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VCE Biology ¾

Gene Expression & The trp Operon I [0.3]

Workshop Solutions

Section A: Multiple Choice Questions (20 Marks)

Question 1 (1 mark)

The outcome of transcription in prokaryotes is the production of:

A. mRNA.

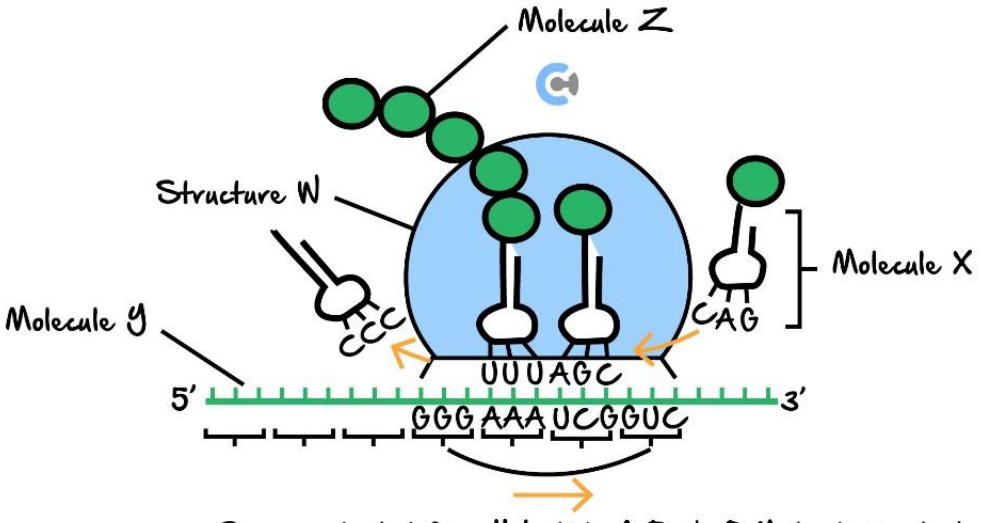
B. A protein.

C. Pre-mRNA.

D. An amino acid chain.

Question 2 (1 mark)

Consider the diagram shown below, with molecules *X*, *Y* and *Z*, and Structure *W* labelled. All arrows depict the movement of molecules or structures.



Source: adapted from H Lodish, A Berk, P Matsudaria et al., Molecular Cell Biology, 5th edition, WH Freeman and Company, New York, 2003, p.119

Which one of the following is a correct statement about the diagram above?

A. Structure *W* is a copy of template DNA found in the nucleus.

B. Molecule *X* carries an amino acid that will be added to the growing polypeptide.

C. Molecule *Y* is being read in the 3′ to 5′ direction.

D. Molecule *Z* contains a codon.

Question 3 (1 mark)

The table below shows all of the mRNA codons for the amino acid leucine and the corresponding tRNA anticodons.

mRNA codons	tRNA anticodons
UUA	AAU
UUG	AAC
CUU	GAA
CUC	GAG
CUA	GAU
CUG	GAC

Based on the information given, it is reasonable to state that:

A. Leucine is a polypeptide.

B. The genetic code is degenerate.

C. The genetic code is universal in nature.

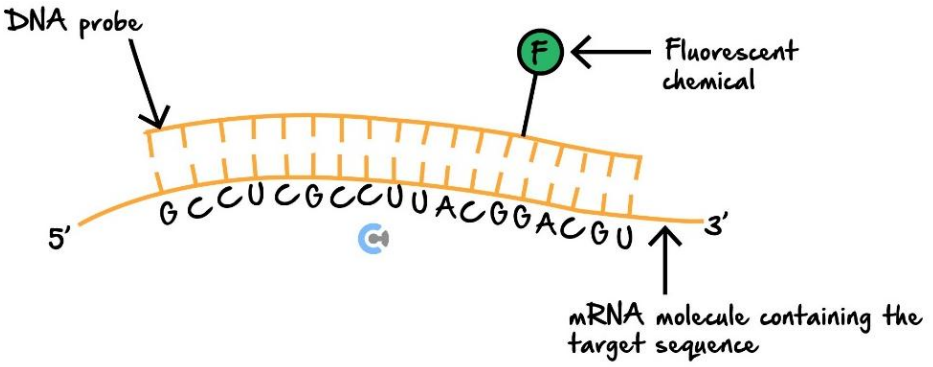
D. Transcription of the mRNA codons gives rise to a functional protein.

Space for Personal Notes

Question 4 (1 mark)

One method that is used to identify and measure quantities of mRNA molecules is called fluorescence in situ hybridisation (FISH).

The fluorescent chemical is attached to the DNA probe. When the DNA probe binds to the target mRNA sequence, as shown in the diagram the fluorescent chemical allows the mRNA molecule to be visualised.



