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VCE Biology ¾
Proteins, Protein Export & Enzymes [0.5]
Workshop Solutions

Section A: Multiple Choice Questions (21 Marks)

Question 1 (1 mark)

Following translation, the insulin peptide is activated when an enzyme cuts a linking peptide chain that connects insulin's A-chain to its B-chain. This suggests that insulin is a:

A. Primary structure peptide.

B. Secondary structure protein.

C. Tertiary structure protein.

D. Quaternary structure protein.

Question 2 (1 mark)

The primary structure of a protein is described as:

A. The sequence of amino acids in a peptide.

B. The three-dimensional arrangement of a polypeptide chain.

C. The closely packed arrangement of several polypeptide chains.

D. Containing the alpha helixes, beta pleated sheets and random coils.

Question 3 (1 mark)

The correct pathway for the production and secretion of a protein in a cell is:

A. Ribosome, endoplasmic reticulum, Golgi apparatus, exocytosis.

B. Endocytosis, ribosome, Golgi apparatus, endoplasmic reticulum.

C. Endoplasmic reticulum, ribosome, Golgi apparatus, endocytosis.

D. Golgi apparatus, ribosome, endoplasmic reticulum, exocytosis.

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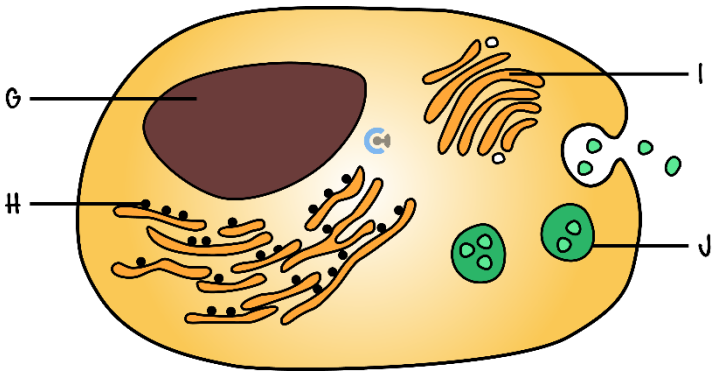
Question 4 (1 mark)

The diagram below represents a cell secreting a protein into the extracellular environment. Structures G-J are part of this process.



In which order are structures G-J involved in the secretion of proteins?

A. G, H, I, J

B. J, I, H, G

C. H, J, G, I

D. I, G, J, H

A is correct. To secrete a protein, the nucleus (structure G) would first transcribe the gene. The ribosomes on the rough endoplasmic reticulum (structure H) would then translate the gene. The protein would move through the lumen of the rough endoplasmic reticulum to the Golgi apparatus (structure I), where it would be modified and packaged into vesicles (structure J) for exocytosis.

B, **C** and **D** are incorrect. These options do not give the correct order of structures G–J.

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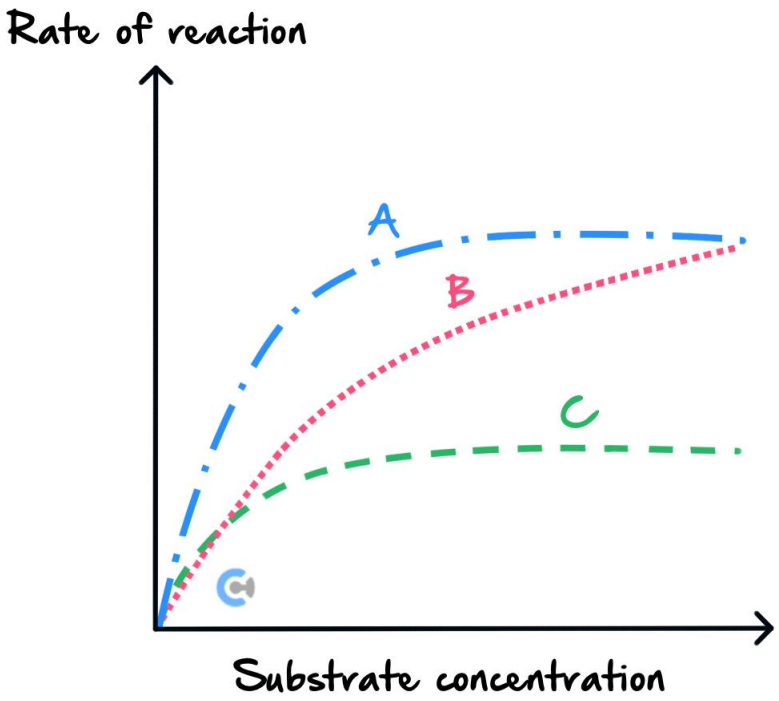
Question 5 (1 mark)

Enzyme CYP3A4 is responsible for metabolising the drug codeine, shown as *A* in the figure below. Grapefruit juice binds irreversibly with this enzyme, limiting the effectiveness of the drug.



Identify the correct statement from the options below.

A. Graph *B* represents the effect of grapefruit juice on codeine.

B. Graph *C* represents the effect of grapefruit juice on codeine.

C. Graph *B* represents the effect of grapefruit on CYP3A4.

D. Graph *C* represents the effect of grapefruit on CYP3A4.

Question 6 (1 mark)

The primary sequence of amino acids is bonded together by:

A. Hydrogen bonds.

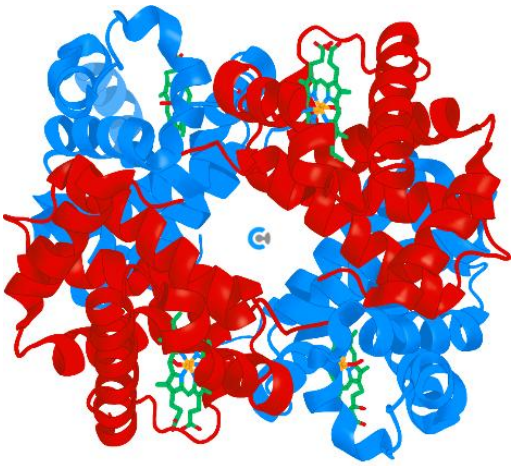
B. Ionic bonds.

