EUNOIA JUNIOR COLLEGE
JC2 Preliminary Examinations 2023
General Certificate of Education Advanced Level
Higher 2

CANDIDATE NAME									
CIVICS GROUP	**2**	**2**	**-**			REGISTRATION NUMBER			

H2 Biology 9744/02

Paper 2 Structured Questions **14 September 2023**

2 hours

READ THESE INSTRUCTIONS FIRST

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

Candidates are to answer:
All questions on the Question Paper.

Write your answers in dark blue or black pen.

You may use an HB pencil for any diagrams or graphs.
Do not use paper clips, highlighters, glue, or correction fluid/tape.

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

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

For Examiner's Use	
1	
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10	
Total	

This document consists of **22** printed pages and **2** blank pages.

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Answer **all** questions.

1 Fig. 1.1 shows an electron micrograph of a eukaryotic cell.

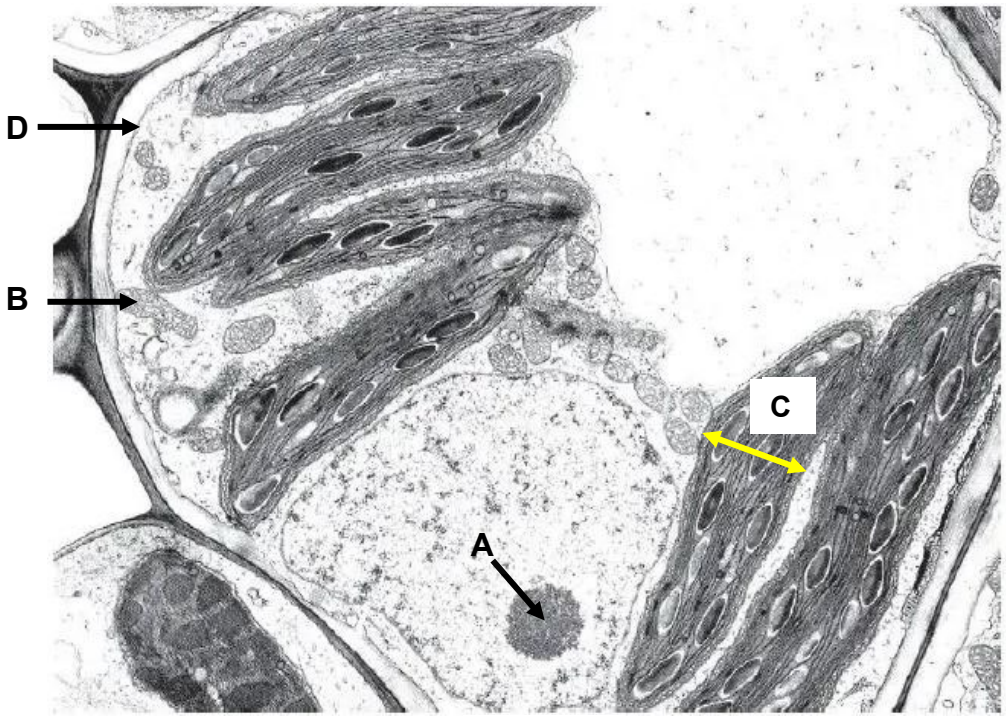


Fig. 1.1

2 μm

(a) (i) Fill in the table to identify structures **A** and **D** and show their functions.

Structure	Identity	Function
A	**Nucleolus** (R: nucleus)	1. Site of **rRNA synthesis**; OR 2. Site of **assembly** of **ribosomal proteins** with **rRNA** to form small and large **subunits** **of ribosomes** / **ribosomal subunits**;
D	**Cell surface membrane** (R: cell membrane) (A: plasma membrane)	It acts as a barrier which **controls the movement** of various substances **in and out of the cell** due to its partial permeability**;**

@ 1 mark per pair [2]

(ii) Using the width of structure **C** as indicated by the arrow in Fig. 1.1, calculate the magnification of the electron micrograph. Show your working clearly.

1. Length of arrow = 1.4 cm = 14,000 μm, actual width of chloroplast = 1.4 x 2 = 2.8 μm;
2. Magnification = 14,000 / 2.8 = x5,000 or 5,000 times

[2]

(R: answers without statement(s) to explain the different components of the equation)

(b) Fig. 1.2 is an electron micrograph of three cells of the same species of bacterium, *Erwinia carotovora*.

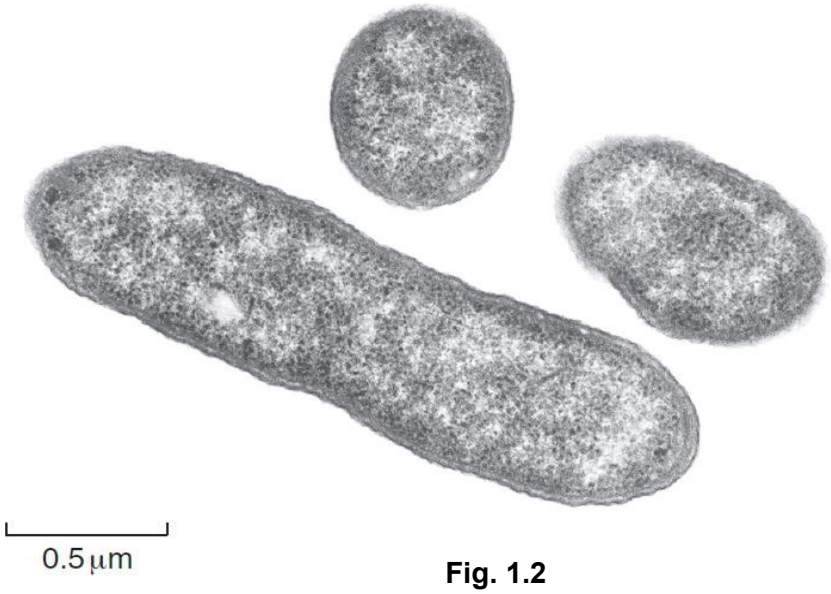


Fig. 1.2

(i) Name two structures found in animal cells which are **not** present in the cells shown in Fig. 1.2. [2]

Any **two** of the following:
1. Mitochondrion / mitochondria; (R: chloroplast)
2. Nucleus / nuclear membrane / nuclear envelope;
3. Nucleolus;
4. DNA associated with, histones / protein(s); (A: chromosomes / linear DNA)
5. Smooth / rough endoplasmic reticulum;
6. Golgi body / apparatus;
7. Lysosomes / Golgi vesicles / secretory vesicles ;
8. 80S ribosomes;
9. AVP; e.g. cytoskeleton, (9 + 2) microtubules, microfilaments, proteasome, peroxisome, cilium / cilia, flagellum / flagella;

(ii) *E. carotovora* is a rod-shaped bacterium.

Explain why two of the bacterial cells in Fig. 1.2 do **not** appear rod-shaped. [1]

1. Cells not sectioned in longitudinal section; WTTE
(A: cross-section shown / depends on angle of cut / cut in different planes / end view)

(iii) Scientists think that the origins of structures **B** and **C** of Fig. 1.1 were very different from that of eukaryotic cells. The evidence for this is that they both have features in common with bacterial cells like *E. carotovora.*

Compare the structural features of **B** and/or **C** with *E. carovotora*; [3]

Similarities:
1. **Circular DNA**;
2. **Small / similar**, size; (A: 0.5–15 μm)
3. **70S ribosomes**;

Difference:

4. **B** (**mitochondria**) and **C** (**chloroplasts**) have **smaller number of genes** / **smaller genome** / **smaller circular DNA** compared to bacteria;
5. **Chloroplasts** have internal membranes folded into **thylakoids**, whereas there are **no thylakoids** in bacteria;

[Total: 10]