Source: adapted from LVJC Mannack, S Eising and A Rentmeister, 'Current techniques for visualizing RNA in cells', F1000 Research, 5:F1000 Faculty Rev-775, 28 April 2016, <https://doi.org/10.12688/f1000research.8151.1>

To make the mRNA molecule containing the target sequence, a cell must:

A. Synthesise DNA polymerase.

B. Attach a poly-A tail to the 3′ end of the gene.

C. Create a nucleotide chain with a ribose-phosphate backbone.

D. Have a ready supply of the N-containing bases adenine, thymine, guanine and cytosine.

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Question 5 (1 mark)

The mRNA molecule identified by FISH is used by the cell to produce a new type of molecule.

Which one of the following statements correctly describes one aspect of the production of this new molecule?

A. The rRNA and its associated proteins create a binding site for the mRNA.

B. The tRNA delivers and attaches a nucleotide to the new growing molecule.

C. The mRNA anticodons are complementarily matched with the tRNA codons.

D. The mRNA attaches to the smaller sub-unit of the ribosome to initiate transcription.

Question 6 (1 mark)

Using the information provided in the diagram and your own knowledge of genetic coding, which of the following is correct? Assume that there are no STOP codons in the target mRNA sequence.

	Probe sequence	Number of amino acids coded by the mRNA target sequence
A.	3′ GCAGGCAUUCCGAUCCGA 5′	5
B.	3′ CGGAGCGGAATGCCTGCA 5′	5
C.	3′ CGGAGCGGAAUGCCUGCA 5′	6
D.	3′ CGGAGCGGAATGCCTGCA 5′	6

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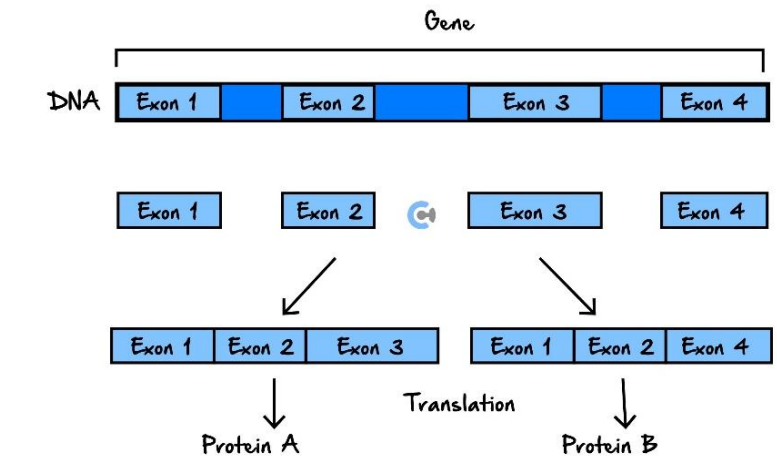
Question 7 (1 mark)



Source: https://study.com/academy/lesson/

What process does the above diagram depict?

A. Alternative splicing.

B. Translation.

C. Transcription.

D. Condensation polymerisation.

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation

The image depicts two different proteins resulting from one gene. This occurs via alternative splicing. The 2017 VCAA Exam, Q1c, demonstrates that students should understand this concept.

Question 8 (1 mark)

This process can explain:

A. How enzyme inhibition occurs.

B. The concept of rational drug design.

C. How the expression of a single gene can lead to the proc proteins.

D. Why do antigens and antibodies agglutinate and are rem .

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation

Alternative splicing leads to variation in the exon order in mRNA. This contributes to a single gene being able to code for the production of different proteins.

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Question 9 (1 mark)

In order for a gene to be transcribed, RNA polymerase must be able to bind to the gene's:

A. Regulator region.

B. Promotor region.

C. Operator region.

D. Repressor region.

Question 2 B
For the gene to be expressed, RNA polymerase must be able to move along the gene from the promotor region.

Question 10 (1 mark)

Proteins that block the movement of RNA polymerase along a gene are called:

A. Operons.

B. Activators.

C. Promotors.

D. Repressors.

Question 5 D
Repressors are repressing the gene from being expressed, hence they are preventing RNA polymerase from functioning.

Question 11 (1 mark)

Within eukaryotic cells, DN

Question 4 B
Once genes are activated, the DNA template can be transcribed into pre-mRNA. The pre-mRNA is then processed and the final mRNA moves to the ribosomes in the cytosol where the mRNA transcript is translated into a protein.

The processes that are involved in the expression of a protein listed in the correct order are:

A. Transcription, translation and RNA processing.

B. Transcription. RNA processing and translation.

C. Translation, transcription and RNA processing.

D. Translation, RNA processing and transcription.

Space for Personal Notes

Question 12 (1 mark)

The main difference between ger

Question 7 **B**

Both prokaryotes and eukaryotes contain double-stranded DNA which provides a blueprint for protein manufacture. RNA polymerase is involved in the process in both cell types. Both cell types have the capacity to activate genes when necessary. It would be a waste of energy for eukaryotic cells to have each gene active all the time. Eukaryotes splice out introns while processing the RNA, whereas prokaryotes do not.