C. Glycosidic bonds.

D. Peptide bonds.

Question 7 (1 mark)

Haemoglobin is a protein consisting of four peptide subunits.



The haemoglobin molecule

The protein structure can be described as a:

A. Primary structure.

B. Secondary structure.

C. Tertiary structure.

D. Quaternary structure.

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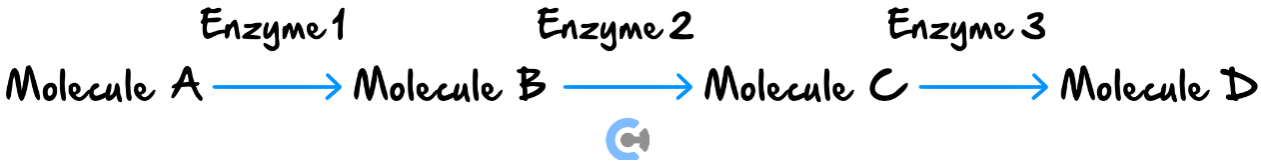
The following information applies to the two questions that follow.



Question 8 (1 mark)

Identify what would happen to the rate of production of molecule *D* if enzyme 1 was not present.

A. It would increase.

B. It would decrease.

C. It would stop.

D. It would be unchanged.

Question 9 (1 mark)

Identify how the rate of production of molecule *D* would be affected if the concentration of enzyme 1 was increased but the concentration of enzymes 2 and 3 remained unchanged.

A. It would increase.

B. It would decrease.

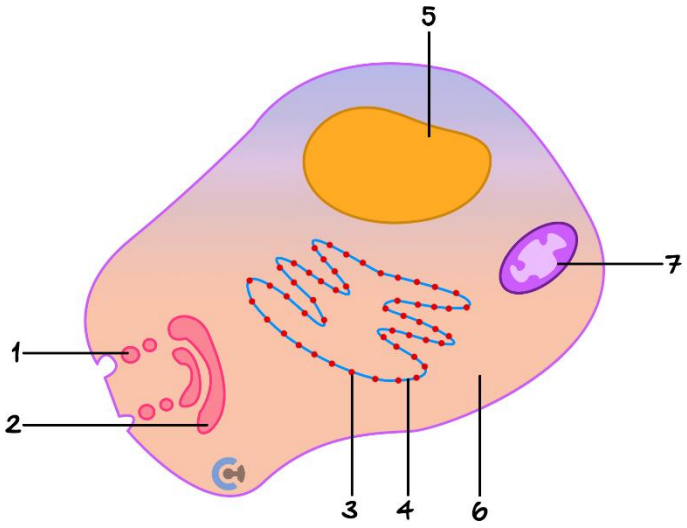
C. It would stop.

D. It would be unchanged.

Space for Personal Notes

Question 10 (1 mark)

The following diagram shows a typical secretory cell, such as the β-cell that secretes the insulin protein and is found in the pancreas. The organelles labelled 1-7 in the diagram are the components of the cell that are involved in the synthesis, internal transport, modification, packaging and export of the substance being secreted from the cell.



In which order are the organelles directly involved in the synthesis, internal transport, modification, packaging and export of insulin?

A. 1, 2, 3, 4, 5

B. 3, 4, 2, 1

C. 7, 6, 5, 2, 1

D. 5, 3, 2, 1

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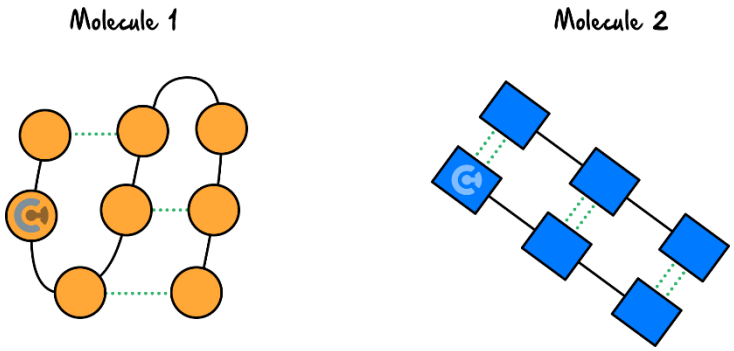
Question 11 (1 mark)

The diagram below shows two biomolecules.



Molecule 1 contains:

A. R-groups.

B. Complementary pairing.

C. Phosphate groups.

D. Antiparallel strands.

Question 12 (1 mark)

The primary structure of a protein is important because it:

A. Is the active, functional form of the protein.

B. Has a very specific three-dimensional shape.

C. Influences the way that the polypeptide folds.

D. Directly controls the way proteins are transported into a cell.

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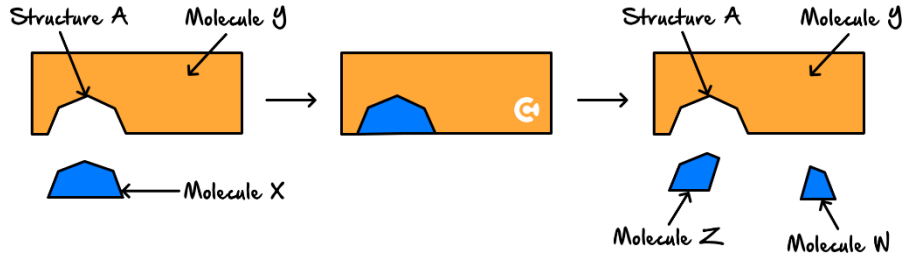
The following information applies to the two questions that follow.

