Surname	StemUp Model Solution	Centre Number	Candidate Number
First name(s)			2

GCE AS

B400U10-1

O20-B400U10-1

MONDAY, 12 OCTOBER 2020 – MORNING

BIOLOGY – AS component 1
Basic Biochemistry and Cell Organisation

1 hour 30 minutes

For Examiner's use only		
Question	**Maximum Mark**	**Mark Awarded**
1.	**12**	
2.	**13**	
3.	**18**	
4.	**10**	
5.	**13**	
6.	**9**	
Total	**75**	

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01

ADDITIONAL MATERIALS

In addition to this paper you will require a calculator and a ruler.

INSTRUCTIONS TO CANDIDATES

Use black ink or black ball-point pen.

Write your name, centre number and candidate number in the spaces at the top of this page.

Answer **all** questions.

Write your answers in the spaces provided in this booklet. If you run out of space, use the continuation page(s) at the back of the booklet, taking care to number the question(s) correctly.

INFORMATION FOR CANDIDATES

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

The assessment of quality of extended response (QER) will take place in question **6**.

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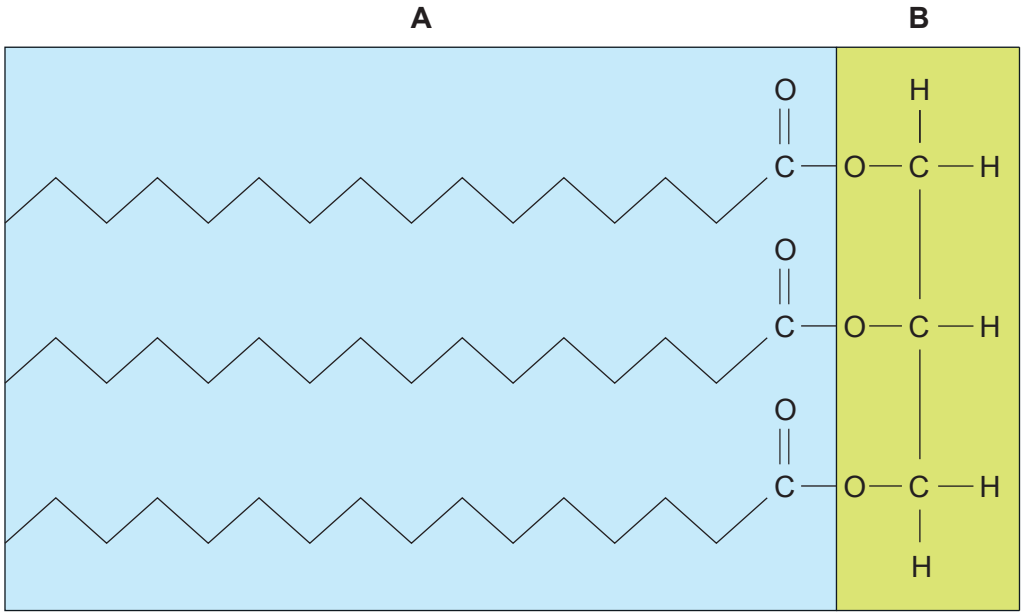
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Answer **all** *questions.*

1. Triglycerides are a class of lipids which are used for long term energy storage and thermal insulation, particularly in mammals and birds. **Image 1.1** shows the structure of a molecule of triglyceride found in a mammal.

Image 1.1



(a) (i) Name the bonds in the triglyceride molecule which are hydrolysed by lipase enzymes. [1]

Ester bonds

(ii) Following hydrolysis of these bonds, name the molecule that would be formed from portion **B** of the molecule in the diagram. [1]

Glycerol

(iii) Explain why it would be incorrect to refer to a triglyceride as a polymer. [1]

A polymer is a long chain of many repeating identical monomers; a triglyceride is one glycerol joined to three fatty acids, so it is not a chain.

(iv) Describe a test which could be performed to detect the presence of triglyceride in a sample. [2]

Emulsion test: shake the sample with ethanol (to dissolve the lipid), then pour the mixture into water.

If triglyceride is present a milky white emulsion forms.

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(v) Identify the specific **type** of molecule shown in portion **A** of **image 1.1**. Explain your answer. [2]

Saturated fatty acids.

There are no C=C double bonds, so the hydrocarbon chains are straight.