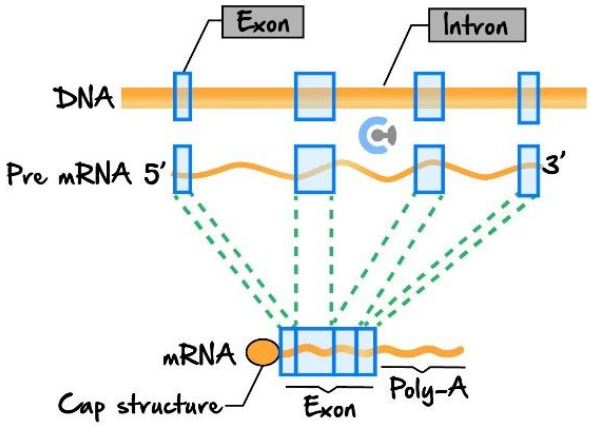
A. Prokaryotes are comprised of DNA.

B. Eukaryotes splice out introns, whereas prokaryotes do not.

C. Eukaryotes involve RNA polymerase, whereas prokaryotes do not involve RNA polymerase.

D. Prokaryotes have a repressor to deactivate genes, whereas eukaryotic genes are always active.

Question 13 (1 mark)



Source: https://cals-best.c.u-tokyo.ac.jp/images/fig/fig03_8.gif

The image above depicts:

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation

A. Translation.

B. RNA processing.

C. Reverse transcription.

D. The polymerase chain reaction.

B *The image depicts introns being removed from pre-mRNA and exons being joined together – this is RNA processing.*

Space for Personal Notes

Question 14 (1 mark)

The use of enzymes including endonucleases (restriction enzymes), l and polymerases

DNA is always read in a 3′ – 5′ direction.

The similarity between DNA and RNA polymerase is that:

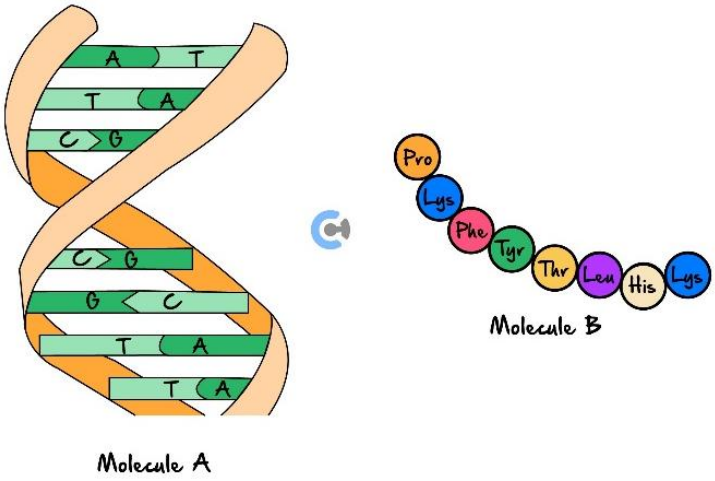
A. They both lead to the production of semi-conservative molec

B. They both act outside the nucleus.

C. They both create a nucleic acid strand consisting of complementary nucleotides in a 3′- 5′ direction.

D. They both read DNA in a 3′-5′ direction.

Question 15 (1 mark)



Which of the following correctly shows the functional link between molecule *A* and molecule *B* in the diagrams above?

A. Transcription then replication.

B. Translation then transcription.

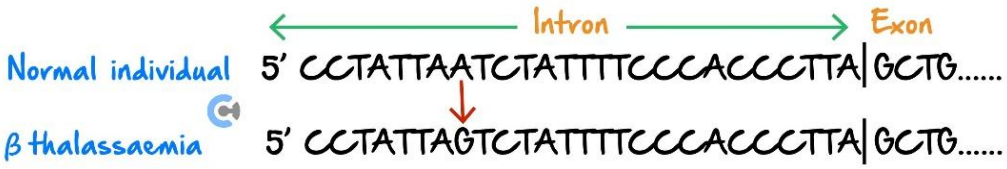
C. Replication then translation.

D. Transcription then translation.

Space for Personal Notes

Question 16 (1 mark)

The diagram below shows a section of the DNA sequence of a normal individual and a person suffering from β thalassaemia.



The best explanation for this mutation causing β thalassaemia would be that this mutation:

A. Changes the amino acid for the codon containing the changed base.

B. Causes a frameshift in the reading of the bases.

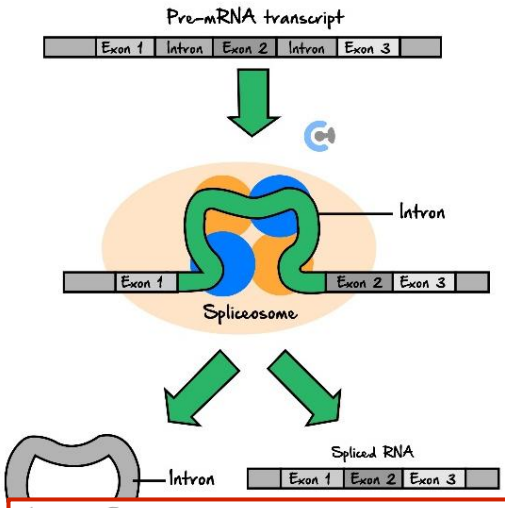
C. Interferes with the splicing out of the intron.

