

JURONG JUNIOR COLLEGE
JC 2 PRELIMINARY EXAMINATIONS
Higher 1

CANDIDATE
NAME

CLASS

BIOLOGY

8875/02

Paper 2 Structured Questions

25 August 2017

Additional Materials: Answer Paper

2 hours

READ THESE INSTRUCTIONS FIRST

Write your name and class in the spaces at the top of this page.

Write in dark blue or black pen.

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

Do not use staples, paper clips, glue or correction fluid.

Section A

Answer **all** the questions.

Section B

Answer **one** question.

Circle the question number of the question attempted.

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

You may lose marks if you do not show your working or if you do not use appropriate units.

At the end of the examination, fasten all your work securely together.

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

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

This document consists of **15** printed pages.

[Turn over

Section A

Answer **all** the questions in this section.

- 1 White blood cells such as dendritic cells synthesise intracellular enzymes.

Fig. 1.1 is a summary diagram of events that occur in a dendritic cell.

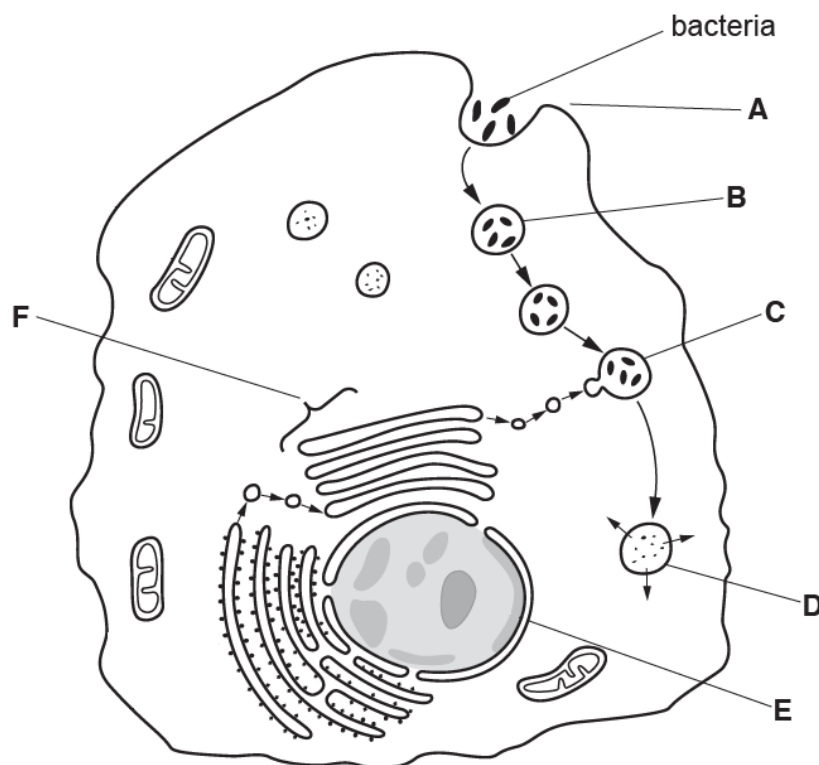


Fig. 1.1

- (a) (i) Name the process at A. [1]

1. **phagocytosis / endocytosis;;**
R pinocytosis / engulfing

- (ii) Name structures B, E and F. [3]

B: phagocytic / endocytic vacuole / phagosome;;

A vesicle

R incorrectly qualified vacuole or vesicle (e.g. large / secretory / Golgi / excretory)
(Ignore) food / pathogenic

E: (outer) nuclear envelope;;

F: Golgi body;;

(b) Describe what happens to the bacteria between C and D. [2]

1. the bacteria are destroyed / digested / broken down / hydrolysed;;
2. (by lysosomes containing) hydrolytic enzymes, e.g. carbohydrase, lysozymes, proteases, nucleases, lipases (*any one*);;
3. catalysed the breakage of glycosidic bond, peptide, ester, phosphodiester bond, ester bond in peptidoglycan, polysaccharide(s), polypeptides, nucleic acids, lipids;; (*bond broken must match substrate*) (*any one*)

(Ignore) fusion of lysosomes with phagosome and diffusion of products of digestion

(c) The gene coding for transcription factor in dendritic cells is known as *Batf3*. The transcription factor is essential for the development of dendritic cells.