(vi) Explain why a diet high in this **type** of molecule could increase the risk of heart disease. [2]

Saturated fats increase the level of LDL cholesterol in the blood.

This increases atheroma (plaque) formation in the coronary arteries (atherosclerosis), which narrows them and reduces the blood supply to the heart muscle.

Many seeds contain large amounts of lipid as a proportion of their mass.

During germination the new plant uses the food reserves within the seed to provide it with the energy it requires for growth. This food reserve is composed mainly of carbohydrate in the form of starch and lipid in the form of triglycerides. **Table 1.2** shows the energy made available to the germinating plant when lipids and carbohydrates are respired.

Table 1.2

Molecule metabolised	Oxygen consumption ($dm^3\ g^{-1}$)	Energy released ($kJ\,g^{-1}$)
Triglyceride	1.96	38
Carbohydrate	0.81	17

(b) With reference to the data in **table 1.2** explain the advantage to plants of using lipid as a food reserve in their seeds as opposed to carbohydrate. [3]

Lipid releases more energy per gram than carbohydrate: 38 kJ g^{-1} compared with 17 kJ g^{-1}, more than twice as much.

So a smaller, lighter food store is needed in the seed to provide the same energy, and the seeds are lighter (easier to disperse).

More energy is available, so the plant can germinate and grow more quickly.

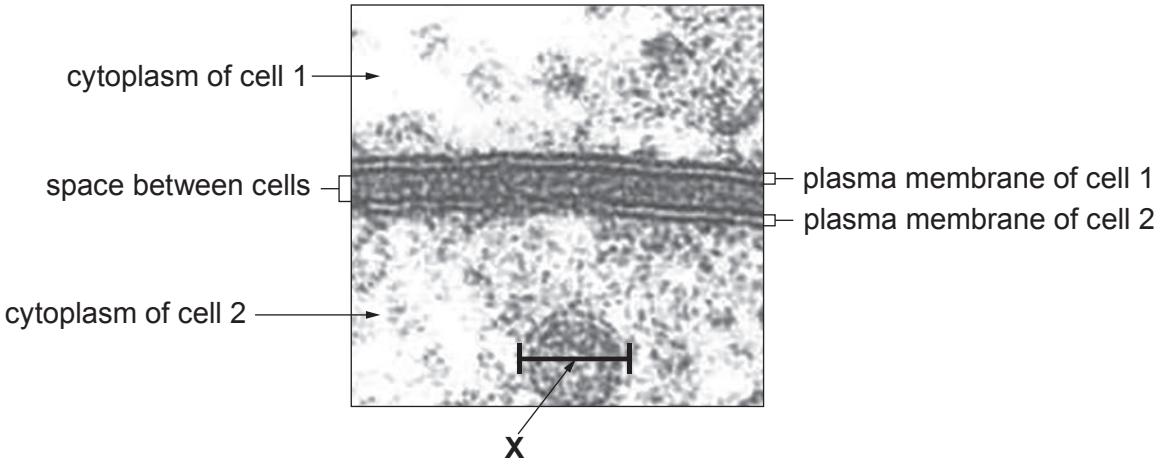
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2. **Image 2.1** is an electron micrograph which shows the plasma membranes of two adjacent cells. A stain was used to make the membranes visible with the electron microscope. The stain binds to negatively charged molecules, making the membranes appear as pairs of parallel dark lines.

Image 2.1



(a) (i) Name the currently accepted model used to describe the structure of the plasma membrane. [1]

Fluid mosaic model

(ii) Explain the distribution of the staining of the membranes in **image 2.1**. [3]

The stain binds to the phosphate heads, as they are hydrophilic and negatively charged, so each membrane shows two dark lines.

It cannot bind to (is repelled by) the hydrophobic, non-polar fatty acid tails in the centre.

(iii) The structure labelled **X** is a secretory vesicle. The magnification of the micrograph is ×34 000. Calculate the actual diameter of the secretory vesicle.
Express your answer to the nearest whole nm. [3]

Diameter on image = 15 mm = 15×10^6 nm

actual diameter = image size ÷ magnification

= $15 \times 10^6 \div 34\,000 = 441.18$ nm

Diameter = 441 nm

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(b) Many single celled organisms, such as yeast, feed by using secretory vesicles to secrete digestive enzymes onto their food. The food is digested extra-cellularly and the products of digestion are absorbed into the cell.