The diagram below represents a generalised biochemical process.



Question 13 (1 mark)

Which one of the following statements is correct?

A. Molecule *Y* represents the substrate.

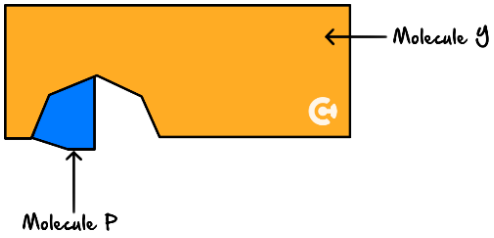
B. Molecule *X* represents an enzyme.

C. Structure *A* is an active site.

D. Molecule *Z* is a reactant.

Question 14 (1 mark)

Another molecule, Molecule *P*, can bind to part of the Structure *A* of Molecule *Y*, as shown below.



Consider a mixture containing molecules of *X*, molecules of *Y* and molecules of *P*. The rate of production of a molecule *Z* and molecule *W* is measured and found to change in the presence of a molecule *P*. In the presence of a molecule *P*, increasing the concentration of a molecule *X* increases the rate of production of a molecule *Z* and molecule *W*.

Which one of the following statements is correct?

A. Molecule *X* changes shape in the presence of Molecule *P*.

B. Molecule *P* is considered a reversible inhibitor.

C. Molecule *Y* is denatured by Molecule *P*.

D. Molecule *P* is made from monomers of nucleotides.

Question 15 (1 mark)

A condensation reaction between two amino acids will produce:

A. Monomers.

B. Water.

C. Energy.

D. DNA.

Condensation reactions release a water molecule as the new bonds form. Hydrolysis reactions release energy. DNA is a polymer of nucleic acids, not amino acids.

Question 16 (1 mark)

The proteome can best be described as:

A. All of the proteins that a cell can produce.

B. All of the genes in a cell.

C. Only the proteins that are needed by the organism.

D. The complete array of the gene pool.

D is incorrect because it refers to multiple organisms. The proteome refers to all of the proteins that are produced by a cell or organism.

Question 17 (1 mark)

When comparing the genome with the proteome of an organism, it is appropriate to say:

A. The genome and the proteome in a particular cell are the same.

B. The proteome controls the genome within the organism.

C. All of the instructions from the genome are transferred to the proteome at some stage within the organism.

D. The genome in each cell in a particular organism is the same but the proteome is different.

The genome is the complete set of genetic instructions (DNA) in the nucleus of a cell. The proteome is all the proteins a cell produces, which is only reliant on a small proportion of the genome. Cells are different, but not due to different genomes - rather it is a result of the different combinations of proteins the cell manufactures. The human genome is made up of about 2% genes and the rest (control, introns or no function as yet discovered) are the remaining 98%.

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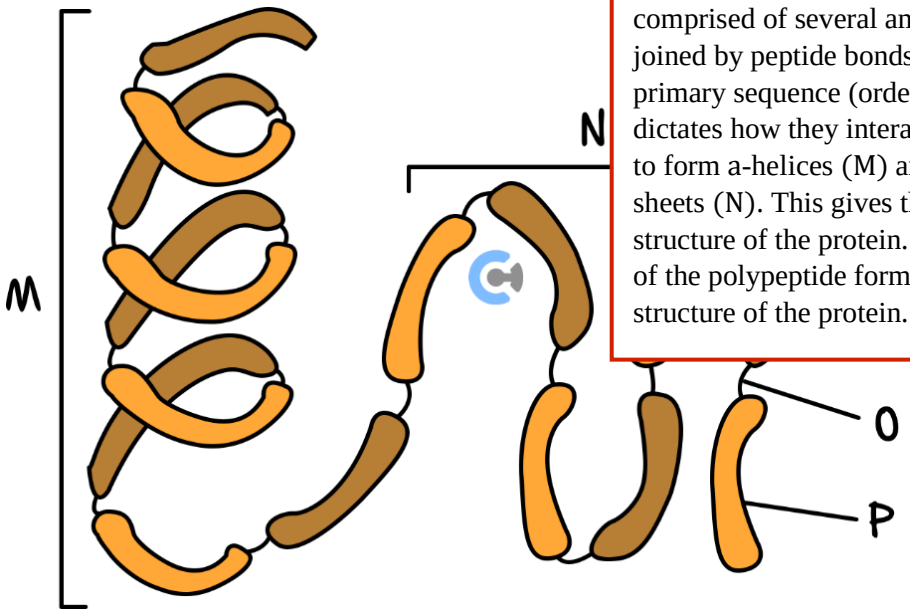
Question 18 (1 mark)

The diagram below shows a globular protein.



Globular proteins are the workhorses of metabolism. Examples of these are enzymes, hormones and antibodies are examples. This particular protein is comprised of several amino acids (P) joined by peptide bonds (O). The primary sequence (order of amino acids) dictates how they interact with each other to form a-helices (M) and β-pleated sheets (N). This gives the secondary structure of the protein. The final shape of the polypeptide forms the tertiary structure of the protein.

Which of the following correctly identifies structures M to P?

	M	N	O	P
A.	α-helix	β sheet	Peptide bond	Amino acid
B.	β sheet	α-helix	Hydrogen bond	Nucleotide
C.	β sheet	α-helix	Amino acid	Peptide bond
D.	α-helix	β sheet	Peptide bond	Nucleotide

Question 19 (1 mark)

Given the critical role of haemoglobin in oxygen transport, how might a mutation affecting the primary structure of haemoglobin impact its function?