(i) Explain what is meant by a *gene*. [1]

1. a specific sequence of nucleotides in the DNA which codes for a polypeptide;;

*A protein for polypeptide / information to produce a polypeptide / codes for sequence of amino acids / primary structure (of a, polypeptide / protein)
R genetic code for a polypeptide*

(ii) There are a number of known mutations for *Batf3*.

Outline how a mutation in *Batf3* can lead to the formation of an altered polypeptide where one amino acid is replaced by a different amino acid. [3]

1. Results in changes in the sequence of DNA nucleotides in the gene;;
2. This includes base-pair substitution / replacement of one nucleotide base pair with another base pair in a gene;;
3. result in a change in the codon in the mRNA;;
4. new amino acid coded for may have different property due to different R groups and result in a change in polypeptide sequence /primary structure;;

[Total: 10]

2 Fig. 2.1 shows some stages in mammalian respiration.

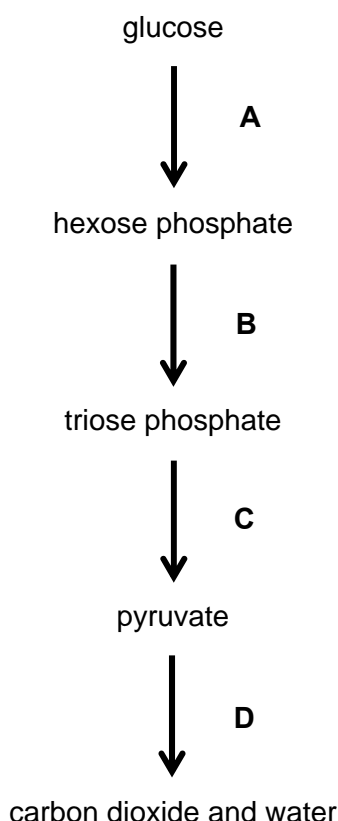


Fig. 2.1

(a) Name the processes taking place during Stage D and state precisely where they occur. [3]

1. **Link reaction – mitochondrial matrix;;**
2. **Krebs cycle – mitochondrial matrix;;**
3. **Oxidative phosphorylation – inner mitochondrial membrane;;**

(b) Intermediates produced at the end of Stages B and C are important in the conversion of carbohydrates to lipids such as triglycerides. Some of the triose phosphate can be converted into glycerol-3-phosphate, while pyruvate can undergo further reactions to form intermediates required for the synthesis of fatty acids.

Describe the formation of triglycerides. [3]

1. **A triglyceride is formed by condensation reactions between 1 glycerol and 3 fatty acids;;**
2. **Each of glycerol's hydroxyl/-OH groups condenses with the carboxyl/-COOH group of a fatty acid;;**
3. **In each condensation reaction, one water molecule is removed, resulting in the formation of an ester bond/linkage;;**

- (c) The first reaction in Stage A is catalysed by the enzyme hexokinase. It has been observed that hexokinase is bound to the outer mitochondrial membrane in muscle cells which undergo high rates of glycolysis.