(i) Name the mode of nutrition seen in yeast. [1]

Saprotrophic (saprobiontic) nutrition

(ii) Describe how the secretory vesicles are produced and how the digestive enzymes are then secreted from the cell. [3]

The enzymes are made on ribosomes on the rough ER and transported in vesicles to the Golgi apparatus (Golgi body).

The Golgi apparatus modifies the enzymes and packages them into secretory vesicles, which bud off.

The vesicles move to the cell surface membrane and fuse with it, releasing their contents outside the cell by exocytosis.

(iii) Suggest why enzyme-secreting cells are observed to contain large numbers of mitochondria. [2]

Mitochondria carry out aerobic respiration to produce large amounts of ATP.

The ATP is needed for protein synthesis (making the enzymes) and for exocytosis (moving and fusing the vesicles).

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3. Some bacteria produce a protease which breaks down milk protein. When the enzyme is added to milk the milk gradually becomes clear as the protein in milk is broken down.
A student investigated the effect of temperature on this protease using the following method.

- Set up five water baths in beakers using ice, hot and cold water at the following approximate temperatures; 10 °C, 20 °C, 30 °C, 40 °C, 50 °C.
- Record the actual temperature of the water baths.
- Add 10 cm^3 of milk to one test tube.
- Add 1 cm^3 of protease at pH 7 to a separate test tube.
- Place both test tubes in the first water bath for five minutes.
- Pour the milk into the protease.
- Record the time taken for the milk to become clear.
- Repeat for the other temperatures.

The results the student obtained are shown in **table 3.1**.

Table 3.1

Actual temperature of water bath / °C	Time taken for the milk to become clear / seconds			
	Trial 1	Trial 2	Trial 3	Mean
8	56	49	54	53
18	31	34	28	31
32	28	34	27	30
42	21	17	21	20
54	45	36	34	38

(a) (i) State **two** *other* variables that should have been controlled during this investigation. [2]

Concentration (volume) of the protease

Type and concentration of the milk (protein)

(ii) Identify **two** sources of inaccuracy in this experimental method **and** describe how accuracy could be improved in each case. [4]

1. The water baths (beakers of ice, hot and cold water) cannot maintain a constant temperature; the temperature changes during the experiment.

Improve by using thermostatically controlled (constant temperature) water baths.

2. It is difficult to judge exactly when the milk has become clear (subjective end point).

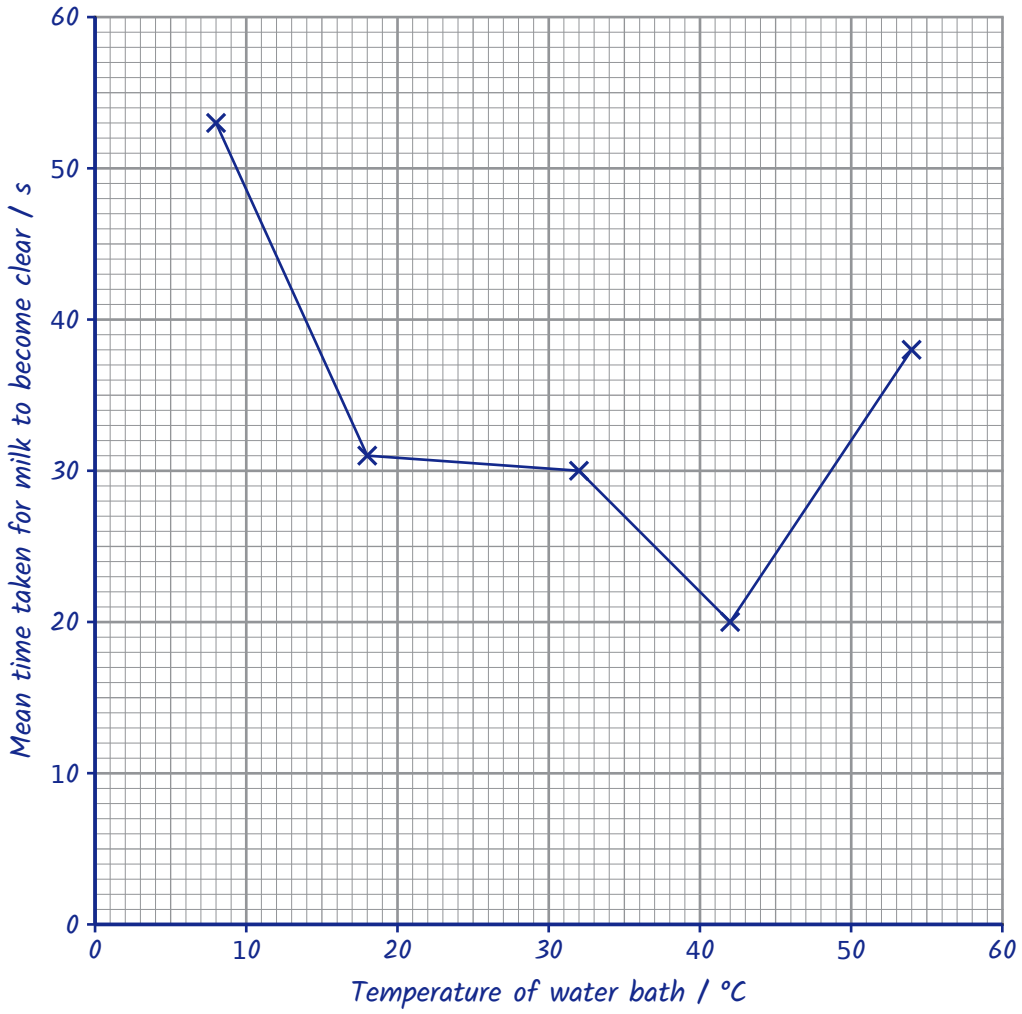
Improve by using a colorimeter to determine when the milk has become clear (a set absorbance), or compare with a colour standard.