2 Fig. 2.1 is a representation of a starch molecule. Starch is a polysaccharide made up of amylose and amylopectin.

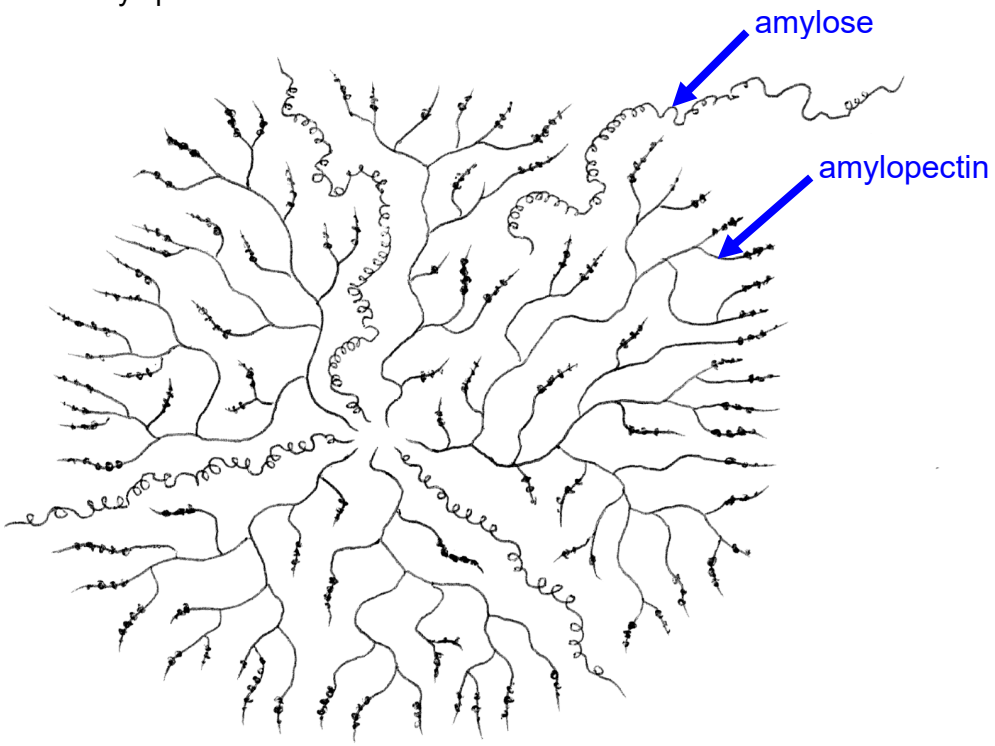


Fig. 2.1

(a) (i) Using arrows, label clearly on Fig. 2.1, amylose and amylopectin. [1]

Clearly and correctly labelled with arrows as shown above. All or none.

(ii) Explain how **one** structural feature of amylopectin is related to its function in living organisms. [3]

1. **Structure:** Amylopectin is a very **large** molecule composed of **many α–glucose** monomers
2. **Property:** Thus it is **insoluble in water** and **does not affect water potential of cells;**
3. **Role:** Good **energy storage** molecule

OR

4. **Structure:** Amylopectin is made up of α-glucose monomers joined together via **α-1,4-glycosidic bonds** giving a **helical shape** within branches;
5. **Property:** Thus making it a **compact** molecule;
6. **Role:** Good **energy storage** molecule**;**

OR

7. **Structure:** Amylopectin has **α-1,6-glycosidic bonds** at branch-points, making it a **highly branched molecule** / contains **numerous branch points;**

8. **Property:** Provides **many ends** for enzyme's easy access to **hydrolyse α-1,4 glycosidic bonds** between α-glucose monomers to enable **rapid release of α-glucose** for respiration to provide ATP **/ faster hydrolysis** / **for amylase act on at the same time**
9. **Role:** Good **energy storage** molecule**;**

(b) Cellulose is another polysaccharide.

Fig. 2.2 shows three monomers from a molecule of cellulose.

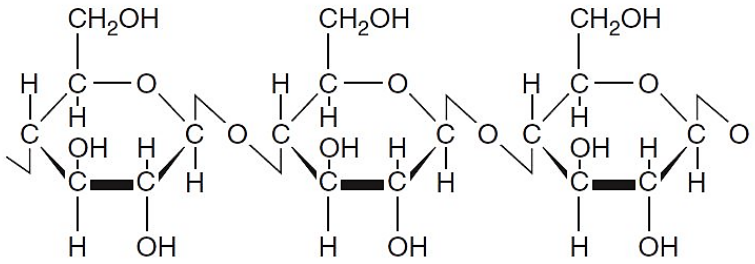


Fig. 2.2

(i) State the name of the monomer that makes up cellulose. [1]

β- glucose

(ii) Cellulose has high tensile strength which makes it suitable for the cell walls of plants.

Explain how cellulose has such a high tensile strength making it suitable for the cell walls of plants. [3]

1. Each cellulose molecule consists of alternate **β-glucose** monomers **rotated 180°** with respect to each other, linked by **β-1,4 glycosidic bond**. This results in a **linear** / **straight cellulose chain**;
2. **Hydroxyl groups** project outwards from **each** linear **cellulose molecule** allows **extensive hydrogen bonds** to form between neighbouring parallel chains, forming **microfibrils**;
3. **Microfibrils** bundle together to form **macrofibrils**, which in turn associate together to form **cellulose fibres**, giving rise to high tensile strength**;**

R:

- reference to few OH groups being able available for hydrogen bonding with water molecules
- β-1,4 glycosidic bond not easily hydrolysed

(c) Glycogen has a similar structure to amylopectin. Glycogen is stored in the liver, kidney and muscles of mammals.

State two ways in which the structure of glycogen differs from the structure of cellulose. [2]

Any two

1. Cellulose consists of **β-glucose monomers** while glycogen consists of **α- glucose monomers;**

2. Cellulose is a **linear molecule /** has **no branching** while glycogen is a highly **branched molecule**
   OR
   Cellulose is a **straight molecule** while glycogen is a **helical molecule**

3. Cellulose contains **β-1,4 glycosidic bonds** between β-glucose monomers, while glycogen contains **α-1,4 glycosidic bonds** between α-glucose monomers**,** and **α-1,6 glycosidic bonds** at branch points;

4. The **alternate / adjacent glucose monomers** in cellulose are **inverted / rotated 180° with respect to each other** while the **glucose monomers** in glycogen have the **same orientation;**

5. Cellulose contains **intermolecular hydrogen bonding** between the hydroxyl groups projecting outwards from each **adjacent cellulose chain**, while glycogen **do not contain intermolecular hydrogen bonds between glycogen molecules;**

[Total: 10]

3 Neutrase® is an enzyme that is used to hydrolyse proteins in solution. When the enzyme is mixed with a 2% protein solution the reaction mixture changes from white to colourless.

A student carried out an experiment to find the effect of copper sulfate and potassium sulfate on the activity of Neutrase®. The student made four reaction mixtures in test-tubes **A** to **D**. The contents of each test-tube are shown in Table 3.1.

Table 3.1

test-tube	volume added / cm^3				
	2% protein	0.05 mol dm^{-3} copper sulfate	0.01 mol dm^{-3} copper sulfate	0.01 mol dm^{-3} potassium sulfate	water
A	0.1	0.1	0.0	0.0	0.0
B	0.1	0.0	0.1	0.0	0.0
C	0.1	0.0	0.0	0.1	0.0
D	0.1	0.0	0.0	0.0	0.1

0.5 cm^3 of a 1% Neutrase® solution was then added to test-tube **A** and immediately placed into a colorimeter. The colorimeter was used to measure the intensity of light that is absorbed by the solution (absorbance) over 100 seconds. The procedure was repeated with the other reaction mixtures, **B**, **C** and **D**.

The results are shown in Fig. 3.1.

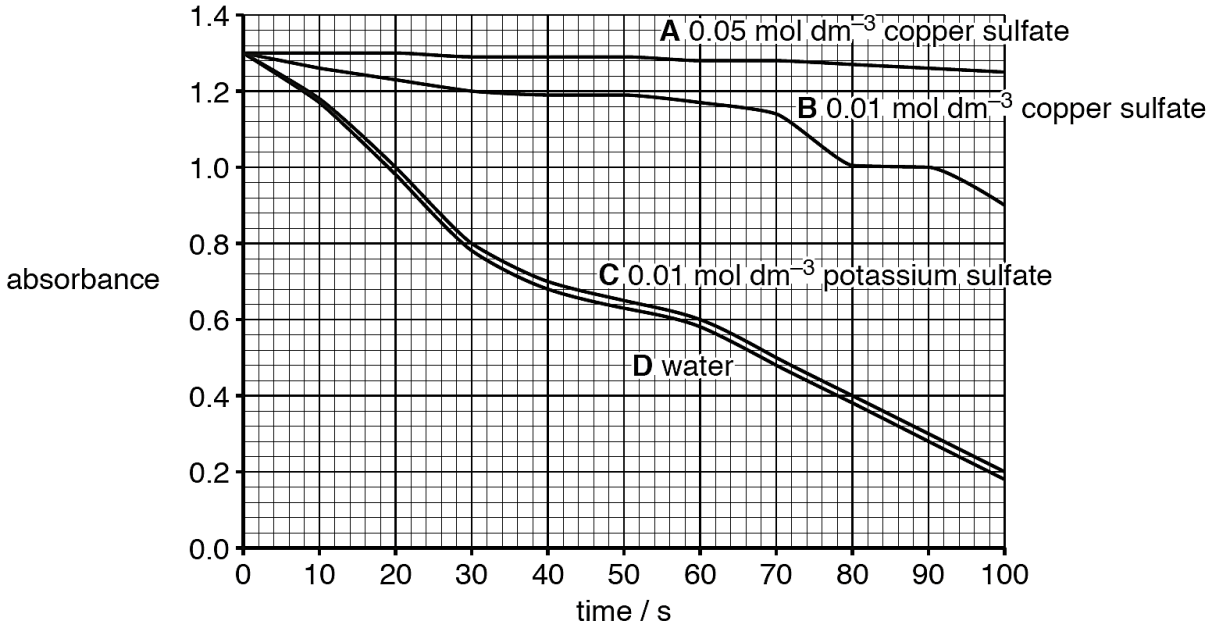


Fig. 3.1

(a) **(i)** Suggest **and** explain why measuring the absorbance of the reaction mixture over 100 seconds is a suitable method for determining the activity of Neutrase®. [2]