A. It could change the protein's three-dimensional shape, impairing oxygen binding.

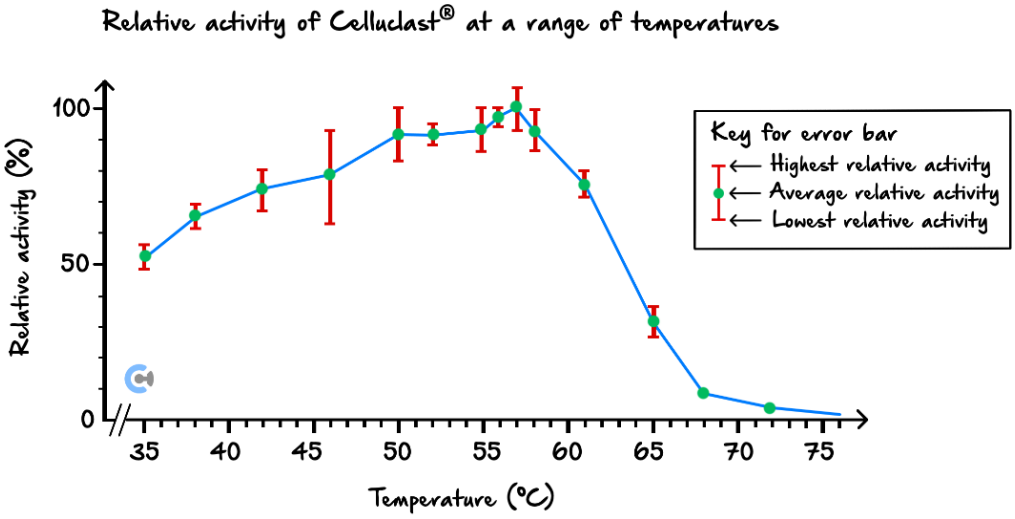
B. It would have no effect since primary structure does not affect function.

C. It could enhance oxygen transport by increasing haemoglobin flexibility.

D. It would prevent haemoglobin from being exported out of the cell.

Question 20 (1 mark)

Celluclast® is an enzyme. The activity of Celluclast® at a range of temperatures and at a pH of 5 was measured. The experiment was repeated five times. The relative activity (%) of Celluclast® was calculated and plotted on a graph, as shown below. The range of the calculated measurements at each temperature is shown as an error bar on the graph.



Source: J Herlet et al.,'A new method to evaluate temperature vs pH activity profiles for biotechnological relevant enzymes', Biotechnology for Biofuels,10,234(2017),<https://doi.org/10.1186/s13068.017-0923-9>

It is reasonable to conclude that:

A. Celluclast® is inactive at 61°C.

B. Celluclast® is denatured at 35°C.

C. The optimum pH for Celluclast® is pH 5.

D. The optimum temperature for Celluclast® is around 57°C.

Question 21 (1 mark)

The error bars on the graph shown above indicate that the measurements taken at:

A. 38°C were more valid than at 35°C.

B. 52°C were more precise than at 46°C.

C. 46°C were more accurate than at 55°C.

D. 58°C had more random errors than at 42°C.

Section B: Short Answer Questions (61 Marks)

Question 22 (2 marks)

Describe the difference between the tertiary and the quaternary structure of proteins.

Define Tertiary Structure – 3D, functional, r groups of amino acids.

Define quarternary – Multiple polypeptides OR prosthetic non-protein group.

Include a comparative term "whereas" "on the other hand" etc.

Question 23 (2 marks)

Explain what is meant by the 'proteome' and account for the functional diversity of proteins.

The proteome refers to the set of all proteins that are expressed and produced by a cell, tissue or an organism.

Protein function is determined by their overall 3D structure, otherwise known as their tertiary structure. This is formed via the interactions of the r groups of different amino acids in the polypeptide, and given that there are 20 different types of amino acids, proteins can be extremely diverse in their function as there are many different arrangments that can be formed from these combinations.

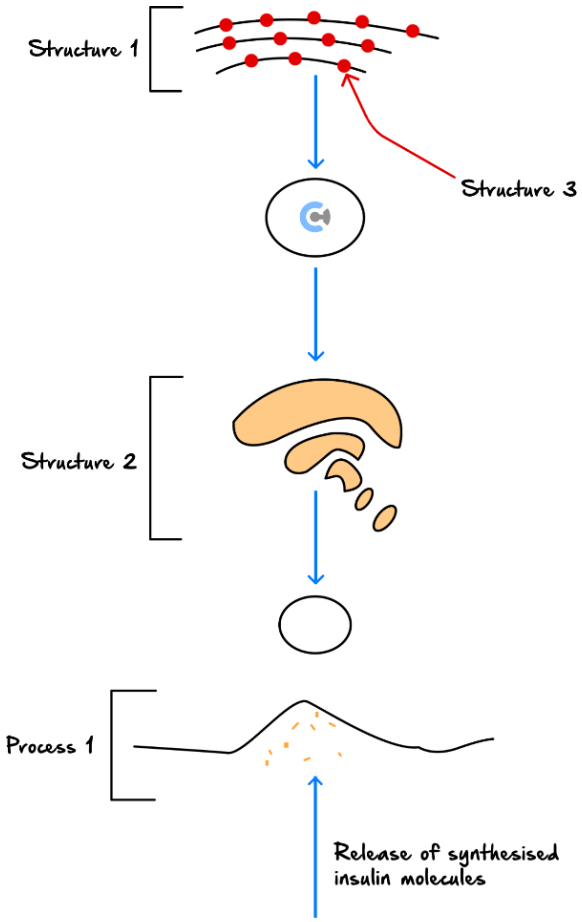
Question 24 (2 marks)

Will all cells within an organism have the same proteome? Explain your answer.