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(b) (i) Plot the mean results of the investigation on the graph paper provided. [4]



(ii) Describe and explain the results of the experiment. [4]

The mean time taken for the milk to become clear decreases from 53 s at 8 °C to a minimum of 20 s at 42 °C, then increases to 38 s at 54 °C.

As temperature rises, molecules gain kinetic energy, so there are more successful collisions and more enzyme-substrate complexes form.

The optimum temperature is about 42 °C. Above it the enzyme denatures: hydrogen bonds break and the active site changes shape, so fewer complexes form.

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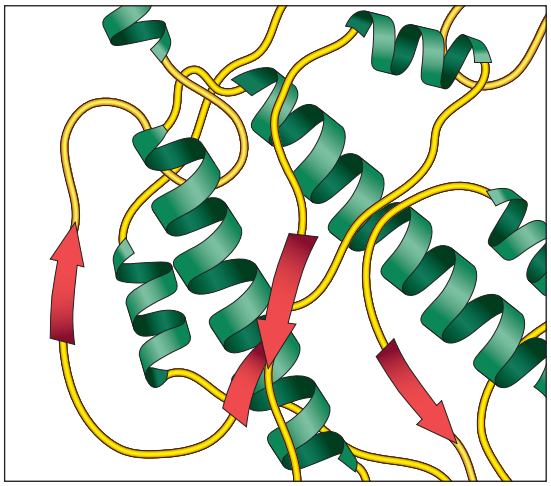
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(c) **Image 3.2** shows part of the structure of the protease used in the experiment on page 6.

Image 3.2



(i) State the highest level of protein structure shown in **image 3.2** and identify the bonds that maintain the structure. [2]

Tertiary structure.

Maintained by hydrogen bonds, ionic bonds and disulphide bonds (and hydrophobic interactions).

(ii) Explain how the shape of the molecule is related to its function. [2]

It is a globular protein with a specific 3D shape, so it has a specifically shaped active site.

The active site is complementary to the substrate (milk protein), so the substrate can bind and form an enzyme-substrate complex.