1. Neutrase® hydrolyses/breaks down protein to **short peptides/amino acids**, which are **more soluble in water**;
2. Hence, as the reaction progresses / as reaction mixture changes from white to colourless / over time, **more light passes through / is transmitted through** (A: less light is absorbed by) the reaction mixture, and the absorbance reading decreases;
3. 100 seconds is long enough to see the progress of the four reactions;
   I: 'the rate of reaction can be calculated'
   R: allow time for reaction to complete'

(ii) With reference to Fig. 3.1, describe the effects of 0.01 mol dm^{-3} copper sulfate solution and 0.01 mol dm^{-3} potassium sulfate solution on the activity of Neutrase®. [4]

copper sulfate:
1. 0.01 mol dm^{-3} copper sulfate **decreases/reduces/lowers the activity** (A: 'inhibits the activity') of Neutrase®; (I: copper sulfate acts as an inhibitor of Neutrase®)
2. Quote data: **absorbance decreases by 0.4 a.u.** (A: 1.3 to 0.9 a.u.) **over 100 s**;

potassium sulfate:
3. 0.01 mol dm^{-3} potassium sulfate **has no/negligible effect** (A: 'very little effect') on the activity of Neutrase®; (I: same effect as water – not describing anything) (R: less effect)
4. Quote data: **absorbance decreases by 1.1 a.u.** (A: 1.3 to 0.2 a.u.) **over 100 s**;

(b) Copper and sulfate ions are not similar in conformation to proteins used in the experiment.

Explain the effect of copper sulfate solution on the activity of Neutrase®. [3]

1. Copper sulfate acts as a **non-competitive inhibitor** of Neutrase®;
2. Copper sulfate **binds to a site other than the active site** and induces a **change in the 3D conformation** of the Neutrase® molecule;
3. As such, the **active site** of Neutrase® is **no longer complementary in conformation** (and charge) **to the substrate** (proteins) and **cannot bind**, thus **enzyme-substrate complex is not formed** (A: lower rate of enzyme-substrate complex formation)
   Hence, fewer products will be formed at any one time as there are fewer available Neutrase® molecules to catalyse the breakdown of proteins;

OR

4. Copper sulfate acts as an **allosteric inhibitor** of Neutrase®;
5. Copper sulfate **binds to allosteric site** of Neutrase® and **stabilises the inactive conformation** of the Neutrase® molecule;
6. As such, the **active site** of Neutrase® is **not complementary in conformation** (and charge) **to the substrate** (proteins) **cannot bind** and **enzyme-substrate complex is not formed**; (A: lower rate of enzyme-substrate complex formation)
   Hence, fewer products will be formed at any one time as there are fewer available Neutrase® molecules to catalyse the breakdown of proteins;

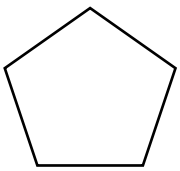
Modified from **CIE 9700/21 May/June 2019 P2 Q3**

[Total: 9]

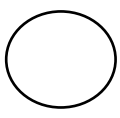
4 Genetic information is encoded in DNA. DNA is made up of monomers called nucleotides.

A DNA nucleotide consists of three types of molecules joined together.

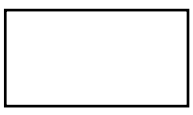
(a) (i) These shapes represent the components of DNA:



deoxyribose sugar

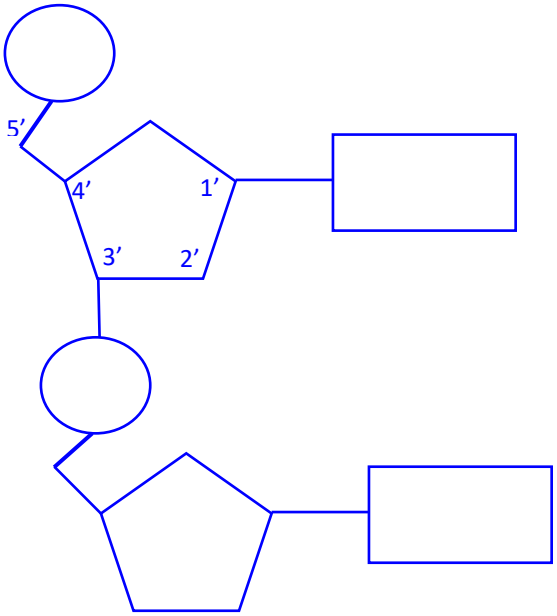


phosphate group

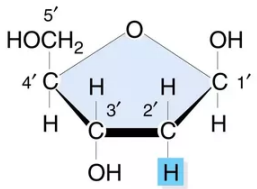


nitrogenous base

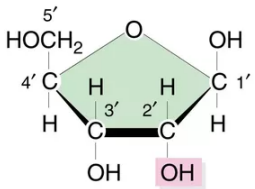
Using the above shapes, draw a diagram to show a dinucleotide. [2]



1. Correct bonding of phosphate group and nitrogenous base to pentose sugar for each nucleotide;
2. Correct bonding of phosphate group between two nucleotides; (Numbering NOT required)



Deoxyribose



Ribose

(ii) A gene was isolated from the DNA of bacterial cells and the base composition of the template strand was analysed.

- 40% of the bases were thymine
- 20% of the bases were guanine
- 10% of the bases were cytosine

Fill in the table below to show the percentage of nucleotides required in these bacterial cells to produce a transcript of this strand of the gene. [1]

Percentage of nucleotides needed with a particular base				
adenine	cytosine	guanine	thymine	uracil
40	20	10	0	30

(b) The DNA molecules are further organised into structures called chromosomes.

Describe the packing of DNA in eukaryotic chromosomes. [3]

1. **Negatively-charged DNA** is coiled around **positively charged histone** octamers via **ionic interactions**, forming **nucleosomes** linked by linker DNA;
2. **Subsequent coiling** results in formation of a **30 nm chromatin fibre / solenoid**;
3. 30 nm chromatin fibre in turn is **further coiled** to form **looped domains** attached to a chromosome scaffold of non-histone proteins, which undergo further **supercoiling** to form **chromosomes**;

(c) Many diseases arise due to gene mutations and/or chromosomal aberrations.

(i) Distinguish between gene mutations and chromosomal aberrations. [2]

Point of Comparison	Gene mutation	Chromosomal aberration
1. Definition	Change in **nucleotide sequence**	Change in **chromosomal structure or number**;
2. No. of genes affected	Affects a **one gene**	Usually affects **many genes** (because involves a

		segment or an entire chromosome hence);
3. Changes in chromosome number	**No change in chromosome number**	May have **changes in chromosome number** e.g. aneuploidy / polyploidy;
4. Mechanisms	**Substitution**, **deletion** or **addition** of nucleotides (any 2)	**Translocation**, **deletion or inversion of chromosomal segments** or **non-disjunction** events during nuclear division (any 2);
5. Frameshift	**Frameshift** is possible	**No frameshift**;

Any two pairs

Fig. 4.1 shows an error occurring during meiosis II.