D. Results in many copies of the gene being made.

Space for Personal Notes

Question 17 (1 mark)

The diagram below shows a process that occurs during the post-transcriptional modification of the pre-mRNA transcript.



Which of the following statements is

A. The spliced RNA will now leave

B. The spliceosome is made up of DNA that will be broken down and reused.

C. A methylated cap needs to be added to the spliced RNA in front of the first exon.

D. All post-transcriptional modification processes protect mRNA from degradation by the actions of nucleases.

Answer: C

Explanatory notes

A is incorrect – the removal of introns and splicing of exons are not the only post-transcriptional modifications to the primary transcript.
B is incorrect – a spliceosome is a molecular construct that is responsible for the removal of introns from pre-mRNA. Material contained in the introns will be broken down and reused.
C is correct – a methylated cap needs to be added to the 5' end of the molecule. This allows for correct orientation as well as protection.
D is incorrect – the methylated cap and polyA tail both provide this type of protection, but the removal of introns and splicing of exons does not.

Question 18 (1 mark)

A small segment of DNA has the sequence:

5′ CTTAGCTAACGTAC 3′

The complementary strand will be:

A. 5′ GTACGTTAGCTAAG 3′

B. 5′ GAATCGATTGCATG 3′

C. 5′ GAAUCGAUUGCAUG 3′

D. 5′ GUACGUUAGCUAAG 3′

Answer is A

Explanatory notes

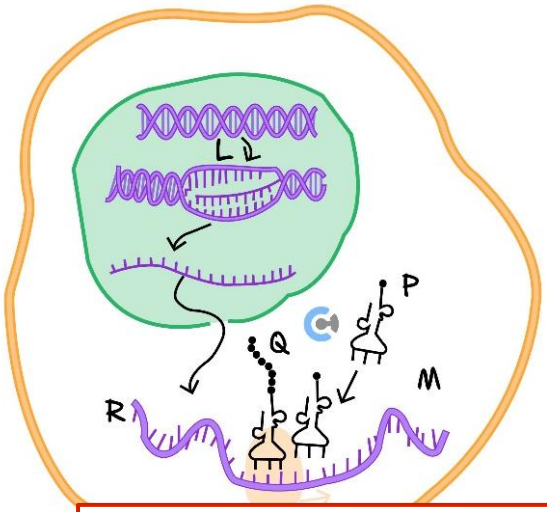
5' CTTAGCTAACGTAC 3'

3' GAATCGATTGCATG 5' (written in 5' to 3' order: 5' GTACGTTAGCTAAG 3')

A is correct – shows matching answer to that shown in the explanation.
B is incorrect – no consideration given to 5' 3' notation; this shows answer in 3' to 5' order.
C is incorrect – a complementary strand will be a DNA strand (ACGT) not RNA (should not contain U).
D is incorrect – a complementary strand will be a DNA strand (ACGT) not RNA (should not contain U).

Question 19 (1 mark)

The diagram below shows a process that occurs in all nucleated cells.



Modified

Question 28

Answer is D

Explanatory notes

A, B and C are incorrect – order of processes and structures are not correct.
D is correct – order of processes and structures is correct.

The correct labelling for this diagram is:

	L	*M*	*P*	*Q*	*R*
A.	Translation	Transcription	mRNA	Protein	DNA
B.	Translation	Transcription	tRNA	Polypeptide	DNA
C.	Transcription	Translation	mRNA	Protein	tRNA
D.	Transcription	Translation	tRNA	Polypeptide	mRNA

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Question 20 (1 mark)

When pre-mRNA is processed to mRNA:

A. Exons are removed, and the remaining introns have a methylated cap at the 5′ end and a poly-A-tail at the 3′ end.

B. Introns are removed, and the remaining exons have a methylated cap at the 3′ end and a poly-A-tail at the 5′ end.

C. Exons are removed, and the remaining introns have a methylated cap at the 3′ end and a at the 5′ end.

D. Introns are removed, and the remaining exons have a methylated cap at the 5′ end and a poly-A-tail at the 3′ end.

Question 23 D

Pre-mRNA is the direct product of transcription. Beyond that, introns are removed and stabilising factors are added prior to mRNA forming. A methylated cap is added to the 5' end to enable the mRNA to bind to the ribosome and a poly-A-tail is added to the 3' end to allow the mRNA to detach from the ribosome.

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Section B: Short Answer Questions (60 Marks)

Question 21 (2 marks)

Why might it be beneficial for a cell to have mRNA as an intermediate between DNA and protein?

mRNA is short-lived and can be degraded after translation, ensuring that the rate of protein gene expression is tightly.

Making a copy of the instructions (DNA) reduces the likelihood of damage to DNA during gene expression.

Question 22 (1 mark)

What principle ensures that the mRNA strand will be complementary to the DNA during transcription?

