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VCE Biology ¾
Gene Expression & The trp Operon [1.3]
Homework Solutions

Homework Outline:

Compulsory Questions	Pg 02 — Pg 20

Section A: Compulsory Questions (53 Marks)

Sub-Section [1.3.1]: Identify and Recall the Process of Gene Expression in Eukaryotes, Comparing How it Differs in Prokaryotes

Question 1 (1 mark)

Which of the following correctly describes the order of gene expression?

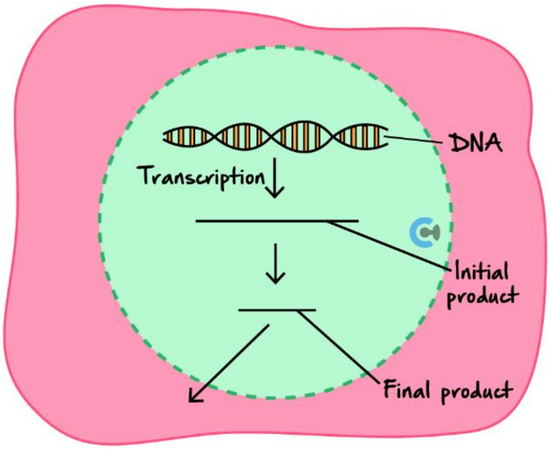
A. Transcription → Translation

B. Translation → RNA Processing → Translation

C. Translation → RNA Processing → Transcription

D. Transcription → RNA Processing → Transposition

The following diagram applies to the two questions that follow.



Question 2 (1 mark)

What is the name of the process that turns the “initial” product into the “final” product?

A. RNA Processing

B. Translation

C. Synthesis

D. Condensation Polymerisation

Question 3 (1 mark)

Why is the final product shorter in length than the initial product?

A. The spliceosome removes the introns leaving a shorter length.

B. Room is required to add the poly-A tail.

C. It is representative of the degeneracy of the genetic code.

D. Exons are spliced out, therefore leaving a shorter mRNA sequence.

Question 4 (1 mark)

Which sequence describes the correct order for the transcription of eukaryotic DNA?

A. DNA polymerase attaches, complementary nucleotides are attached, pre-mRNA, introns are removed, and mRNA leaves the nucleus.

B. RNA polymerase attaches, complementary nucleotides are attached, pre-mRNA, introns are removed, and mRNA leaves the nucleus.

The enzyme is RNA polymerase and introns are removed.

C. RNA polymerase attaches, complementary nucleotides are attached, pre-mRNA, exons are removed, and mRNA leaves the nucleus.

D. RNA polymerase attaches, complementary nucleotides are attached, mRNA, introns are removed, and pre-mRNA leaves the nucleus.

Question 5 (3 marks)

Compare the process of gene expression in eukaryotes and prokaryotes.

- No mRNA processing, and no intron to remove after transcription.
- Transcription and translation occur simultaneously.
- Occur in the same location (the cytosol) as there is no nuclear membrane.

Sub-Section [1.3.2]: Describe the Processes of Transcription, mRNA Processing, and Translation, Recognising the Significance of Each Step to the Final Product

Question 6 (1 mark)

Which of the following accurately describes ‘alternative splicing’?

A. The process by which exons are shuffled around during the splicing of introns.

B. The process of transcription when RNA polymerase begins to transcribe the non-template strand.

C. The process by which the ribosome shuffles codons.

D. The process during RNA processing in which a poly-A tail is added.

Question 7 (1 mark)

During the synthesis of a polypeptide, the molecules most commonly associated with the ribosomes would be:

A. tRNA, mRNA, rRNA

B. tRNA, mRNA, pRNA

C. DNA, mRNA, tRNA

D. cDNA, mRNA, rRNA

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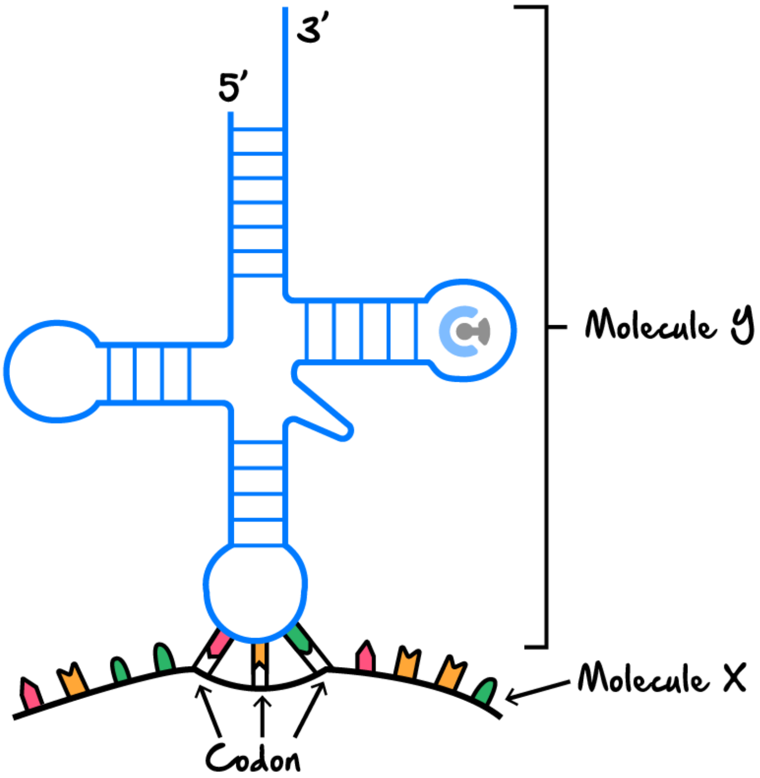
The following diagram applies to the three questions that follow.



Question 8 (1 mark)

Which of the following correctly identifies molecule *X* and molecule *Y* respectively?

A. tRNA, mRNA

B. rRNA, mRNA

C. tRNA, rRNA

D. mRNA, tRNA

Question 9 (1 mark)

At which location in a cell might you expect to see this arrangement?

A. Nucleus

B. Golgi Apparatus

C. Smooth Endoplasmic Reticulum

D. Rough Endoplasmic Reticulum

Question 10 (1 mark)

What is the product of this process?

A. Exons

B. mRNA

C. A polypeptide

D. Amino acid

Question 11 (1 mark)

The function of the ribosome in gene expression is:

A. Read mRNA and synthesise a polypeptide chain.

B. Splice introns out of pre-mRNA.

C. Package and fold proteins for export from the cell.

D. Read DNA and convert it into mRNA.

Question 12 (1 mark)

Following transcription, pre-mRNA is formed. Before pre-mRNA can leave the nucleus, post-transcriptional modification must occur. This included:

A. Addition of a methyl cap at the 3’ end.

B. Addition of a poly-A tail at the 5’ end.

C. Removal of introns.

D. Removal of exons.

Post transcriptional modification involves the addition of a methyl cap to the 5’ ends and a poly A tail to the 3’ end. Introns are removed and exons are spliced together. Therefore, C is the only correct response.

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Question 13 (1 mark)

The following diagram shows a sequence of pre-mRNA. The white regions code for introns, with the black regions coding for exons.

During transcription, a mutation occurred with the nitrogenous base uracil being substituted for a guanine in the white region.

The effect on the protein product:

A. Would be minimal as it is a single base change.

B. Is unable to be determined, as it may create a nonsense mutation.

C. Would have no effect.

As the mutation occurs in the intron, and this is the non-coding region of the protein, any mutation would have no effect.

D. Would create a non-functional protein.

Question 14 (1 mark)

Which of the following describes the termination of translation correctly?