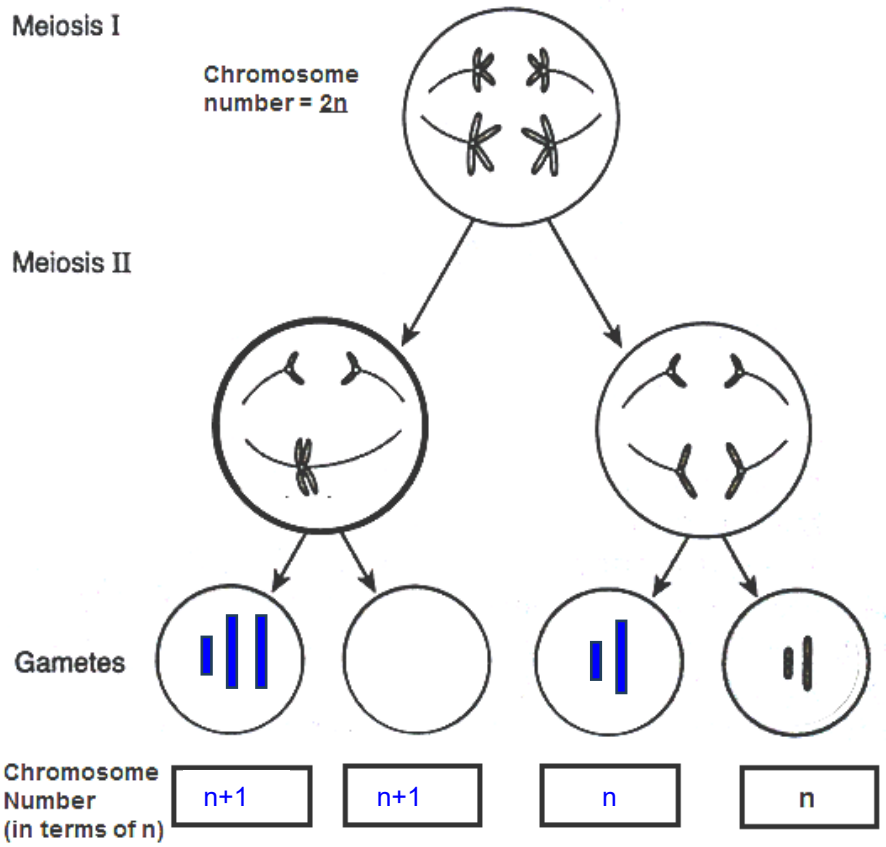


Fig. 4.1

(i) Complete Fig. 4.1 with the correct chromosome structures and chromosome number (in terms of n) in the gametes. [1]

(ii) Describe the error shown in Fig. 4.1. [1]

1. **Non-disjunction** caused by the **failure of sister chromatids to separate** during **anaphase II**;

[Total: 10]

5 The summer squash plant, *Cucurbita pepo*, produces edible fruits that vary in shape. Fruit shape in squashes is controlled by two genes, **A/a** and **B/b**, that are located on different chromosomes.

Fig. 2.1 shows the fruits of three different varieties of squash plants.

Patty pan (disc-shaped) | Di Nizza (spherical) | Alfresco (long)

Fig. 5.1

(a) (i) Table 5.1 shows the possible genotypes of the Patty pan and Alfresco varieties.

Complete Table 5.1 to show the possible genotypes of the Di Nizza variety.

variety	possible genotypes			
Patty pan (disc-shaped)	**AABB**	**AaBB**	**AABb**	**AaBb**
Di Nizza (spherical)	.....	.....	.....	.....
Alfresco (long)	**aabb**			

[1]

AAbb, **Aabb**, **aaBB**, **aaBb** (all or nothing);

(ii) A gardener used pollen from a male flower of Alfresco to pollinate a female flower of Di Nizza. The gardener grew the seeds produced from this cross and found that half the offspring produced spherical fruits and half produced long fruits.

Draw **one** genetic diagram to explain this result.

[4]

1. Parental phenotypes (given in question) → **correct parental genotypes:** EITHER **aabb x Aabb** OR **aabb x aaBb**
2. **Gametes** (must be circled)
3. **Fertilisation**
4. **Offspring genotypic linked to phenotypic ratio**

Parental phenotypes **Alfresco (male)** **X** **Di Nizza (female)**
Parental genotypes **aabb** **Aabb**

Meiosis
Gametes (**ab**) **X** (**Ab**) (**ab**)

Fertilisation

gametes		

	Ab	ab
ab	**Aabb** Di Nizza (spherical)	**aabb** Alfresco (long)

Offspring genotypic ratio **1 Aabb** : **1 aabb**

Offspring phenotypic ratio **1 spherical** : **1 long**

OR

Parental phenotypes **Alfresco (male)** **X** **Di Nizza (female)**
Parental genotypes **aabb** **aaBb**

Meiosis
Gametes **ab** **X** **aB** **ab**

Fertilisation

gametes	aB	ab
ab	**aaBb** Di Nizza (spherical)	**aabb** Alfresco (long)

Offspring genotypic ratio **1 aaBb** : **1 aabb**

Offspring phenotypic ratio **1 spherical** : **1 long**

(b) Explain how **one** event in meiosis can result in genetic variation. [3]

1. **Crossing over** occurs during **prophase I**;
2. Whereby non-sister chromatids of a pair of homologous chromosomes exchange equivalent portions of material (OWTTE);
3. Thus, giving rise to **different combinations of alleles** on daughter chromosomes;

OR

4. **Independent assortment** (A: random assortment) of homologous pairs of chromosomes during **metaphase I**;
5. Whereby each pair of homologous chromosomes align independently of each other along the metaphase plate (OWTTE);
6. Thus, giving rise to **different combinations of maternal and paternal chromosomes**; (R: different combination of alleles)

Modified from **CIE 9700/42 May/June 2020 P4 Q2**

(c) Sex determination in humans depends on the *SRY* gene on the Y chromosome. The product of the *SRY* gene switches on the genes that enable an embryo to start to develop male characteristics.

To transcribe the *SRY* gene, the H3K9 histone must be demethylated by the enzyme coded by the *Jmjd1a* gene.

Define epistasis and state the relationship between the *SRY* gene and the *Jmjd1a* gene. [2]

1. Epistasis is a form of **gene interaction** in which a gene at one locus **masks** the phenotypic **expression** of a gene at a second locus (A: where one gene **masks** the expression of another gene);
2. ***Jmjd1a* gene is epistatic to *SRY* gene** / *SRY* is hypostatic to *Jmjd1a*;
(A: *Jmjd1a* gene masks the expression of *SRY* gene);

Modified from **A-level 9744/01 2021 P1 Q17**

[Total: 10]

6 Mutant Ras proteins have been associated with many types of human cancer. Ras proteins function downstream from cell surface receptors, such as the epidermal growth factor receptor (EGFR).

Fig. 6.1 shows the activation of Ras following binding of the epidermal growth factor (EGF) at its receptor. GRB2 and Sos are cytosolic proteins associated with this signalling pathway.

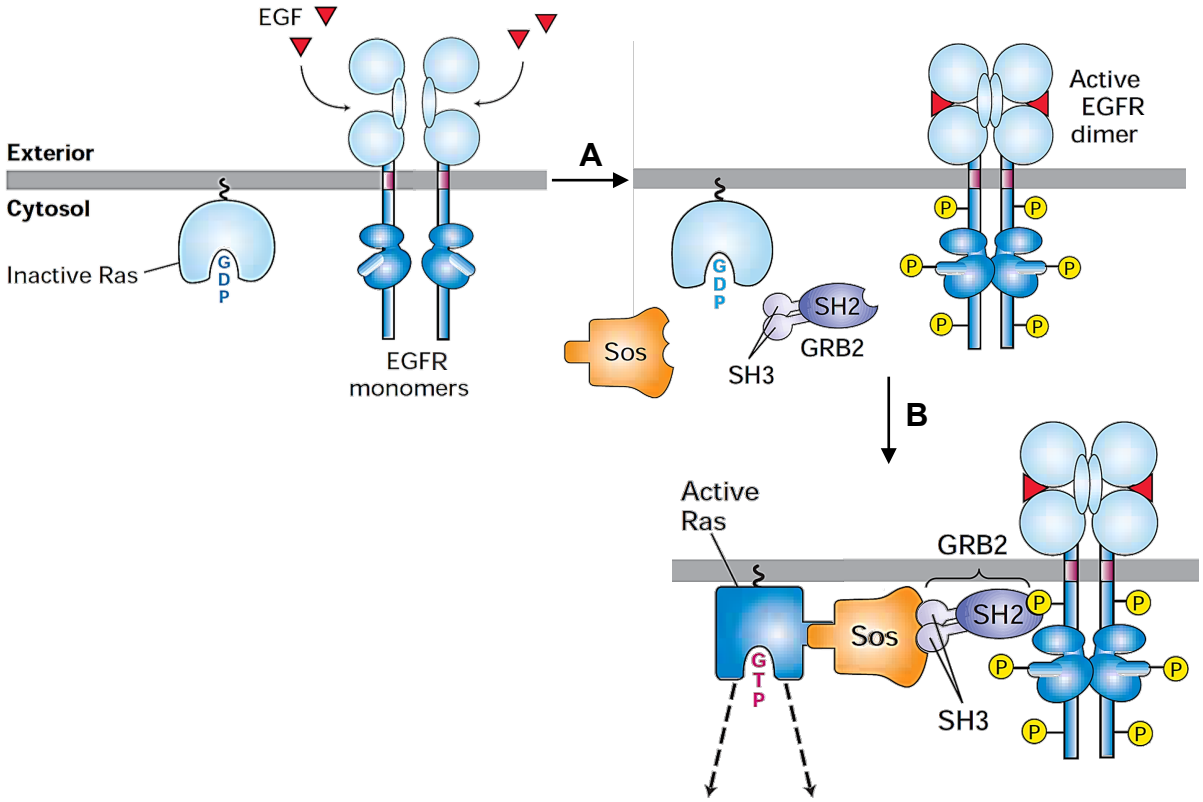


Fig. 6.1

(a) Describe the downstream events that occur after EGF binds to its receptor, as indicated by **A** and **B** in Fig. 6.1. [5]

A

1. Binding of EGF to both EGFR monomers triggers **dimerisation of EGFR monomers**, which induces a **conformational change** in the **intracellular domain** of both subunits;
2. This is followed by **cross-phosphorylation**, where the **tyrosine kinase** (note to marker: don't mark for tyr kinase) of **each receptor subunit phosphorylates** / catalyses the addition of phosphate groups to **specific tyrosine residues of the other subunit**;

B

3. The **GRB2 protein binds to the phosphorylated tyrosine residues** of the EGFR via its **SH2 domain**, and becomes **activated**;
4. The **Sos protein then binds to the SH3 domains** of the activated GRB2 protein, and hence becomes **activated** as well;
5. **Inactive Ras** protein then **binds to the Sos protein**, and **exchanges GDP for GTP** (A: displaces its attached GDP with GTP), and hence is now **activated**;
   (R: GDP phosphorylated to become GTP)

Modified from Cell Signalling tutorial Q4

Active Ras protein can bind and activates other downstream relay proteins within the cell, such as Raf. Raf is a protein kinase that can trigger a sequence of events, as shown in Fig. 6.2.