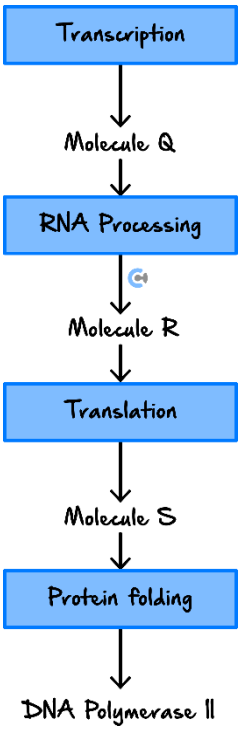
Complementary base pairing.

Space for Personal Notes

Question 23 (2 marks)

Lysozyme is an enzyme comprising a single polypeptide chain. Lysozyme is found naturally in human secretions such as tears and milk. It plays an important part in the body's defence against disease because it digests peptidoglycan which is the major component of gram-positive bacterial cell walls.

The flowchart below shows the steps involved in the synthesis of lysozyme.



a. What is the name of molecule "Q"? (1 mark)

Pre-mRNA (or primary transcript).

b. Name a difference between molecule "Q" and molecule "R". (1 mark)

(One of) There are introns in molecule Q but not in molecule R. Molecule R has a methyl cap on the $5'$ end whereas molecule Q does not. Molecule R has a poly-A tail on the $5'$ end, whereas molecule Q does not.

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Question 24 (5 marks)

Scientists studying the nucleus of the fruit fly *Drosophila melanogaster* observed distinct types of nucleic acid chains.

These scientists noticed that one type of nucleic acid chain was able to pass through the nuclear membrane and move to a ribosome. After the nucleic acid chain attaches to the ribosome, a polymer is produced.

a. Describe the steps occurring at the ribosome that resulted in the production of the polymer. (3 marks)

A good response included the following steps:

- ribosomes use the mRNA code
- tRNA brings a specific amino acid to the ribosome
- tRNA anticodon joins to complementary mRNA codon
- an amino acid is added to the polypeptide chain.

b. One particular length of nucleic acid chain passed through the nuclear membrane and coded for the production of a polymer that was 90 monomers long.

How many nucleotide bases on the nucleic acid chain were involved in the coding for this polymer?

Explain your response. (2 marks)

Three nucleotide bases code for one amino acid and 270 bases in total.

Space for Personal Notes

Question 25 (4 marks)

Consider the template strand of a hypothetical gene, shown below. The exons are in bold type.

3′**TAC AAA** CCG GCC **TTT GCC AAA** CCC AAC CTA **AAT ATG AAA ATT** 5′

Note:

1. The DNA triplet **TAC** indicates START and codes for the amino acid methionine that remains in the polypeptide.
2. The DNA triplets **ATC**, **ATT** and **ACT** code for a STOP instruction.

a.

i. How many amino acids would be present in the polypeptide expressed by this gene? (1 mark)

Eight

ii. An allele for this gene codes for a polypeptide with only five amino acids. This is caused by a mutation in one of the exons. This mutation is a result of one nucleotide change.

By referring to the original sequence above, identify the nucleotide change that must have occurred to bring about this shorter polypeptide. (1 mark)

The original AAA codon codes for the amino acid lysine.A mutation changing AAA to ATT would create a stop codon (UAA in mRNA).This premature stop codon would cause translation to stop early, resulting in a polypeptide that is shorter and consists of only five amino acids.Thus, the correct nucleotide change is from AAA to ATT.

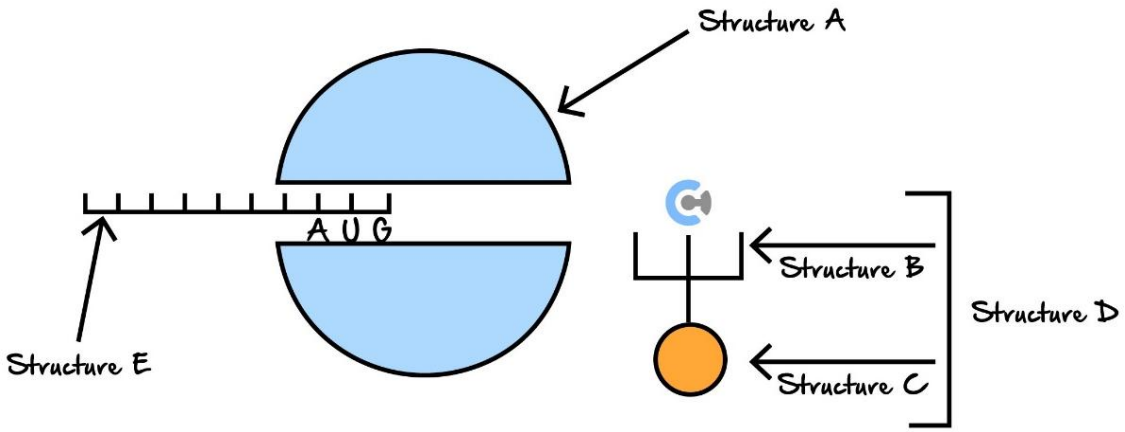
b. Write the mRNA sequence transcribed from this DNA template. (2 marks)