A. A release factor binds to the stop codon, signalling the termination.

B. tRNA delivers a termination amino acid to the stop codon.

C. A hairpin loop is formed in the chain which cuts it off from the ribosomal structure.

D. Once the stop codon is reached, the ribosome binds the repressor terminating translation.

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Question 15 (3 marks)

Translation occurs within the cytosol of a cell. Outline the steps that normally occur in translation. Use specific terms and names of the molecules involved. Name the final product of the process.

Marks	0	1	2	3	Average
%	39	15	16	30	1.4

- mRNA travels to the ribosomes where its codons are read.
- tRNA carries specific amino acids to the ribosomes **or** complementary base pairing occurs between the codons and anticodons.
- product; protein/polypeptide.

This question was well answered by many students. However, some students failed to name the final product, which was significantly asked for in the question. Other students used many irrelevant terms, enzymes and structures which detracted from their answers

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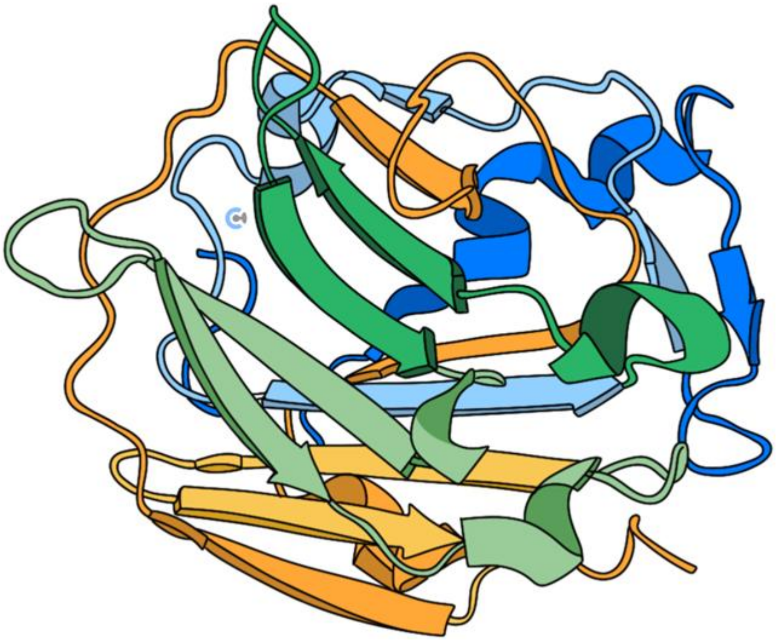
Question 16 (7 marks)

The COL1A1 gene provides instructions for synthesising collagen proteins, such as the one shown below.



Collagens are a family of proteins that strengthen and support many tissues in the body, including cartilage, bone and skin. The COL1A1 gene is 18 kb (18,000 base pairs) in length and codes for the production of a protein that is made up of 1464 amino acids. The image above shows an example of the structure of collagen.

a. Identify the sub-units that make up type I collagen and explain how these sub-units are linked together to form type I collagen. (2 marks)

Amino acids. Amino acids are joined together by a condensation reaction.
As two amino acids are joined together, a water molecule is released.
(The bond that occurs between two amino acids is called a peptide bond.)

Mark allocation:

- 1 mark is awarded for identifying amino acids as the sub-units of proteins.
- 1 mark is awarded for identifying that they are joined together as a result of a condensation reaction, and for stating that a molecule of water is released as each bond is formed.

b. Based on the information provided, calculate the length of the mRNA that was translated to produce the type I collagen. Explain how this answer was determined. (2 marks)

The mRNA that codes for type I collagen is approximately 4,392 nucleotides long, as each of the 1,464 amino acids is encoded by 3 nucleotides ($3 \times 1{,}464 = 4{,}392$). Additionally, the full length of the mRNA includes untranslated regions (UTRs), so the total length of the mRNA is closer to 18,000 nucleotides, corresponding to the size of the COL1A1 gene

Mark allocation:

- 1 mark is awarded for stating that the mRNA would be expected to be 4395 bases in length.
- 1 mark is awarded for explaining that the number of bases was determined by explaining that the mRNA would have been made up of 1465 codons and that the number of bases was determined by multiplying this number by 3.