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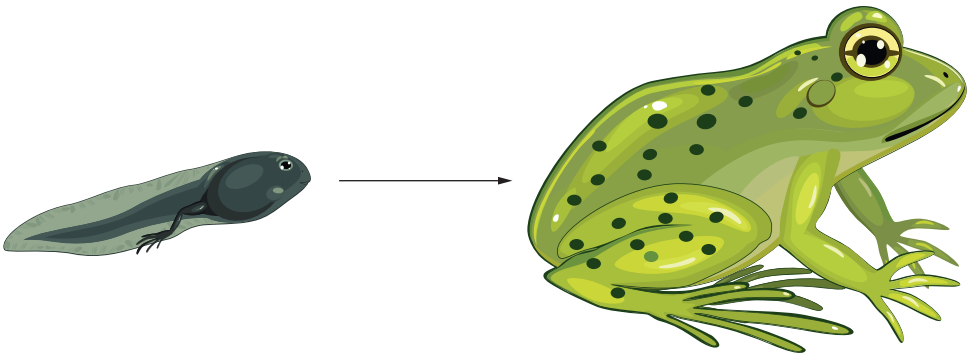
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4. Programmed cell death, also known as **apoptosis**, is an important part of embryonic development. For example, in tadpoles, the cells of the tail undergo apoptosis as the tadpole develops into an adult frog. This is shown in **image 4.1**.

Image 4.1



During apoptosis, the cells in the tail break down into fragments surrounded by membranes. These membranes have signal molecules which are recognised by the tadpole's white blood cells. The cell fragments are then engulfed and destroyed.

(a) (i) Suggest the class of biological molecules to which the signal molecules belong. [1]

Protein (glycoprotein)

(ii) Name the process by which white blood cells engulf and destroy the cell fragments. [1]

Phagocytosis

(b) During apoptosis enzymes hydrolyse the cell's DNA into different lengths. The length of DNA molecules is measured in base pairs (bp).

(i) Name the complementary base pairs found in DNA and state the bond that joins them. [2]

Adenine with thymine and cytosine with guanine; joined by hydrogen bonds.

(ii) Each complete 360° turn of the double helix of DNA is 34 nm long and contains 10 base pairs. The length of a DNA fragment is 6800 nm.
Calculate the number of base pairs in this fragment. [2]

number of turns = 6800 ÷ 34 = 200

base pairs = 6800 × 10 ÷ 34 = 2000

Number of base pairs = 2000 bp

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(iii) With reference to the hydrolysis of DNA, explain why the process of apoptosis would prevent the formation of functional proteins. [4]

Hydrolysis cuts the DNA into fragments, which may disrupt (break up) genes.

Therefore the genes cannot be transcribed, so no mRNA (or a different mRNA) is produced.

So there is no translation, or a different polypeptide is produced, and the proteins made are non-functional (have a different function).

Also the cell fragments may not contain ribosomes or Golgi bodies, which are needed to make and modify proteins.

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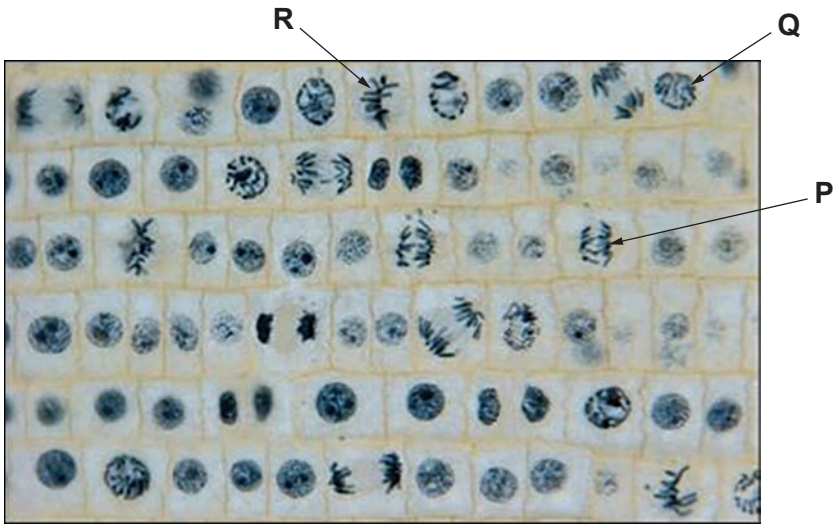
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5. **Image 5.1** shows a section of onion root tip with cells at various stages in the cell cycle.

Image 5.1



(a) (i) Identify the stages of the cell cycle shown by: [1]

P Anaphase

Q Prophase

R Metaphase

(ii) Explain why the slide shown in **image 5.1** was prepared using tissue from a **root tip**. [2]

The root tip is a growing region of the plant containing meristem tissue. Many cells are undergoing mitosis (a high rate of mitosis), so many stages of the cell cycle can be seen.