5’ AUC UUU GGC CGG AAA CGG UUU GGG UUG GAU UUA UAC UUU UAA 3’

Space for Personal Notes

Question 26 (4 marks)

The following diagram shows part of a cellular process involved in the production of the trypsin enzyme within a pancreatic cell.



a. Identify structure D. (1 mark)

Transfer RNA molecule.

b. Outline the function of structure B and structure C. (2 marks)

b. Structure B is the anticodon sequence of the tRNA molecule which complementary base pairs with a specific mRNA codon sequence **(1 mark)**. Structure C is the specific amino acid carried by the tRNA molecule **(1 mark)**.

c. Name the location where structure E is originally produced. (1 mark)

Nucleus

Space for Personal Notes

Question 27 (7 marks)

Messenger RNA Codons and Amino Acids for Which They Code

First base	Second base: U	Second base: C	Second base: A	Second base: G	Third base
U	UUU, UUC: PHE; UUA, UUG: LEU	UCU, UCC, UCA, UCG: SER	UAU, UAC: TYR; UAA, UAG: STOP	UGU, UGC: CYS; UGA: STOP; UGG: TRP	U C A G
C	CUU, CUC, CUA, CUG: LEU	CCU, CCC, CCA, CCG: PRO	CAU, CAC: HIS; CAA, CAG: GLN	CGU, CGC, CGA, CGG: ARG	U C A G
A	AUU, AUC: ILE; AUA: ILE; AUG: MET or START	ACU, ACC, ACA, ACG: THR	AAU, AAC: ASN; AAA, AAG: LYS	AGU, AGC: SER; AGA, AGG: ARG	U C A G
G	GUU, GUC, GUA, GUG: VAL	GCU, GCC, GCA, GCG: ALA	GAU, GAC: ASP; GAA, GAG: GLU	GGU, GGC, GGA, GGG: GLY	U C A G

Source: http://iamqs.blogspot.com.au/2010/05/programming-fundamentals-in-biomedical.html

The following DNA sequence comes from a gene found on chromosome 4.

TTACTGGAACTGCGA

This DNA sequence contributes to producing a polypeptide which forms part of an enzyme involved in the breakdown of a specific carbohydrate.

a. Name the enzyme that is involved in converting this sequence of DNA to RNA via the process of transcription. (1 mark)

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation.

Question 2a (1 mark)
Name the enzyme that is involved in converting this sequence of DNA to RNA via the process of transcription.

Answer:
- *RNA polymerase*

Marking protocol:
One mark for the above point.

b. List the anticodon sequence that corresponds with this DNA sequence. (1 mark)

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation.

Question 2b (1 mark)
List the anticodon sequence that corresponds with this DNA sequence.

Answer:
- *UUACUGGAACUGCGA*

Marking protocol:
One mark for the above point.

c. List the amino acid sequence that corresponds with this DNA sequence. (1 mark)

The genetic code as a degenerate triplet code and the steps in gene expression including transcription, RNA processing in eukaryotic cells and translation.

Question 2c (1 mark)
List the amino acid sequence that corresponds with this DNA sequence.

Answer:
- *ASN, ASP, LEU, ASP, ALA.*

Marking protocol:
One mark for the above point.

A mutation occurred to the original DNA sequence and the following is the new DNA sequence following the mutation:

TTACTGGCAACTGCGA

d. Name the type of mutation that occurred. (1 mark)

_____

_____

	TTACTGG**C**AACTGCGA	
Types of mutations (point, frameshift, block)	**Question 2d** (1 mark) Name the type of mutation that occurred.	**Answer:** • *Point mutation – addition.* **Marking protocol:** One mark for the above point.

e. Describe the impact that this mutation would have on the polypeptide produced. How may this then impact on an individual? (3 marks)

_____

_____

The functional importance of the four hierarchal levels of protein structure	**Question 2e** (3 marks) Describe the impact that this mutation would have on the polypeptide produced. How may this then impact on an individual?	**Answer:** • *The polypeptide produced is likely to be altered as the point mutation has contributed to a frameshift mutation.* • *From the amino acid LEU (inclusive) there is likely to be a change in all the following amino acids.* • *This may cause the enzyme to lose function and this may mean that the specific carbohydrate cannot be broken down.* **Marking protocol:** One mark for each of the above points.

Space for Personal Notes

Question 28 (6 marks)

a. There are several cellular activities that directly alter the number of proteins within a yeast cell. These include transcription, RNA processing, translation, and breakdown of protein.

For each cellular activity liste[illegible]oduct of the activity. (2 marks)

Cellular acti	luct
Transcriptio	
RNA Process	
Translatio	
Breakdown of P	

Acceptable responses were as follows.

Cellular activity	Immediate end product
transcription	pre-mRNA
RNA processing	mRNA
translation	polypeptide
breakdown of protein	amino acids

b. Four *S. cerevisiae* genes and the functions of their gene products are outlined in the table below.