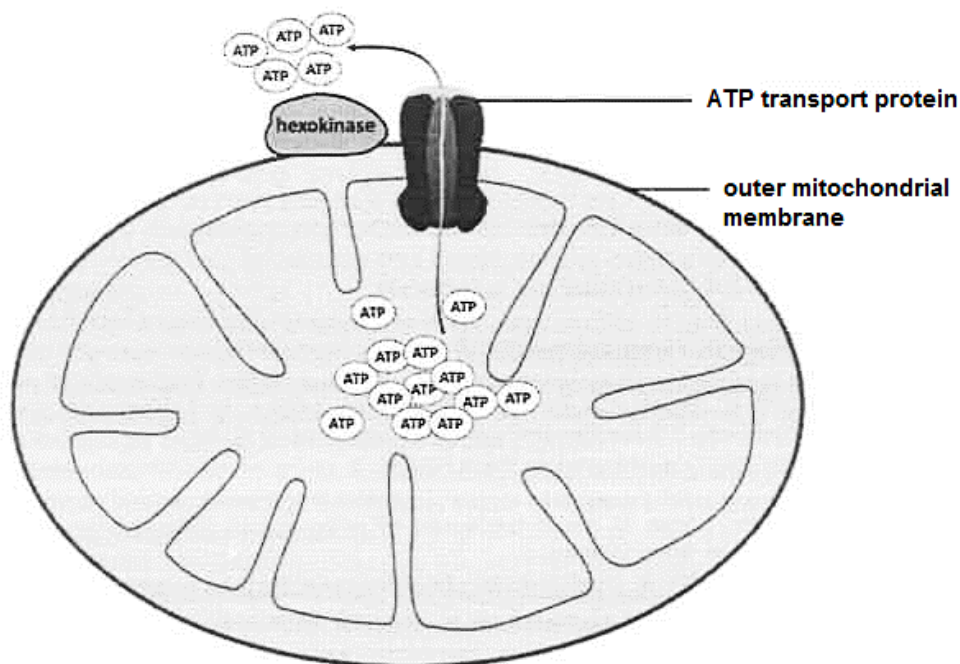


Fig. 2.2

With reference to the role of mitochondria and Fig. 2.2, suggest how the association of hexokinase with mitochondria can lead to high rates of glycolysis. [2]

1. Mitochondria are the site of aerobic respiration to synthesise ATP;;
2. Due to the close proximity of hexokinase to the mitochondria (*mark for idea*), ATP produced by the mitochondria can easily be used by hexokinase to phosphorylate glucose;; increasing the rate of glycolysis.

(d) Fig. 2.3 shows an electron micrograph of a mitochondrion.

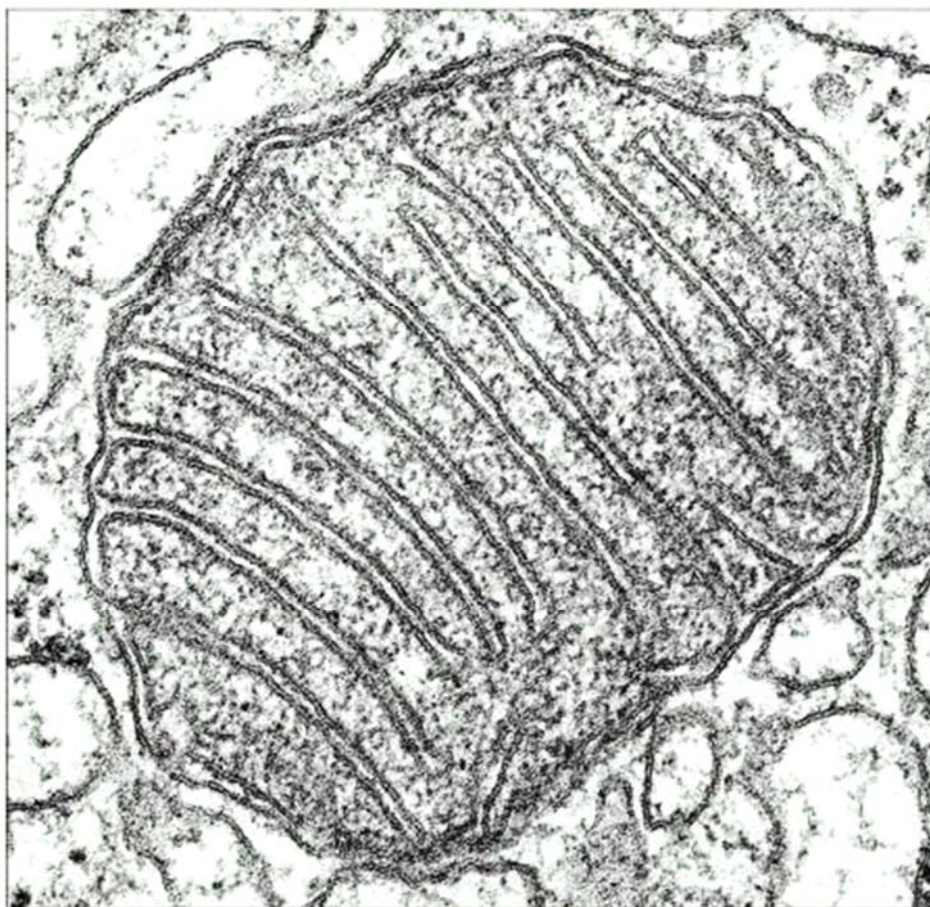


Fig. 2.3

With reference to features visible in Fig. 2.3, outline how the structure of the mitochondrion is adapted for its function. [1]

