DUNMAN HIGH SCHOOL
Promotional Examination
Year 5

H2 Biology Promo Exam 2023
Mark Scheme

Paper 1: Multiple Choice Question

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

Q	**Explanation**
1	Region P refers to the nucleoid region and region Q the nucleolus. Statement 1: True Statement 2: RNA synthesise in P and rRNA in Q. Statement 3: ATP synthesis occurs in mitochondria and chloroplasts. Statement 4: Circular DNA found in bacteria, mitochondria, and chloroplasts.
2	The larger the organelle, the lower the centrifugal speed required for the organelle to sediment. Diagram shows the size of the organelles. Liquid 1 contain all organelles except largest organelle – nucleus Liquid 2 –nucleus and mitochondria removed Liquid 3 –nucleus, mitochondria, and endoplasmic reticulum removed
3	Statement 1 is false: Triglycerides have hydrophobic regions too. Statement 2 is false: The fatty acids in a triglycerides may not be always saturated. Statement 3 true. Statement 4 is false: Phospholipids is polar whereas triglycerides is non-polar.
4	Statement 1: glucose monomers arranged in the same orientation will give a helical structure thus structure is compact and thus suitable as energy store. Statement 2: Fact. But does not account for starch being suitable as an energy storage molecule. Statement 3: amylopectin is more branched than amylose. So more compact and thus a suitable as energy store. Statement 4: will remain insoluble at room temperature so suitable as energy store. Statement 5: Fact. But does not account for starch being suitable as an energy storage molecule.

5 Graph is an endothermic reaction activation energy graph.

Statement 1: X shows potential energy of reactants.
Statement 2: Y shows activation energy.
Statement 3: you need to see another graph showing lowering of activation energy to be sure that enzyme is added to the reaction.
Statement 4: This is factual statement but cannot be concluded from the graph since there is no information about proximity effect.
Statement 5: can see from graph.
.

6 X has ribose sugar and Y has deoxyribose sugar.

Statement 1: True, X forms 2 hydrogen bonds with T.
Statement 2: X has ribose sugar, not deoxyribose sugar.
Statement 3: True, Y forms 2 hydrogen bonds with U.
Statement 4: No uracil used in replication.

7 Types and amount of DNA in:

Picture 1: all double stranded $^{15}N^{15}N$
Picture 2: all double stranded $^{15}N^{14}N$,
Picture 3: 50% double stranded $^{15}N^{14}N$ and 50% double stranded $^{14}N^{14}N$. So, it is 25% of DNA is ^{15}N and 75% of DNA is ^{14}N.

8 Statement 1: Fact but not answering question.
Statement 2: True, need to have the genome sequence to synthesize primers.
Statement 3: Factors e.g. length of genome, type of DNA polymerase used, may determined the temperature used for the three stages.
Statement 4: Only sterile technique can ensure that there is no contamination.

9 All bands in the son should be either accounted for by the mother or the father. The bands chosen should undeniably come from the husband aka band 1 and 4.

Band 1 inherited from husband.
Band 2 can be inherited from wife or male.
Band 3 cannot be determined if is inherited from husband or male.
Band 4 inherited from husband.
Band 5 inherited from either husband or wife.
Band 6 can be inherited from husband or wife or male.
Band 7 can be inherited from wife or male.
Band 8 inherited from wife.

10 DNA fragment 3’ **A**CCGTC**AA**T 5’
mRNA codon 5’ **C**GGCAG**CC**A 3’
amino acid N-Terminus arg glut pro C-Terminus

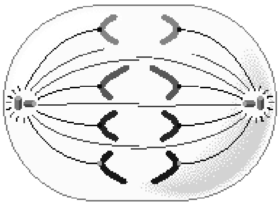
11 X: Lysis process in the cycle indicates that it is a lytic cycle.
Y: Excision of prophage indicates that it is a lysogenic cycle.
A: The bigger one is bacterial DNA.
B: Phage genome in bacterial chromosome is called prophage.

12 Since CFU is increasing, this shows that lactose is being used so the entire Lac operon is being transcribed.

13 Statement 1: Unwinding of DNA likely results in upregulation of transcription.
Statement 2: May be true but not shown in diagram. Also, it is usually acetylation or deacetylation of histone protein.
Statement 3: True.
Statement 4: Binding of TAP and TBP to their binding sites is dependent on complementary shape between TAP and TBP and their DNA binding sites.

14 16 chromosomes in diagram.
Sister chromatids are separated into 2 daughter cells.

15 Centrioles exist as a pair. It is more accurate to call the structure a pair of centrioles. The diagram shows 2 pairs of centrioles. The duplicated centrioles are separated to the opposite poles.



During anaphase, centriole to centromere microtubules become shorter so that the sister chromatids are pulled apart.