***S. cerevisiae* genes and the functions of their gene products**

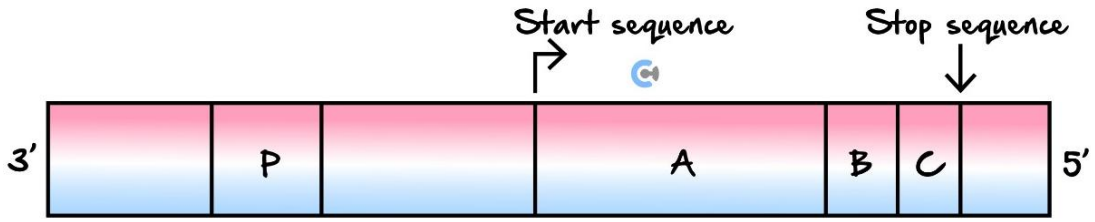
Gene	Function of the gene product
HSP82	Active on the plasma membrane to pump protons out of the cell.
ADR1	Binds to DNA and acts as a transcriptional factor.
GCN4	Controls the activity of RNA polymerase.
AQY1	A water channel in the plasma membrane.

Identify the regulatory genes in the table above and justify your response. (2 marks)

The correct response was ADR1 and GCN4. Both of their gene products regulate, for example, transcription.

Many students were able to identify the regulatory genes. However, it was common for students to repeat the function of the gene product information given in the table, which was not an acceptable justification.

c. One particular *S. cerevisiae* protein, PFY1, assists with the organisation of a cell's cytoskeleton. In the diagram below, the gene for the PFY1 protein is shown with a promoter region (labelled *P*), start and stop transcription sequences, and a single intron (labelled *B*).



Give the general name of the sections labelled *A* and *C*, and outline the function of these sections. (2 marks)

The correct answer was exons, with a suitable function such as:

- code for a protein
- be translated into a protein
- code for mRNA
- be transcribed into mRNA.

Space for Personal Notes

Question 29 (10 marks)

Klotho is a fascinating protein that has garnered significant attention in ageing research due to its potential anti-ageing properties. It was originally identified in mice, where a mutation in the Klotho gene resulted in a syndrome that mimicked accelerated human ageing, including shortened lifespan, infertility, osteoporosis, and skin atrophy.

In humans, Klotho is primarily expressed in the kidney, brain, and reproductive organs. It functions as a co-receptor for fibroblast growth factors (FGFs) and is crucial in regulating phosphate and calcium homeostasis in the body. This regulation is essential for maintaining healthy bone density and preventing vascular calcification.

Beyond its role in mineral metabolism, Klotho has been shown to exert protective effects against oxidative stress and inflammation, which are key contributors to ageing and age-related diseases. Interestingly, higher levels of Klotho in the body have been associated with increased longevity and improved cognitive function.

However, one of the detriments of Klotho is that any regulation of it would be difficult to manage given that shares a gene in the code with Glucagon, a blood sugar-controlling hormone. Any increase in glucagon may cause dangerous increases in blood sugar.

a. Explain how a single gene can code for multiple different proteins. (3 marks)

A single gene can code for multiple different proteins due to the RNA processing occurring in gene expression. Specifically, during alternative splicing, exons can be shuffled around and introns can be retained, thus resulting in many possible mRNA products, producing many different proteins form a single gene.

The first step in producing Klotho in the body is transcription.

b. Why must the DNA be unwound before it can be read during transcription? (1 mark)

The DNA must be unwound before it can be read during transcription to expose the nucleotide bases so that the RNA polymerase can read the template strand and synthesize the mRNA.

c. What direction is the template strand read in during transcription? Explain why this is the case. (3 marks)

The template strand is read in the 3' to 5' direction during transcription. This is because RNA polymerase synthesizes the mRNA in the 5' to 3' direction, adding RNA nucleotides to the 3' end of the growing strand. The template strand is read in the opposite direction (3' to 5') to ensure that the RNA sequence is complementary to the DNA template. This ensures that the mRNA is transcribed with the correct sequence of nucleotides, corresponding to the coding strand of the DNA.

d. What happens to the primary transcript after transcription before it is converted into a polypeptide? (3 marks)

After transcription, the primary transcript (pre-mRNA) undergoes several modifications before it is converted into a polypeptide:

a) 5' Capping: A 5' cap, a modified guanine nucleotide, is added to the beginning of the mRNA. This cap protects the mRNA from degradation and helps with the binding of the ribosome during translation.

b) Splicing: The pre-mRNA contains non-coding regions called introns, which are removed. The remaining coding regions, called exons, are spliced together to form the mature mRNA.