1. The inner mitochondrial membrane is highly folded, providing a large surface area where stalked particles, enzymes and electron carriers of the electron transport chain (ETC) (*any 1 e.g.*) needed for aerobic respiration can be located;;
2. The mitochondrion is enclosed by double membranes separated by (an extremely narrow fluid-filled space) intermembrane space, allowing for compartmentalisation within the mitochondrion / specialised metabolic pathways to take place in different areas;;

- (e) Phosphatidylcholine (a phospholipid) is present in membranes such as those of the mitochondrion. The molecular structures of tristearin (a triglyceride) and phosphatidylcholine are shown in Fig. 2.4.

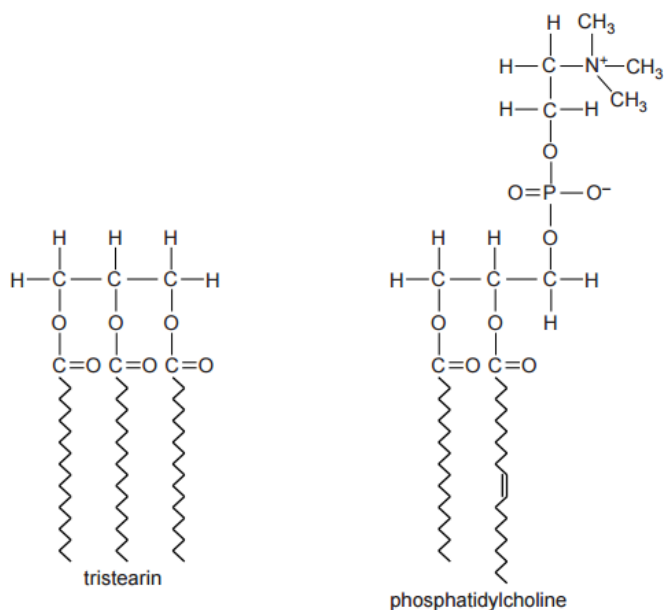


Fig. 2.4

State two structural differences between tristearin and phosphatidylcholine, other than in numbers of the different types of atoms. [2]

structural feature	triglyceride	phospholipid
phosphate (group)/contains phosphorus	×	✓
nitrogen	×	✓
charged/polar	×	✓
(number of) fatty acids	3	2
number of ester bonds	3	2
number of phosphate ester bonds	0	1
<i>award one mark for any of the following comparisons</i>		
number of double bonds (in hydrocarbon chain)	0	1
number of saturated fatty acids/ORA	3	1
presence of double bonds	×	✓
presence of unsaturated fatty acids	×	✓

These are alternatives – award one mark only

[Total: 11]

- 3 A type of pheasant occurs in a range of colours, especially when bred in captivity. It may, for example, have green or purple plumage as seen in Fig. 3.1.



Fig. 3.1

Sometimes when a green male is crossed with a green female all the offspring, male and female, are green. However, sometimes a green male crossed with a green female results in offspring in which the majority of the offspring are green, but in which some of the females are purple, as shown in Table 3.1.

Table 3.1

phenotype	number of offspring
green male	7
green female	3
purple female	4

Plumage colour in pheasants is sex-linked.

In birds, the sex chromosomes are referred to as W and Z, rather than Y and X as in mammals. The W chromosome has no genes that affect plumage colour. The heterogametic sex is the female, **not** the male. Thus the male has two Z chromosomes (ZZ) and the female has one W and one Z chromosome (WZ).

