you may not score very well depending on the question type. Only 1 out of the whole cohort actually write only what is needed and still score very well. All of you can do it!!! There are quite a number of students who try to "forcefully" fit the end replication problem section with this (no-end-replication-problem in prokaryotes) question from the tutorial. BUT it is a different question in the tutorial!

*There is a shocking number of students who got the **content** of the four viruses all mixed up. You need to be super familiar and accurate in them since they are learning outcomes of the syllabus. Some even thought that animal viruses are phages, viruses are bacteria, half way through the essay you suddenly write about phages instead, all sorts of mistakes. One common misconception is that HIV provirus will behave like Lambda prophage. It is wrong to say HIV provirus replicate with host or excise and circularize. When activated, HIV DNA will be transcribed into (+)RNA when serves as the genome and also the mRNA for translation to form proteins.*

*Some are also very careless and reckless with their **verbs**, e.g enzyme create product vs enzyme synthesis product, DNA polymerase synthesizes RNA strand vs RNA polymerase synthesizes RNA, question is about genome so that is a random and wrong use of strand, genome, segment or just RNA/DNA. Please do not try to use your own words and rephrase to the point that the sentence has a different meaning.*