No, they will not. The proteome refers to the proteins that are expressed by specific cells. As in a multicellular organism an advantage in the specialisation of different cells, they will produce different proteins according to their function, and hence, will have different proteomes.

Question 25 (10 marks)

The human insulin protein is secreted by pancreatic cells and functions to enable the cellular uptake of glucose essential for the process of cellular respiration. The figure below is a simplified outline that shows the production of insulin in a cell.



a. Name and outline the role of Structures 1 and 2 in the process shown in **the figure.** (4 marks)

Structure 1 is the rough endoplasmic reticulum **(1 mark)**. It functions to transport the human insulin protein to the Golgi body **(1 mark)**. Structure 2 is the Golgi body. **(1 mark)**. Its role is to package and modify the human insulin protein for export out of the cell **(1 mark)**.

b. Name Process 1 in **the given figure.** (1 mark)

Exocytosis **(1 mark)**.

c.

i. Name Structure 3 in **the given figure.** (1 mark)

A ribosome **(1 mark)**.

ii. Identify and briefly describe the process that occurs at this structure in relation to human insulin production. (4 marks)

The process occurring in Structure 3 is translation **(1 mark)**. The mRNA strand carries the code for the production of human insulin **(1 mark)**. mRNA is read at the ribosome and attracts corresponding tRNA molecules **(1 mark)**. tRNA molecules recognise specific mRNA codons via their anticodon sequences and ddeliveramino acids in the order specified by the mRNA sequence, building the primary structure of the insulin protein chains **(1 mark)**.

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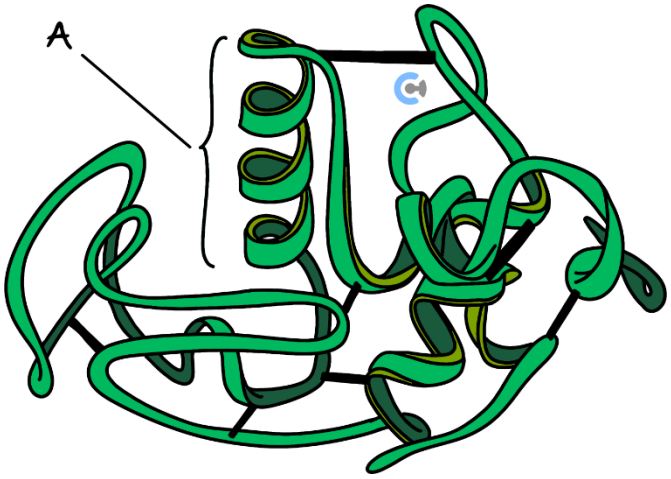
Question 26 (8 marks)

Lipase is an enzyme that catalyses the hydrolysis of triglycerides. It is a soluble globular protein. The function of an enzyme depends upon the precise nature of its tertiary structure. The diagram below represents the structure of an enzyme. The black strips represent the disulphide bonds that help to stabilise its tertiary structure.



a. What is this secondary structure called? (1 mark)

α helix or alpha helix.

b. Explain why the function of an enzyme depends upon the precise nature of its tertiary structure. (2 marks)

The tertiary structure determines the three-dimensional shape (conformation) of the protein molecule (1) and so determines the (three-dimensional) shape of the active site or the specificity of the enzyme (1).

c. Describe the effect of breaking the bonds between the R groups of the amino acids of the protein on lipase function. (2 marks)

It will after the three-dimensional shape of the active site preventing it from binding with the triglyceride (1), thus preventing lipase from functioning (1).

d. After being synthesised, lipase is released from mast cells via exocytosis.

Complete the table below by naming three different organelles directly associated with the transport of the synthesised lipase within or from mast cells and state the role of each organelle in this process. (3 marks)

Organelle	Role
Rough endoplasmic reticulum	Transports lipase within cell, including to the Golgi body.
Golgi body	Packages lipase into vesicles for export from the cell.
Vesicles	Carries lipase to plasma membrane where it fuses and releases the lipase from the cell.
Plasma membrane	Vesicles fuse with it and are released by exocytosis.
Mitochondria	Provides the energy required, e.g., for packaging.

Some students wrote RER or ER but these were not suitable abbreviations and were only accepted if the student defined their abbreviation.

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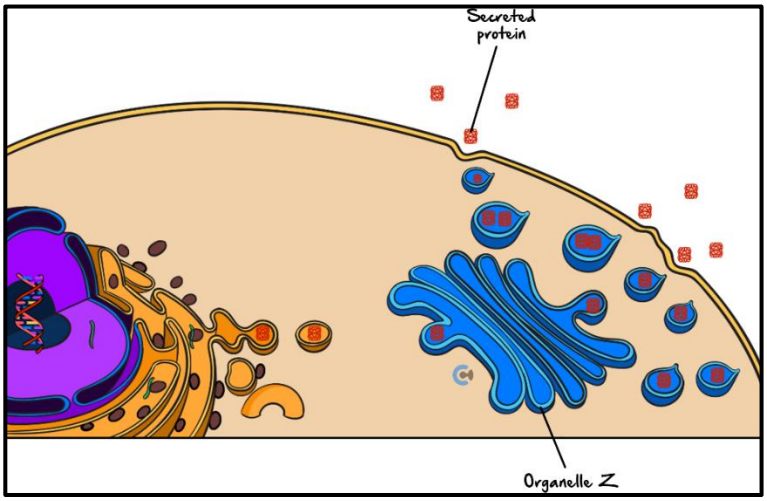
Question 27 (7 marks)