(a) Use a genetic diagram to explain the results in Table 3.1. [3]

Parental phenotypes:	green male	x	green female	
Parental genotypes:	$Z^G Z^g$	x	WZ^G	;;
Gametes	Z^G	Z^g	W	Z^G ;;

Punnett Square

	Z^G	Z^g
W	WZ^G	WZ^g
Z^G	$Z^G Z^G$	$Z^G Z^g$

Offspring genotype : $Z^G Z^G$: WZ^G : WZ^g ;
 $Z^G Z^g$

Offspring phenotype : green male : green female : purple female ;

Offspring phenotypic ratio: 2 : 1 : 1

(b) Using the same symbols as in (a), indicate the genotypes of the parents which could give rise to purple male offspring. [1]

1. $Z^G Z^g \times WZ^g$;;

OR

2. $Z^g Z^g \times WZ^g$;;

(c) Using the information provided, state which allele for plumage colour is dominant and explain your answer. [2]

1. *dominant allele* –

allele coding for green feather (carried on the Z chromosome);;

2. *explanation* –

Heterozygote male appeared green, thus showing the gene product of the allele coding for green feather masked the effect of the gene product expressed by the allele coding for purple feather;;

(d) Describe how you would determine the unknown genotype of a green male. [2]

1. **Carry out a test cross by breeding with a purple female;;**

2. **If all the offspring have green plumage then the male must be homozygous dominant;;**

OR

3. **If some of the offspring have purple plumage then the male must be heterozygous;;**

[Total: 8]

- 4 Human growth hormone (hGH) is a peptide hormone that is important for human development. Recombinant hGH can be synthesised via genetic engineering with the use of plasmids.

(a) (i) State the type of organism that contains plasmids. [1]

1. **Bacterium/prokaryotes;;**

(ii) Describe one feature of plasmids that make them suitable to be used for genetic engineering. [2]

1. **contain an origin of replication;;**
2. **so that the vector and the inserted gene of interest can replicate independently of the bacteria chromosome to produce multiple copies within the host cell;;**
OR
3. **contain genetic/selectable markers;;**
4. **e.g. antibiotic resistant genes that confer resistance of the host cell to antibiotics / lacZ gene coding for β -galactosidase which enable selection;;**
OR
5. **possess restriction sites;;**
6. **which can be recognised, bound and cut by restriction enzymes for insertion of gene of interest;;**

The polymerase chain reaction (PCR) can be used to amplify the gene coding for hGH before genetic engineering is carried out.

(b) Describe what occurs during the first two stages in PCR.

(i) Stage 1 [2]

1. **Denaturation by heating to 95°C;; (A) 90-100°C**
2. **Hydrogen bonds between (complementary bases of) double-stranded DNA break, separating the double-stranded DNA into single-stranded DNA;;**

(ii) Stage 2 [2]

1. **Annealing of DNA primers by cooling to 65°C;; (A) 30-65°C**
2. **Primers base pair via complementary base pairing with (complementary sequences at the) 3' end of the single-stranded DNA;;**

(c) Outline how a recombinant plasmid can be produced for genetic engineering after the gene coding for hGH was isolated from human cells and amplified using PCR. [3]

1. **Same restriction enzyme was used to recognise, bind and cut the gene coding for hGH and plasmid;;**
2. **to produce restriction fragments with complementary sticky ends that would anneal/complementary base pair via hydrogen bond formation;;**
3. **DNA ligase would then seal the nicks between fragments by formation of phosphodiester bonds between adjacent nucleotides, forming a recombinant plasmid;;**

- (d) With the advancement in technology, plasmid-free bacteria cells have been constructed for the production of hGH with the gene coding for hGH inserted directly into the host chromosome instead of using plasmid.

Suggest how this new method is an improvement over the previous method. [1]

1. **No need for antibiotic selection / lower costs as no antibiotics needed/no need to remove the antibiotics used for selection;;**
2. **Less metabolic burden on host strain;;**
3. **Genes are more stable;;**

[Total: 11]

Section B

Answer **one** question.

Write your answers on the separate answer paper provided.

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

Your answers must be in continuous prose, where appropriate.

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

- 4** Early ancestors of today's horses were browsers. Their teeth were adapted for eating woody shrubs and trees. In the early Miocene (23 million years ago), the first groups adapted for grazing emerged. Modern horses are grazers, with teeth adapted for grinding tougher, grassy materials.