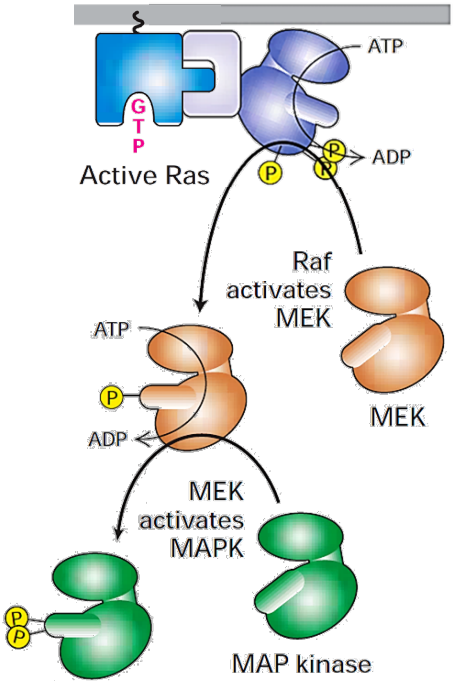


Fig. 6.2

(b) Describe the sequence of events triggered by Raf and explain its importance in signal transduction. [3]

1. Raf triggers a **phosphorylation cascade**;
2. In which **Raf phosphorylates and activates MEK**, and **MEK** then phosphorylates and activates **MAPK**;
3. This facilitates **signal amplification**, where only a **small amount of signal molecules** (e.g. ligand or activated Ras protein) is required to **elicit a large response** from the cell;
   OR
   This facilitates **signal amplification**, where each protein kinase **phosphorylates and activates many** protein kinases in the series (A: specific examples);

(c) In a separate signalling pathway, activated EGFR can also result in the activation of PLC-γ. PLC-γ is an enzyme that cleaves a modified phospholipid molecule called PIP_2 into IP_3 and DAG. Both IP_3 and DAG function as second messengers.

Describe the role of second messengers. [2]

.....

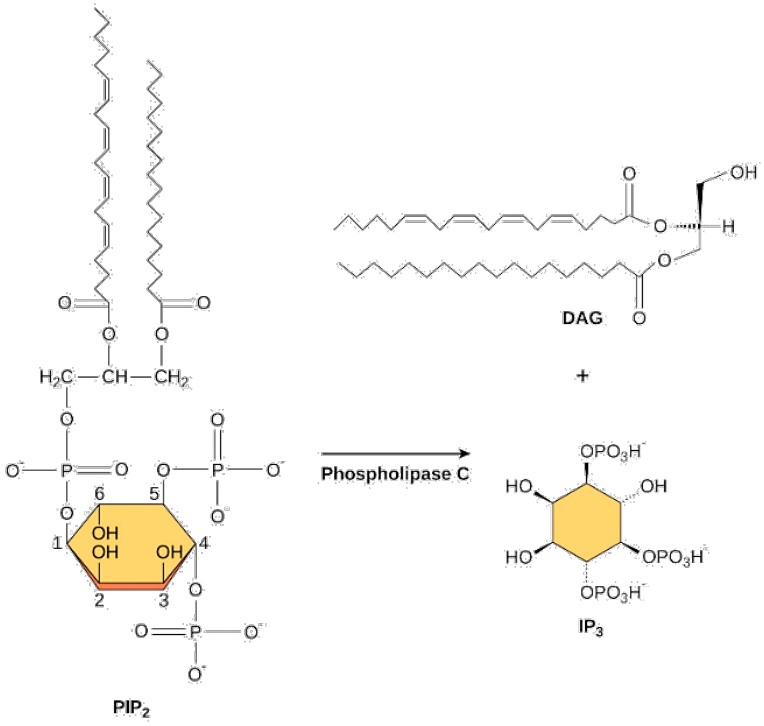
.....

.....

.....[2]

1. Second messengers **bind** and induce a conformational change in a downstream protein kinase / relay protein, thus **activating** it;

2. In this way, the 'signal' is passed on/relayed to the next protein kinase / relay protein during signal transduction;



Modified from 2021 EJC Prelim P2 Q8(a)

[Total: 10]

7 In experiments it was found that, in an intact mitochondrion:

- there is a membrane potential across the inner mitochondrial membrane whereby there is an unequal distribution of charges across the membrane
- the membrane potential arises because the mitochondrial matrix has a negative charge and the intermembrane space has a positive charge.
- the transport of ATP, ADP and inorganic phosphate (Pi) is driven by the membrane potential across the inner membrane

Fig. 7.1 shows the location of some inner mitochondrial membrane carrier proteins.

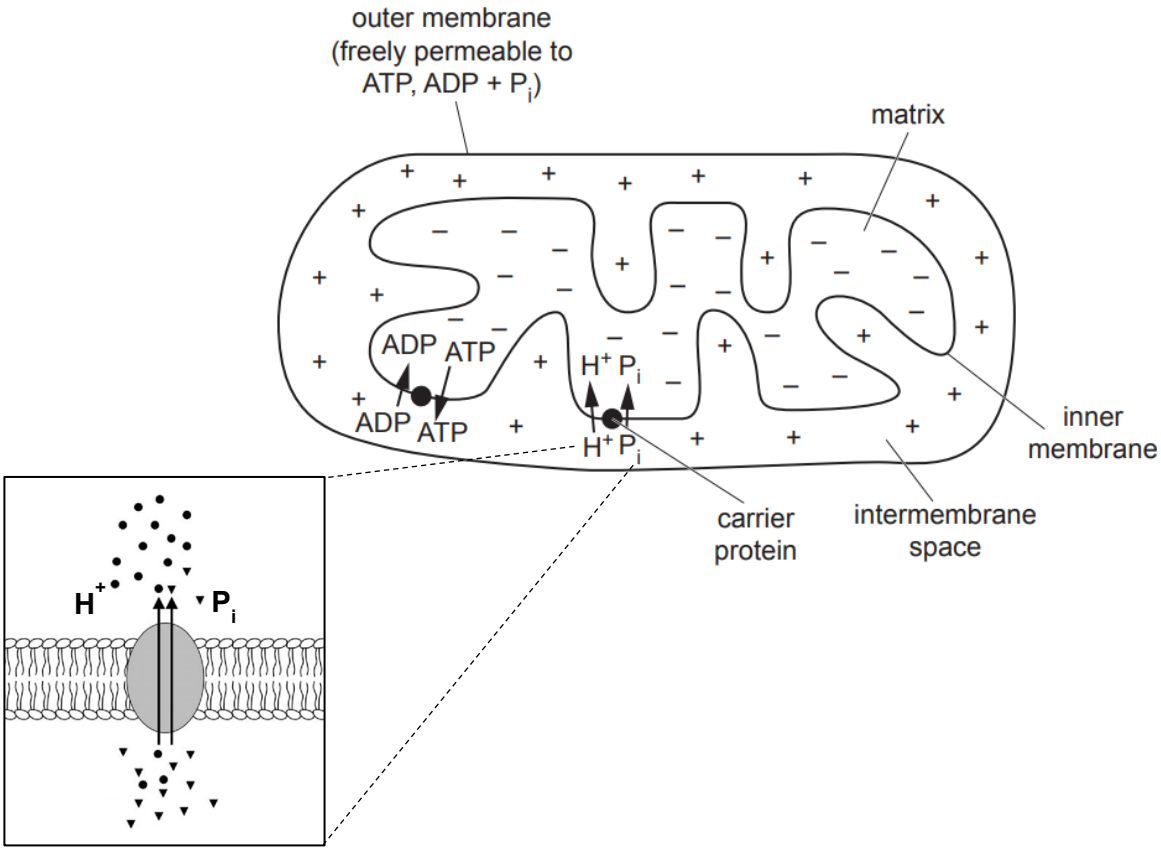


Fig. 7.1

(b) (i) Reduced NAD and reduced FAD transfer hydrogen atoms to carriers located in the inner mitochondrial membrane.