This diagram shows a human cell secreting a protein.



a. Where, specifically, is the polypeptide of this protein synthesised in this cell? (1 mark)

The ribosomes are studded on the rough endoplasmic reticulum.

b. Briefly describe the process by which this polypeptide is synthesised. (3 marks)

Translation is divided into-
Initiation: The ribosome attaches to the mRNA at the start codon (AUG), and the first tRNA carrying methionine binds to the codon.
Elongation: The ribosome moves along the mRNA, matching tRNA anticodons to mRNA codons, forming peptide bonds between amino acids, and elongating the polypeptide chain.
Termination: Translation ends when a stop codon is reached, causing the ribosome to release the completed polypeptide.

c. What is an organelle Z? Describe its function in protein secretion. (2 marks)

Golgi Apparatus – responsible for adding modification to protein structure (sugar groups for glycoproteins) and packaging them into secretory vesicles for export via exocytosis.

d. By what process does the protein exit the cell? (1 mark)

Exocytosis – a secretory vesicle binds to the plasma membrane and expels the protein into the extracellular space.

Question 28 (7 marks)

Baker's yeast (Saccharomyces cerevisiae) is a unicellular, eukaryotic organism. Biologists have studied its proteome. A single yeast cell contains approximately 100000 different proteins.

a. Consider the 100000 different proteins. The concentration of each protein may change with a change in environmental conditions.

Give **one** example of a **type** of protein within a yeast cell that may change in concentration and explain why this change is necessary. (3 marks)

An acceptable answer was one of the following types of proteins with the explanation.

Enzyme: If there is a change in substrate concentration, then more or less enzyme may be produced to conserve ATP.
OR
Structural protein: Repair or synthesis of organelles if organelles are damaged due to increased or decreased temperature.
OR
Regulatory/Repressor protein: More or less repressor protein is required to inhibit or promote a reaction when there is a change in substrate availability.
OR
Transcription factors: More or less is required for transcription if environmental conditions result in increased or decreased need for protein synthesis.

b. Explain how yeast could produce over 100,000 different proteins from 20,000 genes. (2 marks)

Alternative splicing and post translational modifications – the way that they fold may be different.

c. What is the functional difference between a regulatory gene and a structural gene? (2 marks)

Structural genes code for proteins required for the body to function, whereas...

....a regulatory gene produces proteins that act to switch on or off structural genes.

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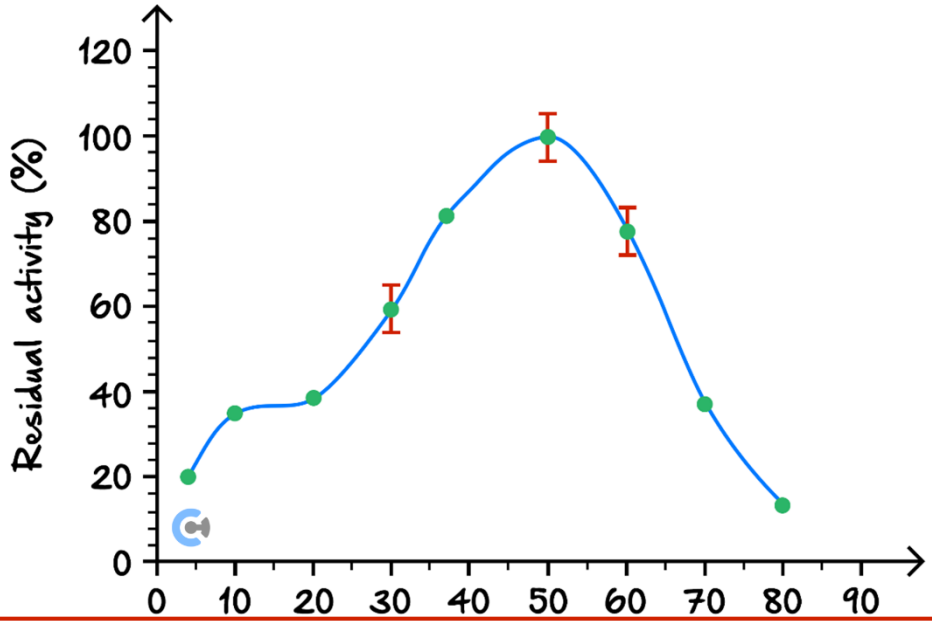
Question 29 (13 marks)

In the human body, the enzyme amylase is found in both saliva and the digestive tract, and is responsible for catalysing the hydrolysis of starch to maltose. This maltose is then broken down by the enzyme maltase to become glucose, which is the most common energy source for a cell in the body.

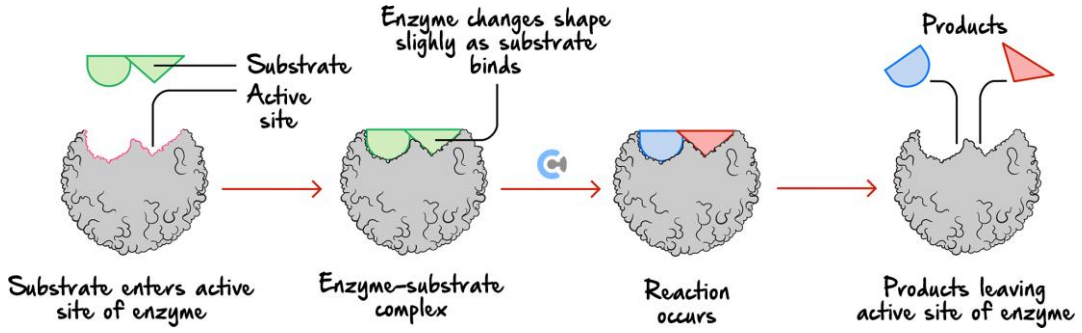
Some students, upon hearing about amylase being an enzyme, wanted to investigate the impact of different factors on the rate at which amylase hydrolyses starch.