The foot structure evolved from four separate toes to three, then to only one that touched the ground with two smaller side toes higher than the ground. In more modern horses, the two side bones are fused together. Modern horses are of much greater size than their ancestors.

(a) Describe the causes of variation in horses.

[6]

Causes of variation

1. Gene mutations and chromosomal aberrations;;

OR

2. Gene mutations + one example e.g. base pair substitution / insertion / deletion;;

3. Chromosomal aberrations + one example e.g. duplication / translocation;;

4. Independent assortment and segregation of chromosomes in meiosis;;

OR

5. Independent assortment and segregation of homologous chromosomes during metaphase I and anaphase I, respectively;;

6. Independent assortment and segregation of chromatids during metaphase II and anaphase II, respectively;;

7. Crossing over between non-sister chromatids of homologous chromosomes during prophase I in meiosis I;;

8. Give new combination of alleles;;

9. Random fusion of gametes during sexual reproduction;;

(b) Explain how natural selection could lead to evolution of modern horses with distinct phenotypic differences. [6]

1. Spontaneous mutation results in genetic variation in horses within a population;;
2. There were phenotypic variation / difference in characteristics in the populations in each habitat e.g. teeth / foot structure;;
3. The horses were exposed to different environments in each habitat and were subjected to different selection pressures;;
4. Examples of phenotypic variation e.g. teeth / foot structure OR different selection pressures e.g. type of foot and ground type / habitat;;
5. Since there was variation within the populations, individuals who are better adapted to the environment / with favourable characteristics will be at a selective advantage;;
6. These individuals will survive to maturity, reproduce and pass down their favourable alleles to their offspring;;
7. With each succeeding generation, the proportion of individuals having the favourable characteristics increases while the proportion of individuals lacking the characteristics decreases;;
8. Over time / successive generations, there is a change in allele frequency in the populations, leading to evolution and thus distinct phenotypic differences between the populations of horses;;
9. Diverse forms of horses have thus arisen by descent with modifications from ancestral species by accumulation of modifications as the population of horses adapt to the new environment;;

(c) Explain, with examples, what is meant by anatomical and molecular homologies in horses. [8]

1. Diverse forms of horses have thus arisen by descent with modifications from ancestral species by accumulation of modifications as the population of horses adapt to the new environment;;

OR

2. Homologies show “descent with modification + Comparisons of homologies between species show how an ancestral homology in a population may have been modified in descendent species through natural selection and changes in allele frequency;;

3. Homology is similarity in characteristics resulting from common ancestry;;

4. and developed as a result of natural selection and changes in allele frequency;;

5. Homologies suggest common ancestry + Similarity in anatomical / molecular homology between species suggests that they are descended from a common ancestor which had a basic form of the structure / homologous genes;;

6. Species with common ancestors should display underlying similarities even in features that no longer match in function;;

7. Species with a higher level of similarity diverged from a common ancestor more recently (than species with a lower level of similarity) and thus are more closely related;;

8. Organisms with anatomical homologies have physical structures that are derived from a common ancestor;;

9. E.g. teeth, foot structure in horses, with different forms in different species;;

10. Organisms with molecular homology have similar DNA nucleotide / amino acid sequences of homologous genes that are derived from a common ancestor;;

11. Examples of homologous genes in different horses are the haemoglobin genes and the cytochrome oxidase genes which are derived from a common ancestor;;

Pt 8-11 are required.

12. Homologies provide the basis of comparison + Comparison of molecular homologies between species by comparing homologous DNA nucleotides/amino acid sequence OR Comparison of homologous traits/structures/teeth/foot structure between species (as they are derived from a common ancestor) shows the modification process from a basic ancestral form;;

[Total: 20]

- 5** Invertase, a major enzyme present in plant tissues such as the developing roots of carrots, catalyses the hydrolysis of sucrose (a non-reducing sugar) to fructose and glucose (reducing sugars).

A scientist carried out an investigation into the effect of pH on the activity of invertase in carrots, by recording the time taken for the reducing sugars to change the colour of pink potassium manganate (VII) solution to a colourless end point. From the results obtained, the scientist concluded that the optimum pH of invertase was pH 5.0.