Explain how hydrogen atoms from reduced NAD and reduced FAD lead to a membrane potential forming across the inner mitochondrial membrane during oxidative phosphorylation. [4]

1. Hydrogen atoms from reduced NAD and reduced FAD dissociate into **protons and electrons**;
2. The **high energy electrons** are **passed down the electron transport chain** (ETC) which is made up of electron carriers of decreasing energy levels.
3. During which, **energy is released** and is used to **pump protons** from the **mitochondrial matrix into the intermembrane space**,
4. making the **intermembrane space more positively charged**;
5. A **proton motive force / proton gradient** is thereby **formed across the inner mitochondrial membrane**;

(CIE mark scheme) any four from:
1 (H atoms) split into protons and electrons ;
2 electrons, flow / move, down ETC ;
3 (releases) energy used to move H+ to intermembrane space ;
4 more / build-up of, H+ / positive charge, in intermembrane space ;
5 (causes / sets up) proton / electrochemical, gradient ;

(ii) Suggest and explain how Pi is transported across the inner membrane of the mitochondrion into the matrix. [2]

1. A **carrier protein** transports Pi across the inner mitochondrial membrane via **facilitated diffusion**;
2. together with proton;

(CIE mark scheme) any two from:
1 (Pi) by facilitated diffusion or through a protein, channel / carrier ;
2 Pi and H+ move together ;
3 (as) H+ ions diffuse (through ATP synth(et)ase / to matrix) ;

The production of reduced electron carriers from the first three stages of aerobic respiration are shown in Fig. 7.2.

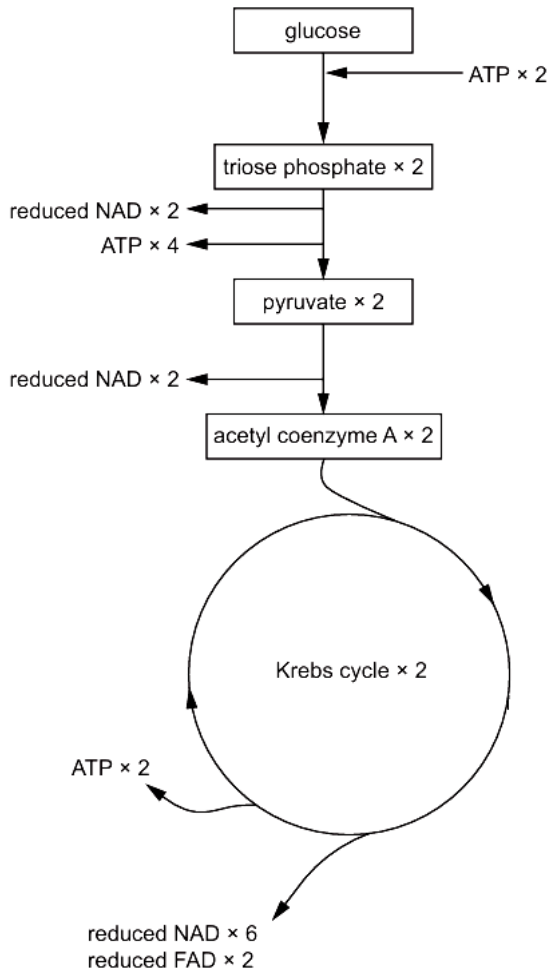


Fig. 7.2

At one time it was thought that the oxidative phosphorylation of:

one molecule of reduced NAD results in the synthesis of 3 ATP molecules
one molecule of reduced FAD results in the synthesis of 2 ATP molecules. Using Fig. 7.2, a theoretical value for the net number of ATP molecules that are synthesised for each molecule of glucose can be calculated.

Modern research has shown that the actual net number of ATP molecules synthesised for each glucose molecule respired is much lower than this theoretical value.

(c) **(i)** Using Fig. 7.2, calculate the theoretical value for the net number of ATP molecules that are synthesised for each molecule of glucose respired in all phosphorylation reactions.

Show your working. [2]

answer = ...

(glycolysis) + (Krebs)
(ATP + reduced NAD) + (ATP + reduced NAD + reduced FAD)
$(4 - 2) + (4 \times 3) + 2 + (6 \times 3) + (2 \times 2)$ **OR**
2 + 12 + 2 + 18 + 4 ;

38 ;

(ii) Suggest one reason why the actual net number of ATP molecules synthesised is less than the theoretical number. [1]

any 1:
1. Electrons from NADH in the cytoplasm are passed on to FAD instead of NAD in the mitochondrial matrix;
2. ATP used to transport pyruvate from cytoplasm to mitochondrial matrix;
3. Some protons leaked form the intermembrane space;
4. Glucose may not be completely broken down / some intermediates are used in different metabolic processes;
5. Reduced NAD or reduced FAD may be used for other metabolic reactions;

(CIE mark scheme) any two from:
1 ATP / energy, used to transport, pyruvate / reduced NAD / products of glycolysis, into (named part of) mitochondria ; 2 some protons leak from intermembrane space ; 3 some energy lost as heat ; 4 glucose may not be completely broken down / some intermediates are used in different metabolic processes ; 5 reduced NAD may be used for other (metabolic) reactions ;

Photosynthesis is another important energy transfer process.

(d) Explain why temperature can be a limiting factor of photosynthesis. [3]

1. **Enzymes** such as **Rubisco** are involved in Calvin cycle;
OR
Enzymes such as **ATP synthase** are involved in photophosphorylation / light-dependent reaction / chemiosmosis;

2. **Increasing temperature up to optimum increases kinetic energy** of **Rubisco, CO_2 and RuBP**;
OR
Increasing temperature up to optimum increases kinetic energy of **ATP synthase, ADP and inorganic phosphate**;

OR
Increasing temperature up to optimum increases kinetic energy of **enzyme and substrate molecules**;

3. This **increases the rate** of **effective collisions** between **enzymes and substrates** and **increases** the **rate of formation** of **enzyme-substrate complexes**, resulting in increase in rate of product formation;

R: mention of temp beyond optimum and denaturation

(CIE mark scheme) any three from:
1 ref. (named) enzymes ;
2 high(er) temperature increases rate ; 3 (temperature affects) photophosphorylation / light-dependent / Calvin cycle / light-independent / ESC formation ; ora 4 enzymes denature at, too high a temperature / very high temperature / above optimum temperature ; 5 AVP ;

[Total: 12]

8 Genome-wide association studies find links between single nucleotide polymorphisms (SNPs) and phenotypic features such as human diseases. SNPs are points on the DNA that vary in the population because of single base substitutions.

Fig. 8.1 summarises results for three diseases – rheumatoid arthritis, type 1 diabetes and type 2 diabetes. The 22 human autosomes and the X chromosome (chromosome 23) are shown.

Chromosome locations with SNPs that are associated with a disease at a statistically significant level (greater than 5 arbitrary units) are shown in black.

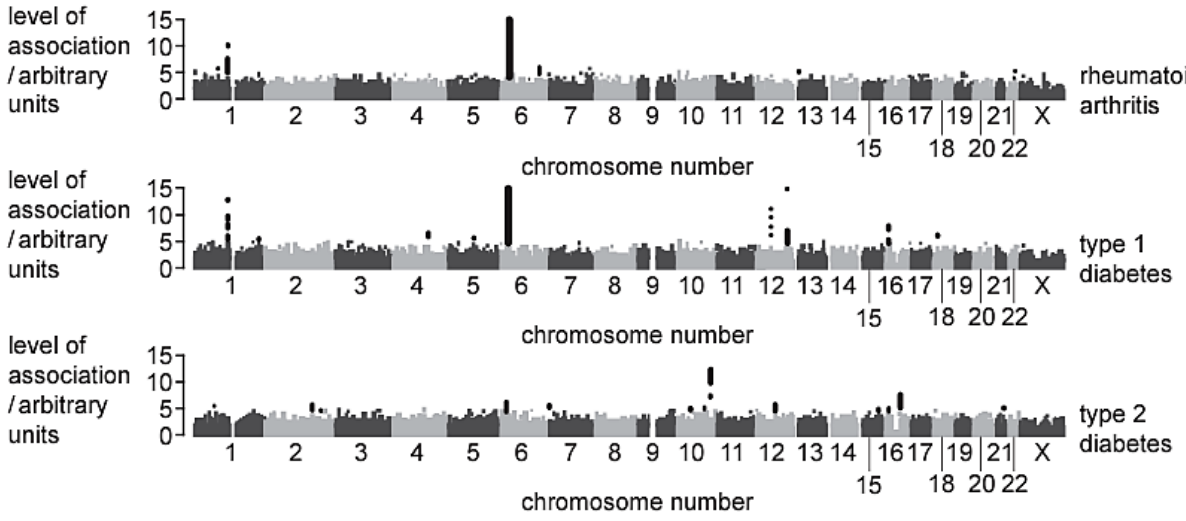


Fig. 8.1

(a) (i) Identify the chromosomes that contain SNPs that have a high level of association with **both** rheumatoid arthritis and Type 1 diabetes. [1]

Chromosomes 1 and 6;

(ii) Genetic diseases are caused at the level of the gene and the chromosome.