The following results are achieved when comparing the activity of amylase at different temperatures.

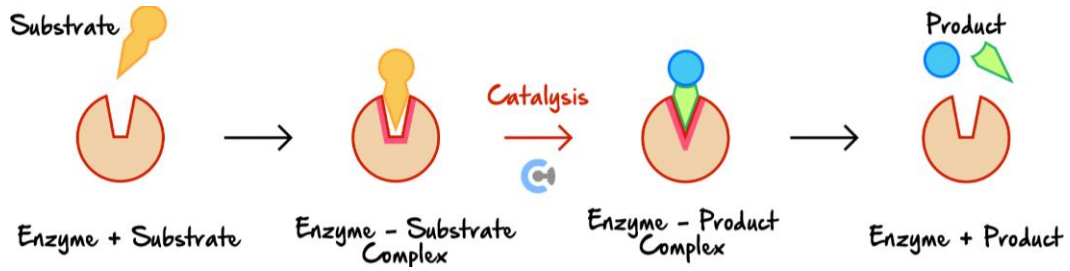


Lock and key model – where the active site and the substrate are perfectly complementary in shape to each other.

a. Exp ed fit mo



Induced fit – where the active site conforms slightly to the substrate to catalyse the reaction.



b. Explain the shape of the graph generated. (3 marks)

At low temperatures, the rate of reaction is low, as there are fewer collisions between substrate and enzyme molecules.

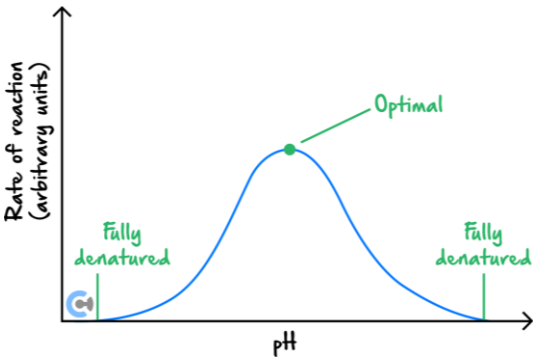
Temperature increases the collisions, thus increasing the rate until the optimal temperature, which is the temperature at which the highest rate or activity was achieved.

However, at temperatures higher than that, the heat breaks the bonds in the structure of the enzyme, causing it to lose its 3D shape, altering the active site and denaturing it, with the enzyme no longer able to catalyse the reaction.

c. How might this graph look different if the students were investigating the impact of pH? Use a diagram in your response. (3 marks)

pH also impacts the tertiary structures of enzymes.

Where low temperature slows the reaction, the pH change denatures the enzyme as long as it is outside its optimal range, which is at a certain pH depending on the enzyme.



d. Describe how non-competitive inhibitors impact the rate of enzyme function. (3 marks)

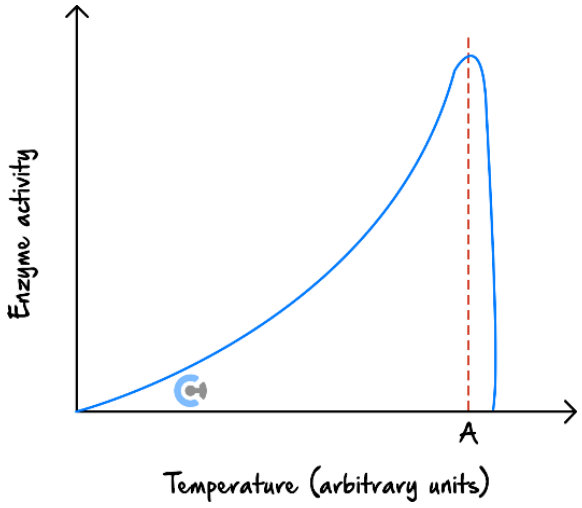
Non-competitive inhibitors bind to an allosteric site on an enzyme, which causes a conformational shape change in its active site.

This prevents the enzyme form binding to the substrate, thus preventing it from catalysing the reaction.

Hence, it reduces the rate of enzyme function.

Question 30 (7 marks)

Below is a graph showing how enzyme activity changes with temperature.



a. For most mammalian enzymes, what is the temperature at *A*? (1 mark)

36°C-37°C

b. Explain the shape of the graph. (2 marks)

The enzyme activity increases until the optimum temperature is reached. (1 mark)
After this, the enzyme is denatured, so enzyme activity ceases. (1 mark)

c. Referring to the graph, explain how food is preserved by refrigeration. (2 marks)

At lower temperatures, enzymes are inhibited from functioning. (1 mark)
Keeping food at low temperatures increases its shelf life as reactions are slower. (1 mark)

d. In order to store vegetables, such as carrots, for long periods, they are first 'blanched' (boiled for a few seconds) and then deep frozen.