After additional analyses, the scientist also found that the invertase is:

- made up of several subunits
- synthesised with a signal peptide required for entry into the rough endoplasmic reticulum and thus into the secretory pathway
- glycosylated and bound to the cell wall

(a) Describe how invertase can be synthesised from mRNA. [8]

Amino acid activation [max 1m]

- 1. A specific amino acid is joined to the 3' end of a tRNA, forming an amino acyl-tRNA, reaction catalysed by a specific aminoacyl-tRNA synthetase;;**
- 2. The amino acid that the tRNA attaches to is determined by the specific anticodon of the tRNA (which is complementary to the mRNA codon);;**

Initiation

- 3. A small ribosomal subunit recognises and binds to the 5' end of the mRNA and travels along the mRNA until it reaches the first AUG codon that serves as the start codon;;**
- 4. An initiator tRNA carrying the amino acid methionine (Met), with anticodon UAC, binds to the start codon AUG on the mRNA (via complementary base pairing);;**
- 5. The union of mRNA, initiator tRNA and a small ribosomal subunit is followed by the attachment of large ribosomal subunit, completing a translation initiation complex;;**
- 6. Initiation factors and GTP are required to bring all these components together;;**
- 7. At the completion of the initiation process, the initiator tRNA fits into the P site of the large ribosomal subunit and the vacant A site is ready for the next aminoacyl tRNA;;**

Elongation

8. The anticodon of the next incoming aminoacyl-tRNA, carrying its specific amino acid, undergoes complementary base pairing and forms hydrogen bonds with the mRNA codon in the A site of the ribosome;;
9. A peptide bond is formed between the amino end of the amino acid in the A site and the carboxyl end of the growing chain in the P site, catalysed by peptidyl transferase;;
10. After the peptide bond has been formed, the ribosome translocates one codon downstream along the mRNA in a 5' to 3' direction;;
11. This moves the tRNA, carrying the growing polypeptide in the A site, to the P site and the tRNA in the P site now moves to the E site and leaves the ribosome and A site is free to receive the next aminoacyl-tRNA;;

Termination

12. Elongation continues until a stop codon, UAA, UAG or UGA reaches the A site of the ribosome;;
13. A protein release factor recognises and binds to the stop codon on the mRNA, causes the addition of a water molecule to the polypeptide chain;;
14. This reaction hydrolyses the completed polypeptide from the tRNA that is in the P site, freeing the polypeptide from the ribosome;;
15. remainder of translational complex then comes apart / are disassembled;;

(pt 3-15: must have at least 1 pt from each stage of translation for full credit)

Extra points

16. (Each) polypeptide chain/subunit may undergo folding into a specific shape due to formation of hydrophobic interactions, disulfide bonds, ionic bonds and hydrogen bonds between (R groups of) amino acids;;
17. and aggregate with other polypeptide chains/subunits to form a functional protein, invertase;;

- (b) Outline structural features and roles of the rough endoplasmic reticulum. [4]

Structure of rER

1. consists of a network of sheets (called cisternae);;
2. ribosomes are present / bound / attached to the membrane of the rough ER;;

Roles of rER

3. Site of protein/invertase synthesis – (the polypeptides of) invertase are synthesised by ribosomes attached to the rough ER;;
 4. Biochemical/Chemical modification – the polypeptides/invertase is transported through the pore in the ER membrane into the ER lumen, where carbohydrate chains are added to them – glycosylation;;
 5. Intracellular transport – the rough ER forms part of the intracellular transport system which transports the synthesised/modified (polypeptides of) invertase to other compartments within the cell by transport vesicles budding off from the ER membrane;;
- (c) Describe the investigation carried out by the scientist to examine the effect of pH on the activity of invertase in carrots. [8]

Variables

1. The independent variable of the experiment would be pH;;
2. The dependent variable would be the rate of reaction, measured by the time taken for the reducing sugars to change the colour of pink potassium manganite (VII) solution to a colourless end point;;