Centriole to centriole microtubules will become longer instead of shorter

Paper 2
Section A: Structured Questions

Question 1

(a) [2]

1. a stack of **smooth surfaced flattened membranous sacs** / no ribosomes;
2. not connected to / **continuous with (outer membrane of) nuclear envelope**;
3. **swellings at end of sacs** (for vesicle formation) / vesicles at ends of sacs;

Accept reverse argument
Max 2

(b) [2]

$$\text{Magnification} = \frac{XY}{\text{Actual diameter}}$$

$$\text{Actual diameter} = \frac{XY}{\text{Magnification}} = \frac{1.35\text{ cm}}{47000} = 0.0000287\text{ cm} = 287\text{ nm} \;;$$

Correct calculation;
A 276/7 nm (for 13)
A 287 nm (for 13.5 mm)
A 297/8 nm (for 14 mm)

(c) **(i)** accept points from a diagram [3]

1 phospholipid **bilayer**;
2 membrane protein;

plus any two from:

3 **hydrophobic core** / fatty acid tails orientated inwards;
4 phospholipids **move laterally**;
5 integral and peripheral proteins / AW **proteins scattered** (in phospholipid bilayer) proteins / phospholipids, can move around (in phospholipid bilayer)
6 correct ref. to, **hydrophobic / hydrophilic, regions** / AW, on, phospholipid / protein;

(ii) any two from: [2]

ref. reduced gaps between membrane molecules;
higher proportion of phospholipids with saturated fatty acids (means closer packing);
fewer unsaturated fatty acids so, fewer 'kinks' in tails / closer packing;
ref. lower number of channel / carrier / transport proteins;
smaller diameter of channels in non-specific channel proteins;
fewer types of (specific), transport/ carrier, proteins;
AVP;

Question 2

(a) (i) **Correct polypeptide product + water molecule formed;** [3]
(R: R used instead of H for glycine)

Peptide bond: correct identification + labelling;

Condensation process;
(Reject translation since ribosomes and mRNA are not shown).

(ii) **Peptidyl transferase**; [1]
(R: ribosome)

(b) any three from: [3]

accept answers in the context of lactase:

1 ref. to controlled variables; e.g. constant pH / temperature
2 take samples at timed intervals; Accept regular intervals
3 determine, substrate / lactose, concentration
or determine, product / glucose / galactose concentration;
4 plot graph of, substrate concentration / product concentration, against time;
5 ref. to rate of disappearance of substrate or ref. to rate of appearance of product;

(c) One of the **amino acid/G is changed to a much larger amino acid residue** which **disrupts the close/compact packing of triple helix / three polypeptides** ; (R: no collagen molecule/tropocollagen formed). [2]

Less/no covalent cross-links between adjacent collagen molecules, reducing formation of collagen fibrils, and disrupting structure of collagen fibre formed from staggered arrangement of collagen fibrils;

(d) As pH increases from **pH 5** to pH 7 to **pH 10**, the **swelling ratio** of collagen **increases** from around **150%** to 400% to **850%** by end of 8 hours; [2]

Excess OH$^-$ ions at high pH neutralise the **positively charged R group** of **amino acids**, breaking the **ionic bonds and hydrogen bonds**, creating **larger / more gaps** between collagen molecules, resulting in higher swelling ratio;

Question 3

(a) Mitosis [1]

(b)
1 **Longer poly-A tail** of the mRNA template; [2]
2 which allows for **longer** availability / **half-life**/ higher stability of the mRNA template **for translation**, resulting in **more proteins**;

OR

3 **More translation initiation factors**, hence;
4 **promoting assembly / longer** assembly of the translation initiation complex / ribosomes;

(c) (i)
1 There is **no clear trend** / correlation **between** average body size and average genome size; [2]

2 [**Data**] for example, Hominidae has a **relative large body size of almost 200 cm**, but the **genome size is only about 10 pg**, while the Poaceae family has a **much smaller body size between 10 cm and 100cm**, and a **similar genome size of 10pg**;

Accept other comparative data

(ii) Answer should have an understanding that salamanders are **eukaryotes**, and Enterobacteriaceae are **prokaryotes** (so as to point out the points below.) [2]

any two from:
1 Hence, there are **more genes**/ genetic material coding for more proteins present in the salamanders' genome than in the bacterial genome;
2 Eukaryotic **genes** are larger / **longer** than the prokaryotic genes;
3 Eukaryotic chromosomes **contain a lot of repetitive DNA** / telomeres / centromeres/ non-coding DNA /regulatory sequences e.g. enhancers, silencers / introns / promoters / other non-coding sections between genes which are **absent in prokaryotic** chromosomes;

Question 4

(a) Natural Method [2]

1 Naturally **competent bacteria** possess cell-surface proteins that **can bind to and transport** DNA construct **into** the cell;

Artificial method:

2 Bacteria cell **made competent** by immersion in culture medium containing **calcium chloride**/ ($CaCl_2$);

3 Followed by treated at 42°C / **heat shock** with the DNA construct;

4 AVP (**Electroporation**)

(b) (i) There should have an understanding that in the initial medium of lactose, the entire DNA construct is transcribed into 6 types of mRNA and then translated into proteins. After transferring to another medium with lactose and tryptophan, (since tryptophan is in excess, the operon will be repressed. (so as to point out the points below.) [4]