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A student counted the number of cells in each stage of the cell cycle in a section of plant tissue similar to the one shown in **image 5.1**. The results obtained are shown in **table 5.2**.

Table 5.2

Stage of cell cycle	Number of cells in each stage	Percentage cells in each stage
Q	24	21.2
R	8	7.1
P	6	5.3
S	7	6.2
T	68	60.2

(b) With reference to the data in **table 5.2**, identify which stage of the cell cycle is represented by the letter **T** in the table. Explain your answer. [2]

Interphase.

There are more cells in T (68 cells, 60.2%) than in any other stage, so this is the longest stage in the cell cycle.

A group of herbicides (weedkiller) known as the dinitroaniline herbicides were once used commonly to control weeds. Dinitroaniline works by inhibiting the formation of the spindle microtubules during cell division.

(c) (i) Identify which stage of mitosis would be affected by dinitroaniline. Explain your answer. [2]

Metaphase.

The spindle microtubules cannot form, so the chromosomes cannot attach to the spindle and align on the equator.

(ii) Suggest how the herbicide would affect the growth of a plant. [2]

It prevents cell division (mitosis), so the growing regions (root and shoot tips) are most affected.

The plant cannot grow, so it stays small and underdeveloped.

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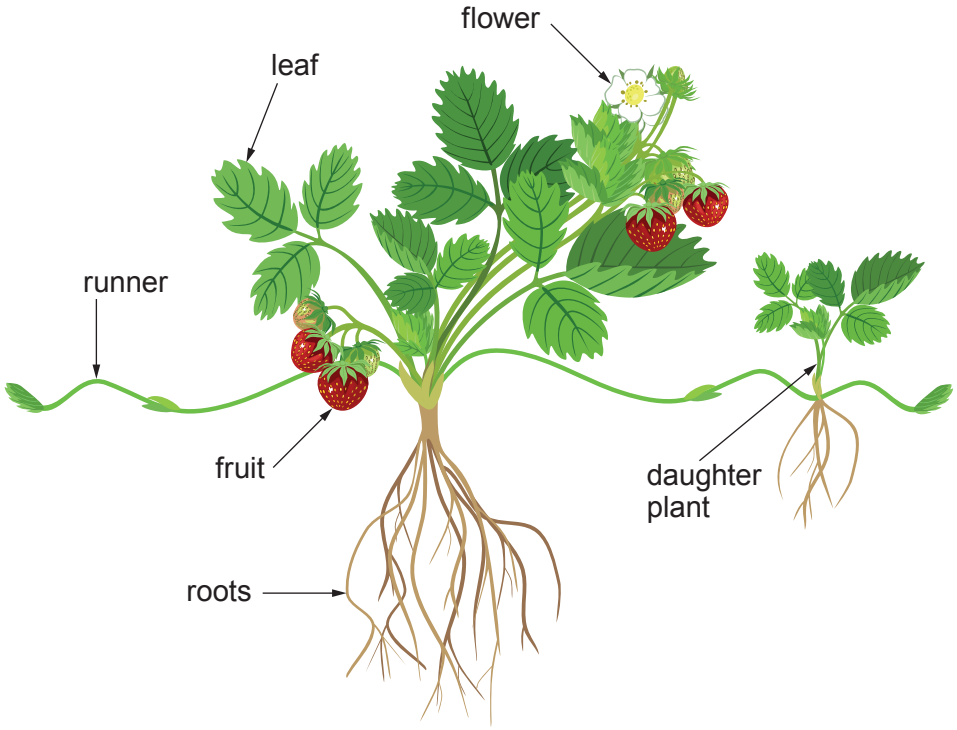
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Image 5.3 shows two methods by which strawberry plants reproduce.

- Strawberry plants can reproduce using seeds.
- Another method involves a runner growing out from the parent plant and when it touches the soil a new daughter plant will grow. In this type of reproduction the daughter plants are produced entirely through mitosis.

Image 5.3



(d) The cells in the runner of the parent plant contain 8 sets of chromosomes giving a total number of 56.

(i) State how many chromosomes there would be in a root cell in the daughter plant. [1]

56

(ii) When growing plants for commercial strawberry crops, growers prefer to use runners rather than seeds to produce new plants. Explain why it is an advantage to produce new plants in this way rather than using seeds. [3]

Using mitosis, the daughter plant is genetically identical to the parent plant (a clone).