Referring to the graph, explain how this method works. (2 marks)

Blanching denatures the enzymes, as above 65°C there are no units of sugar produced, (1 mark) vegetables can then be stored without cellular activity. (1 mark)

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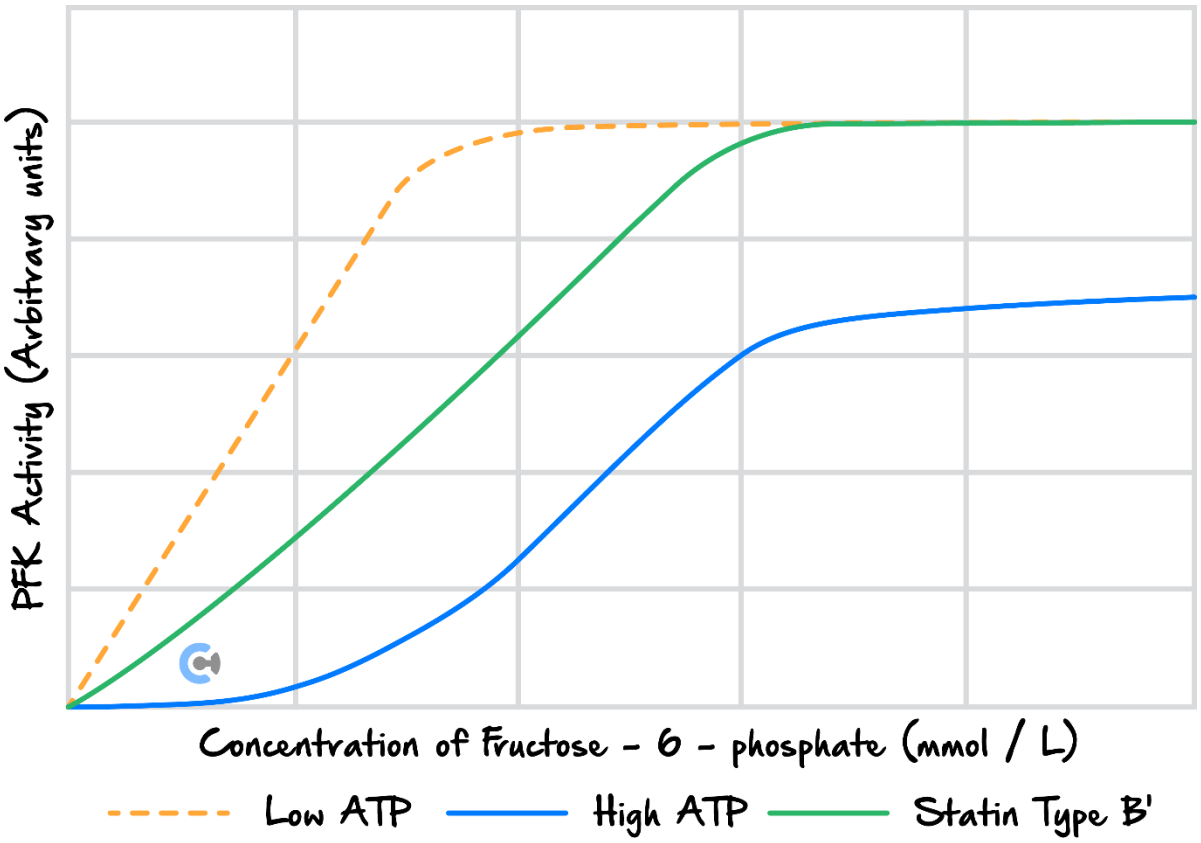
Question 31 (3 marks)

The diagram below shows one of the reactions that occur during the regulation of cholesterol synthesis. The enzyme **HMG-CoA reductase** is responsible for catalysing the conversion of HMG-CoA into mevalonate, a key step in the cholesterol biosynthesis pathway. ATP and statins both act as allosteric inhibitors of HMG-CoA reductase. Statins type B can act as active inhibitors of HMG-Coa reductase.

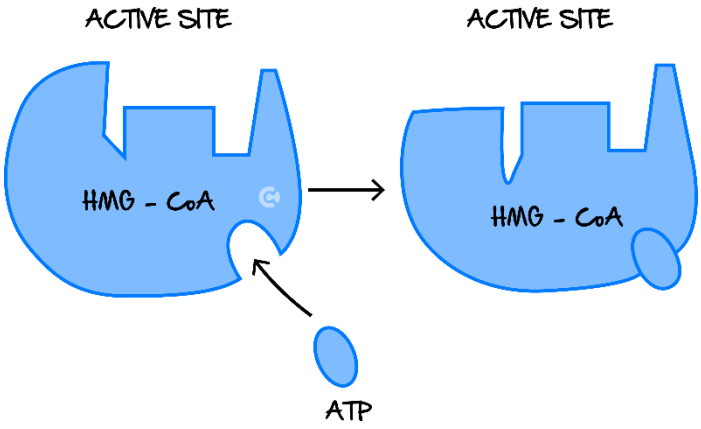
During cholesterol synthesis, the following reactions occur:

Acetyl-CoA → HMG-CoA → Mevalonate → Cholesterol

An experiment was conducted to determine the effect of ATP on HMG-CoA reductase activity and the results are shown on this graph.



A student draws the following diagrams to illustrate the effect of ATP on HMG-CoA reductase.



Does this diagram accurately convey the role of ATP in HMG-CoA reductase regulation?
Circle the correct answer: Yes / No.

Explain your answer:

No, the diagram does not accurately convey the role of ATP in HMG-CoA reductase regulation.
1. ATP functions as an allosteric inhibitor, binding to a regulatory site, not the active site.
2. The diagram incorrectly depicts ATP binding directly to the active site, which disrupts the enzyme's function.
3. Allosteric binding alters the enzyme's shape, reducing its catalytic activity on HMG-CoA.

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- After school weekdays and all-day weekends.

1-on-1 Video Consults	Text-Based Support
➢ Book via bit.ly/contour-biology-consult-2025 (or QR code below). ➢ One active booking at a time (must attend before booking the next).	➢ Message +61 440 137 387 with questions. ➢ Save the contact as "Contour Biology".

Booking Link for Consults
bit.ly/contour-biology-consult-2025

Number for Text-Based Support
+61 440 137 387