With reference to Fig. 8.1, compare the genetic basis of the three diseases. [2]

Similarity (max 1)

All three diseases

1. are **autosomal** diseases / **not sex-linked** / **not associated with X chromosome**;
2. are associated with SNP on **chromosome 6**;

Difference (max 1)

3. **Type 1 and type 2 diabetes** are associated with **chromosomes 12 and 16**, but **rheumatoid arthritis is not**;
4. **Only type 2 diabetes** is associated with **chromosome 10**;
5. **Rheumatoid arthritis and type 1 diabetes** have **more SNPs in common than with type 2** diabetes;
6. **Rheumatoid arthritis** has the fewest SNPs
   OR
   Type 1 and type 2 diabetes has **more SNPs than rheumatoid arthritis**;

One of the SNPs associated with rheumatoid arthritis results in the introduction of an additional restriction site for *Sma*I, as shown in Fig. 8.2. The restriction sites for *Sma*I are indicated by the arrows.

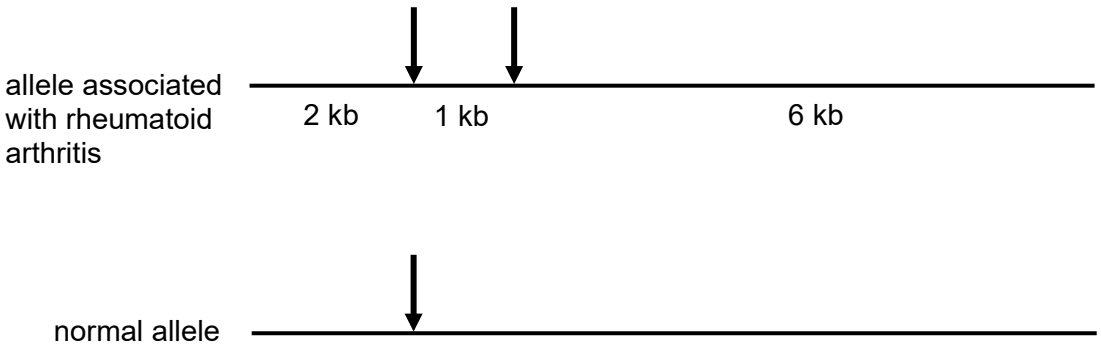


Fig. 8.2

(b) (i) Various probes can be used in Southern blotting for disease detection.

Design a probe such that a different band pattern will be produced for the various genotypes. Draw this probe on Fig. 8.2 to show where will it bind on the allele associated with rheumatoid arthritis. Label this probe clearly as **(b)(i)**. [1]

Anywhere along the 1kb and/or 6kb region.

(ii) The allele associated with rheumatoid arthritis is a dominant allele.

Using the probe you have designed for **(b)(i)**, draw the band pattern that will result for all genotypes in the population in Fig. 8.3. [4]

Fig. 8.3

1. size of bands indicated clearly (e.g. 1kb, 6kb, 7kb)
2. band pattern for homozygous normal allele, homozygous rheumatoid arthritis allele, heterozygous drawn + genotypes labelled clearly
3. band pattern correctly correlates with probe designed in (b)(i)
4. thickness of each band for heterozygote is half that of the homozygous individuals

(iii) Not all probes will be useful in producing a distinct band pattern between those who have rheumatoid arthritis allele and those who do not.

On Fig. 8.2, draw to show where such a probe will anneal to the allele associated with rheumatoid arthritis. Label this probe clearly as **(b)(iii)**. [1]

Anywhere along the 2kb region only.

[Total: 9]

9 The main cause of tuberculosis (TB) in humans is the bacterium, *Mycobacterium tuberculosis*. Generally, a healthy person who inhales these droplets has effective defence mechanisms in their respiratory airways to prevent infection.

One example of a defence mechanism against such pathogens in the respiratory airways involves the action of resident phagocytes.

(a) State the specific type of phagocyte that acts as the primary defence against *M. tuberculosis*. [1]

Alveolar macrophages;

(b) Describe the mode of action of this phagocyte in killing bacteria cells. [3]

1. Alveolar macrophages detect/recognise pathogens in the respiratory airways and form **pseudopodia** that surround/wrap around *M. tuberculosis*;
2. The macrophage then **engulfs** (A: phagocytose) the bacteria cells, placing them within a **phagocytic vesicle**;
3. The phagocytic vesicle then **fuses with a lysosome**, which releases **hydrolytic enzymes** into the phagolysosome to **digest/break down** the bacteria cells;

(c) It is sometimes possible for *M. tuberculosis* to survive within these phagocytes without being destroyed.

Suggest **one** way in which *M. tuberculosis* may survive within these phagocytes. [1]

Any one of the following:

1. After being phagocytosed by alveolar macrophages, *M. tuberculosis* **prevents fusion of phagosome with lysosome**;
2. *M. tuberculosis* is **resistant to hydrolytic enzymes** in the lysosome / produces inhibitors of lysosomal enzymes to prevent digestion of the bacterial cell (OWTTE);
3. *M. tuberculosis* may **form spores** that are resistant to degradation by lysosomal enzymes;

Modified from 2018 HCI Prelim P2 Q10(a)

Fig. 9.1 shows the reported number of new cases of tuberculosis (TB) in the USA and the number of new cases per 100000 of the population of the USA between 1993 and 2018.

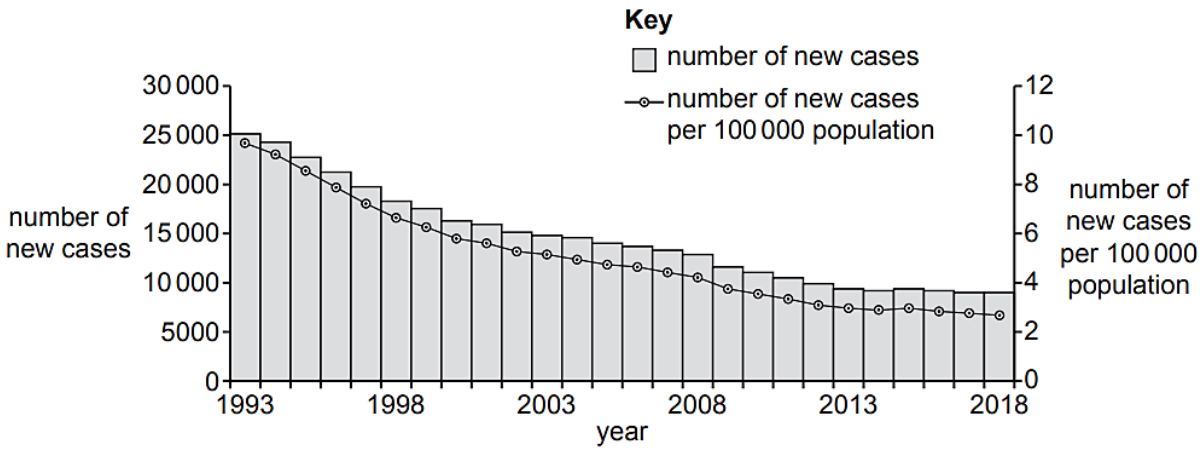


Fig. 9.1

(d) **(i)** Calculate the percentage decrease in the number of new cases of TB in the USA between 1993 and 2012. Show all your working. [1]

Percentage decrease
= (25000 – 10000) / 25000 x 100%
= 15000 / 25000 x 100%
= 60%

1. number of new cases for 1993 and 2012 shown
2. correct final answer

(ii) Suggest an advantage of calculating the number of new cases per 100000 each year in the prevention and control of TB across the world. [1]

1. Able to make **statistical / valid comparisons** between **years**
   OR
   Able to make **statistical / valid comparisons** between **countries** as it considers the differences in population sizes of different countries;
2. Able to **set targets for the control of TB** / able to determine demand of vaccines / drugs for treatment of TB;
3. Able to **monitor success of TB control programmes** of various countries;
4. AVP

I references to (more) accurate

can make, statistical / valid, comparisons between, years / countries ;
A takes into account the population sizes of different countries

AVP ; e.g. can set targets for the control of TB (e.g. keep below n per 100 000) ref. to supply of, vaccines / drugs / hospital beds / AW can, monitor / evaluate, success of TB control programmes to find out which countries have high, rates / incidence, of TB

R 'high numbers'

(e) TB is endemic (always present) in many populations across the world and many countries have high numbers of cases.