Seeds are produced by meiosis (and fertilisation), which results in increased genetic variation.

With runners favourable genes are passed on, so desirable characteristics (e.g. large fruit) are retained; production is also faster.

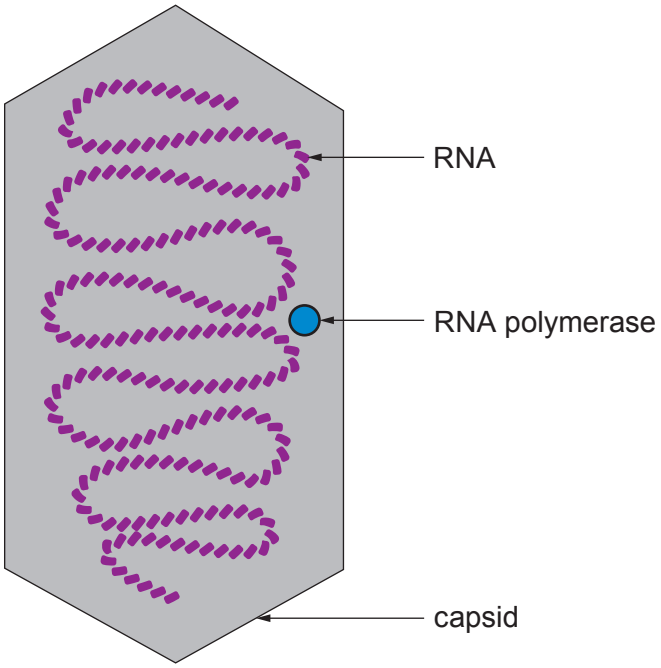
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6. Viruses cause infections in many mammals including humans. The basic structure of a virus is shown in **image 6.1**.

Image 6.1



The virus must enter a host cell in order to reproduce. Once inside, the viral RNA is replicated using viral RNA polymerase enzyme. Viral RNA then acts as a code to synthesise the capsid protein using the host cell's organelles.

Compare the structure of the virus shown in **image 6.1** with the structure of a human cell. Describe and explain how the viral RNA is replicated and then used to make viral protein molecules. [9 QER]

Structure: a human cell's genetic material is DNA, whereas this virus has only RNA. The human DNA is organised into chromosomes (linear DNA with histone proteins) inside a nucleus surrounded by a nuclear envelope; the virus has no chromosomes and no nucleus, its single RNA molecule lies free inside the capsid.

A human cell is surrounded by a cell (plasma) membrane made of a phospholipid bilayer; the virus has no membrane but a protein coat called a capsid.

A human cell has cytoplasm and organelles such as mitochondria, ribosomes, Golgi apparatus and rough and smooth ER; the virus has no cytoplasm and no organelles, only one enzyme, RNA polymerase. This is why the virus cannot reproduce on its own and must use a host cell.

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Replication: once the virus has entered the host cell, the RNA is released from the capsid into the cytoplasm. The viral RNA polymerase enzyme 'reads' the base sequence of the viral RNA, which acts as a template. Free RNA nucleotides in the cytoplasm pair up with the exposed bases on the viral RNA by complementary base pairing: C pairs with G and U pairs with A. RNA polymerase catalyses the formation of phosphodiester bonds between adjacent nucleotides (condensation reactions), forming a new RNA molecule. This complementary copy can itself be used as a template, so many copies of the original viral RNA are made.

Protein synthesis: the replicated viral RNA acts like mRNA and attaches to a ribosome in the host cell (on the rough ER). The ribosome moves along the RNA reading the codons (triplets of bases). Each tRNA molecule carries a specific amino acid and has an anticodon; tRNAs match their anticodons to the complementary codons on the viral RNA by complementary base pairing, bringing the amino acids to the ribosome in the correct sequence. Adjacent amino acids are joined by peptide bonds in condensation reactions, forming a polypeptide chain, which folds into the capsid protein.

Other host organelles are needed: mitochondria provide ATP for amino acid activation and protein synthesis, the rough ER transports the proteins and the Golgi apparatus modifies and packages them. The new capsid proteins then assemble around the new copies of viral RNA (with RNA polymerase) to form new virus particles, which are released from the host cell.

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