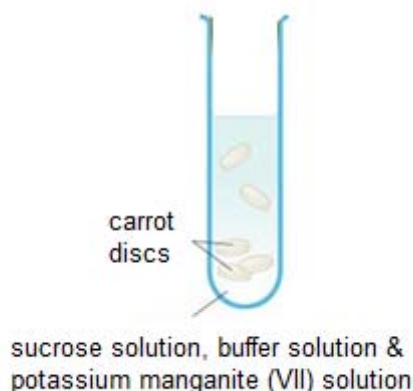
Variables to be kept constant [max 2m]

3. Volume and concentration of invertase
Carrot discs/cubes of identical sizes were cut from a single carrot and 5 discs/slices were added to a boiling tube;;
OR
Invertase is obtained by blending a single carrot to obtain a homogenous liquid carrot solution to ensure that the concentration of invertase is constant throughout the solution. 5 cm³ of invertase solution was placed in the boiling tube;;
4. Volume and concentration of sucrose solution
Equal volumes of sucrose solution (of a fixed concentration) to be placed in the boiling tube, e.g. 5 cm³ of (10.0%) sucrose solution was placed in the boiling tube;;
5. Temperature – enzyme activity is affected by temperature
Temperature of experiment must be kept constant at 35°C by placing boiling tubes in a thermostatically controlled water bath;;
OR
The experiment was carried out at room temperature of 26°C, which is assumed to remain constant throughout the experiment;;

(pt 3-5: award 1m for stating 2 variables to keep constant; 1m for describing how variables are to be kept constant)

Procedure

6. Set up the apparatus as shown (fully labelled diagram);;



OR

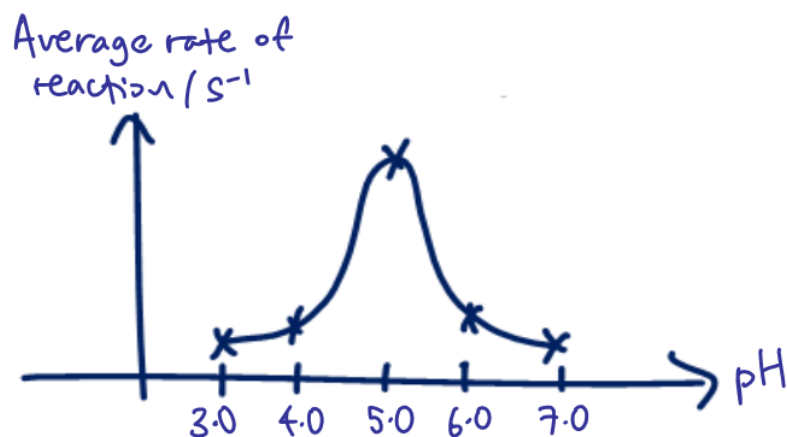
7. Add 5 carrot discs/cubes containing invertase / Add (5 cm³ of) invertase solution to the boiling tube containing (5 cm³ of) sucrose solution, (5 cm³ of) potassium manganite (VII) solution and (5 cm³ of) pH 3.0 buffer solution;;
8. The buffer solution helps to keep the pH constant at pH 3.0;;
9. Using a stopwatch, start timing and measure the time taken for the reducing sugars to change the colour of pink potassium manganite (VII) solution to a colourless end point;;
10. Repeat twice to get a total of 3 readings;;
11. Repeat steps 6 to 10 using different buffers at pH 4.0, pH 5.0, pH 6.0 and pH 7.0;;
12. Calculate the average rate of reaction (1 / average time taken for the reducing sugars to change the colour of pink potassium manganite (VII) solution to a colourless end point) and record these data in a table;;

13. Table of results

pH	Time taken for the reducing sugars to change the colour of pink potassium manganite (VII) solution to a colourless end point / s				Average rate of reaction / s ⁻¹
	Reading 1	Reading 2	Reading 3	Average Reading	
3.0					
4.0					
5.0					
6.0					
7.0					

Graph

14. Plot a graph of average rate of reaction against pH using the data in the table;;



Safety issues

15. As the buffers used are corrosive, wear gloves / protective goggles when handling the buffer solutions to prevent contact with skin / eyes;;
16. As the scalpel is sharp / glassware is fragile, handle them carefully / place them away from the main work area after use;;

[Total: 20]