1 From <u>0 minutes to 60 minutes</u>, mRNA level decreased from <u>2000 arbitrary units to 20 arbitrary units</u> for all genes;

2 **Tryptophan** (corepressor) **binds to trp repressor** and **change repressor to its active form** / complementary conformation to operator;

3 Active **trp repressor binds to operator**, which **prevents binding of RNA polymerase to promoter**;

4 hence **preventing transcription** of all structural genes into mRNA; (thus mRNA level drop)

(ii) 1 *Trp* and *Lac* structural genes are **under the control of the same** tryptophan **promoter**; [2]

Any one from:

2 When RNA polymerase binds to promoter, structural genes are **transcribed together**

3 Producing a **polycistronic** mRNA;

Section B: Long Structured and Free-Response Questions

Question 1

(a) (i) [3]

1 **RNA polymerase** binds to the **promoter** to initiate **transcription**;

2 It **unwind+unzips** double stranded DNA, and uses **one DNA strand** as a **template** to synthesise an mRNA strand;

3 Via **complementary base pairing** between adenine & uracil, cytosine & guanine, thymine & adenine (must have all three);

4 It catalyses the formation of **phosphodiester bonds** between ribonucleotides to form the mRNA strand;

5 mRNA strand is synthesised in the **5' to 3'** direction (A: template DNA strand is read in the 3' to 5' direction);

max 3

(ii) [2]

1 After transcription of this DNA sequence, there are **two start codons AUG** in the mRNA strand;

2 **Ribosome** begins translation <u>four nucleotides apart</u> / in <u>different reading frames</u> / reads a <u>different sequence of mRNA codons</u> (OWTTE), hence producing two different amino acid sequences can be produced from the same mRNA strand;

(b) (i) [1]

(C-terminus) **Glu– Pro– Ser– Leu– His – Val** (N-terminus)

(ii) [3]

1 (from Fig 1.2) **G is replaced with T**

2 (from Table 1) introduces a **premature stop codon UAA** (instead of UCA - Serine);

3 Translation is prematurely terminated, resulting in a **truncated polypeptide**, which then folds into **a protein of different 3D conformation** that is non-functional;

4 ref. **nonsense mutation** (no excuse for not writing after we finish mutation tutorial)

max 3

(c) (i) [3]

J metaphase; K prophase; L telophase (Accept anaphase);

(ii) [1]

This cell is large size / same size as cells in mitosis / same size as the cells labelled in stages of mitosis;

accept reverse argument, i.e. Cells are regular size/smaller in early interphase

(iii) [2]

1 chromosomes, orientated / arranged / AW, at, spindle equator / metaphase plate;

plus any one from:

2 chromosomes attached to, spindle / spindle fibres at centromere / kinetochore;
3 (sister) chromatids still attached at centromere;
4 spindle fully formed;
5 nucleolus has disappeared;
6 nuclear envelope, has disassembled / broken down / AW;

Question 2

The body's immune response to the influenza virus can lead to damage of the collagen matrix in the affected tissues, leading to possible tissue remodeling and other related physiological effects.

Compare the structure of collagen fibril and influenza genome and describe how new strains of influenza virus might arise.

Differences (Max 8)

	Feature (not marked)	Collagen fibril	Influenza genome	
1	monomer	Amino acid	Ribonucleic acid	;
2	linked by	Peptide bond	Phosphodiester bond	;
3	Repetitive monomer	Each collagen chain consists of a repeating sequence of [**Gly-X-Y**], where X and Y are usually proline and hydroxyproline, respectively	The RNA sequence in all 8 segments are unique and not repetitive	;
4	Length of chain	Each collagen chain is about 1000 amino acids long	8 RNA segments of varying length	;
5	Structure of chains	3 collagen chains wound together to form tropocollagen	All 8 RNA strands are single stranded	;
6	Bundles	The collagen chains are bundled into microfibrils then fibrils	RNA segments do not form bundles	;
7	Bonds within bundles	Covalent crosslinks and hydrogen bonds can be found in between collagen chains, microfibrils and fibrils	There is no bond formation between each RNA segment	
8	Chain / Fibril numbers	Number of collagen chains / fibrils are not fixed and will increase as muscles developed	Segments number do not change	;
9	Bound proteins	No proteins attached to collagen	Enzyme RNA-dependent RNA polymerase attached on RNA segment	;

At least one similarity:

10 Monomers are linked by condensation reaction with loss of one water molecules;

11 Overall shapes are linear;

how new strains of Influenza virus arise(Max 5)

12 Antigenic drift;

13 Random gene mutation result in change in base sequence, change in amino acid sequence and change in viral protein structure;

14 Which may make the virus more / less virulent / new strains;

15 Antigentic shift;

16 In the same host cell/ Co-infection of one host cell by different strains;

17 Involving reassortment of RNA segments from different origins (e.g. human strain and avian strain);

18 Which may result in result in a new strain of virus that is capable of infecting multiple host types, e.g. birds and humans in avian flu; [pt 14/18 only mark once]

Max 14

QWC 1M: 2pts differences + 1pt similarity + 2pts new strains