Suggest two reasons why it is difficult to reduce the number of cases of TB across the world. [2]

1. Mycobacterium / TB bacteria remains dormant in the body (A: reference to latent TB / TB bacteria in the body but infected person has no symptoms);
2. The presence of **antibiotic-resistant strains of TB bacteria** makes it more **difficult to treat** infected persons;
3. Takes a **long time / minimum of 6 months** to **complete the treatment**;
4. **Many** people **do not complete the treatment**;
5. **Many** do **not have access to treatment** for TB;
6. **Reluctance to be vaccinated** against TB / vaccination is not effective for adults;
7. **Migration of people infected with TB** to other countries;
8. **Overcrowded living conditions** perpetuate the spread of TB;

9. **Lack / poor education** in **preventing spread of TB**;

any two from:
1 Mycobacterium / pathogen / TB bacteria, remains dormant in the body ; A ref. to latent TB / bacterium present in the body but no symptoms 2 treatment takes a, long time / minimum of 6 months ; 3 many people do not complete treatment ; 4 many people do not have access to treatment ; 5 drug-resistant / antibiotic resistant, strains of Mycobacterium / pathogen / TB bacteria ; R 'immune' 6 HIV/AIDS or any other medical condition that increases susceptibility to TB ; e.g. weakened immune system / increased activation of dormant bacteria I TB is opportunistic, infection / disease, without further detail 7 vaccine reluctance ; 8 movement / migration, of people, infected with TB / from countries with high rates of TB ; 9 poor housing / overcrowded living conditions / homelessness ; 10 malnutrition / poor diet ; 11 transmission from cattle by, drinking unpasteurised contaminated milk / eating meat from contaminated cattle ; 12 lack of education / AW, about preventing spread of TB ; 13 AVP ; e.g. vaccination is not effective for adults / AW TB is difficult to diagnose

The genes in bacteria are commonly arranged into operons.

Fig. 9.2 shows the structure and control of the *trp* operon.

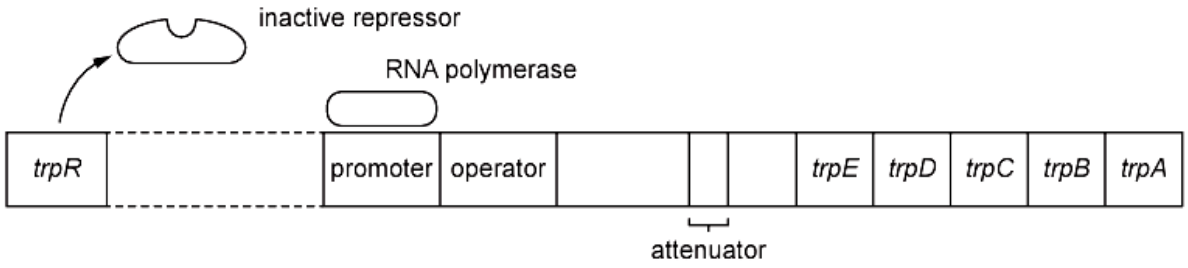


Fig. 9.2

(f) Describe the differences in structure **and** control between the *lac* operon and the *trp* operon. [3]

Difference in structure (max 2)

1. *Lac* operon has **3 structural genes** whereas *trp* operon has **5 structural genes**;
2. There is a **CAP-binding site** within the promoter of the *lac* operon but **none** in *trp* operon;
3. The promoter and operator overlap in the *lac* operon, while the promoter and operator of *trp* operon do not overlap;
4. *Trp* operon contains an **attenuator** sequence but this is **absent** in the *lac* operon;

Difference in control (max 2)

5. The **lac repressor** is synthesised in an active form and hence the lac operon is usually not expressed whereas the **trp repressor** is synthesised in an inactive form and the trp operon is usually expressed
   OR
   Inducer/(allo)lactose binds to lac **repressor** to **inactivate** it while the **corepressor/tryptophan binds** to trp **repressor** to **activate** it;

6. The **presence** of an **inducer molecule / (allo)lactose** will result in **expression of the *lac* operon**, but the ***trp* operon is expressed without the presence of an inducer molecule**;

7. The **presence of a corepressor / tryptophan** will result in ***trp* operon not being expressed**, whereas the **presence of glucose** will result in the ***lac* operon not being expressed**;
8. AVP (*Lac* operon has positive regulation while the *trp* operon does not / CAP vs no CAP)

*any **three** from:*

1 *trp* operon regulatory gene / *trpR*, codes for an inactive repressor
and
lac operon regulatory gene / *lacI*, codes for active repressor ;

2 *lac* operon does not have an attenuator ; **ora**

3 *lac* operon has fewer structural genes
or
3 vs 5 structural genes ;

4 *lac* operon uses, an inducer / (allo)lactose
and
trp operon uses, a repressor / tryptophan ;

5 (allo)lactose, binds / inactivates, repressor, so repressor, leaves / cannot bind to, **operator**
and
tryptophan, binds / activates, repressor, so repressor can bind to **operator** ;

6 (allo)lactose causes genes to be, transcribed / switched on / expressed
and
tryptophan causes genes to be **not**, transcribed / switched on / expressed ;

(g) Explain why structural genes in operons are transcribed together. [2]

1. The structural genes are **under the control of the same promoter**;
2. **Enzymes / products** coded by the structural genes are involved in the **same metabolic pathway**;
3. This will allow the bacteria to **respond quickly to environmental changes**; (R: minimise wastage)

either points 1+2 or 2+3

[Total: 15]

10 The global demand for meat is growing. Over the past 50 years, meat production has more than tripled. However, the production of meat has large environmental impacts.

Fig. 10.1 shows the mass of meat eaten from 1980 to 2010.

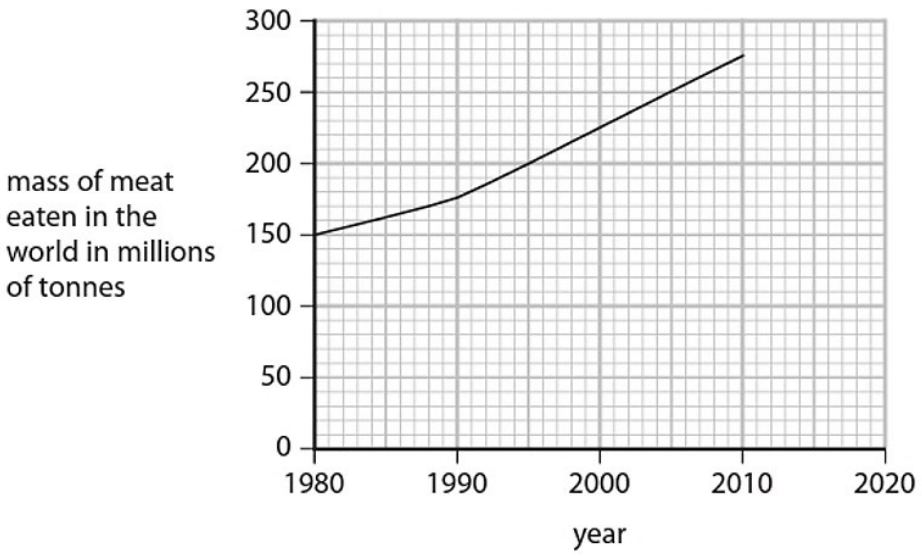


Fig. 11.1

(a) With reference to Fig. 10.1, calculate the rate of increase of the meat eaten in the world from 2000 to 2010. [1]

Rate of increase of meat eaten in the world from 2000 to 2010
= (275 -225) / 10
= 50/10
= 5 millions of tonnes per year

…… millions of tonnes per year

(b) Ruminant animals such as cows, buffaloes and sheep produce large amounts of methane when they digest food, adding to greenhouse gases in the environment.

Explain how increased meat production contributes to an increase in another greenhouse gas such as carbon dioxide in the environment. [2]

1. **Deforestation** to convert land into farmland to raise livestock;
2. **Carbon stored by trees** **released** into the atmosphere **as carbon dioxide** when trees are **burned** / **decomposition** of the remaining organic matter
   OR
   fewer trees to take in carbon dioxide from the environment;

   OR
3. **Increased burning of fossil fuels** for the production / transportation / handling of food/livestock;
4. **releases carbon dioxide** into the environment;

(c) Explain how a large increase in the mass of meat eaten will impact global food supply in the future. [2]

1. Global food supply will decrease / there will be less food for people to eat;
2. Farming livestock does not produce as much food per acre as growing crops
   OR

more land used for farming livestock / growing animal feed, means less land to grow crops for humans;

[Total: 5]