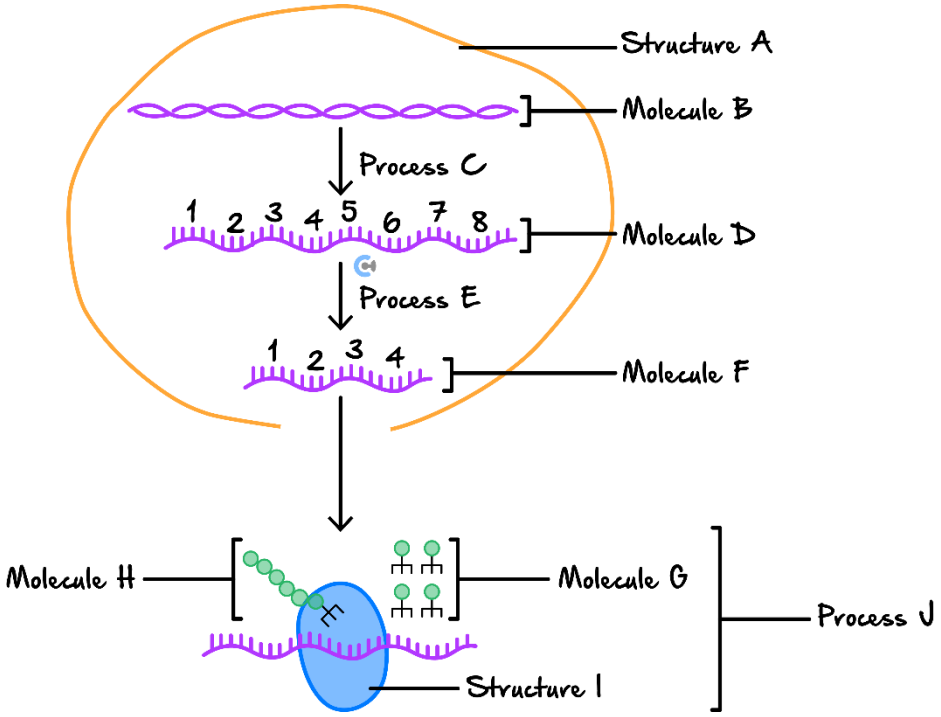
c) Polyadenylation: A poly-A tail is added to the 3' end of the mRNA. This tail stabilizes the mRNA, protects it from degradation, and assists in its export from the nucleus to the cytoplasm.

These modifications ensure the mRNA is mature and ready for translation into a polypeptide.

Space for Personal Notes

Question 30 (9 marks)

A simplified diagram of gene expression is shown below. Labels *A*-*G* represent various structures, molecules, and processes involved in gene expression.



a.

i. Identify structure *A*. (1 mark)

Nucleus

ii. Identify structure *E*. (1 mark)

Alternative splicing **OR** RNA processing.

iii. RNA polymerase is involved in the production of molecule *D*.

Identify molecule *D*. (1 mark)

Pre-mRNA

b.

i. Molecule *G* translates a message.

Identify the **two** parts of molecule *G* that enable it to do this. (2 marks)

Amino acid
Anticodon

ii. Molecule *D* has eight sections. Each section comprises 30 nucleotides.

Based on this information, determine and justify the length and composition of molecule *H*, which is formed at the end of process *J*. In your response, identify any relevant structures, molecules and processes. (4 marks)

Molecule F is mRNA and comprises four exons. Each of these exons has 30 nucleotides; therefore, molecule F has a total of 120 nucleotides. 1 mark

The 120 nucleotides are read at the ribosome in groups of three nucleotides. These are called codons. 1 mark

Process J is translation. During translation, each codon binds to an anticodon on tRNA that has a specific amino acid attached to it. 1 mark

Therefore, molecule H is a polypeptide that has a length of 40 amino acids. 1 mark

Note: Molecule F, process J and molecule H must be identified in order to obtain full marks.

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Question 31 (4 marks)

Many structures have important functions in gene expression.

a. Explain the function of RNA polymerase in transcription. (2 marks)

RNA polymerase is the enzyme responsible for catalysing the production of an mRNA strand complementary to the DNA template strand.

It synthesises the strand by joining together free nucleotides via condensation polymerisation that bind to the template through complementary base pairing, adding them to the 3' end.

b. The next stage in the production of pepsin is translation which happens at the ribosomes. Describe the relationship between mRNA and tRNA in this process. (2 marks)

tRNA **anticodons align with complementary codons** on the mRNA. (1 mark)

tRNA molecules bring (specific) amino acids to the ribosome **based upon the mRNA sequence**. (1 mark)

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Question 32 (2 marks)

Identify **TWO** differences in gene expression between eukaryotes and prokaryotes.

1. In eukaryotes, transcription occurs in the nucleus, while translation occurs in the cytoplasm. In prokaryotes, both transcription and translation occur simultaneously in the cytoplasm.
2. Eukaryotic mRNA undergoes post-transcriptional modifications (such as splicing, 5' capping, and polyadenylation) before translation, whereas prokaryotic mRNA is typically not processed and can be translated directly after transcription.

Question 33 (4 marks)

Outline two events that happen during RNA processing and the significance of both to gene expression.

Addition of 5' Methyl G cap – allows the mRNA to be recognised by the ribosome to initiate translation, whilst also ensuring stability as it exits the nucleus.

3' Poly A-tail – prevents the degradation of the mRNA chain at the 3' end as it leaves the nuclear membrane.

Splicing – removal of non-coding regions (introns) to generate mature mRNA
Alternative splicing - alternative splicing, exons can be shuffled around and introns can be retained, thus resulting in many possible mRNA products, producing many different proteins form a single gene.

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