Two students are discussing the information provided and they conclude that the mRNA is much shorter than expected compared with the DNA.

c. Use the i

The length of the mRNA is approximately 4,392 nucleotides, calculated by multiplying the 1,464 amino acids by 3 (since each amino acid is encoded by a codon of 3 nucleotides).

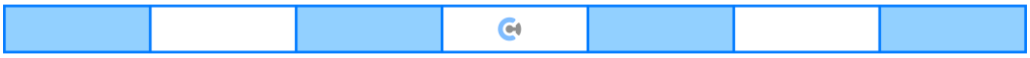
Mark allocation: 1 mark is awarded for identifying the substantial difference between the length of the DNA and the calculated length of the mRNA.

Note: Reference to the provided data is required. It is not enough to state that the DNA is

d. Produce an annotated diagram to describe how and why the difference between the length of the DNA and the mRNA occurred. Refer to the appropriate cellular processes in your answer. (2 marks)

The double-stranded template strand of DNA contains both introns and exons.

A primary transcript (pre-mRNA) is produced after the leading strand of DNA is transcribed. This strand of RNA contains both introns (non-coding regions) and exons (coding regions).



During post-transcriptional modification, the introns are removed and the exons are spliced together. Because mRNA only contains exons, this molecule will be shorter than the template strand of DNA and the pre-mRNA.

Mark allocation:

- 1 mark is awarded for producing a diagram showing the double-stranded DNA as well as the single-stranded pre-mRNA. It is essential to show the difference between the introns and the exons. The accompanying notation should refer to the process of transcription and identify that the pre-mRNA contains both introns and exons.
- 1 mark is awarded for drawing an appropriate diagram representing mRNA. The accompanying notation should explain that the introns are removed from the pre-mRNA during post transcriptional modification and therefore the mRNA molecule will be shorter than the template strand of DNA because it only contains exons.

Note: A methylated cap and poly-A tail may also be drawn (as this would be more accurate), however, based on the context of the question, these structures are not required.

Sub-Section [1.3.3]: Explain How a Single Gene Can Give Rise to Multiple Proteins

Question 17 (1 mark)

The genetic code contains codons that code for the 20 amino acids that are used to assemble proteins. Humans are believed to produce approximately 20,000 different proteins that perform a wide variety of functions.

This functional div

A. Multiple codo

B. Amino acids b

C. Proteins being

D. Post-translatio

Option A is incorrect. While this statement is accurate, the degeneracy of the genetic code does not contribute to the functional diversity of proteins.

Option B is correct. The primary structure of a protein is determined by the order in which the amino acids are assembled.

Option C is incorrect. Most proteins do not change shape, and if they denature they lose the ability to carry out their function. Proteins that can change shape normally carry out variants of the same function (e.g. a repressor protein will either bind to or release an operator region).

Option D is incorrect. Although a polypeptide chain is modified in the Golgi apparatus and results in the formation of a functional protein, the same type of polypeptide chain will be folded in the same way.

Question 18 (2 marks)

Explain how a single gene can give rise to many different proteins.

Alternative splicing allows different exons of the pre-mRNA to be joined in various combinations, leading to the production of multiple distinct mRNA transcripts from one gene, and thus different protein variants. After translation, proteins can be chemically modified (e.g., phosphorylation or glycosylation), which can alter their function, activity, or localization, resulting in different functional forms of the same protein.

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Sub-Section [1.3.4]: Identify and Recall the General Principles and Reasons for Gene Regulation in Both Prokaryotes and Eukaryotes

Question 19

Definitions:

a. Regulatory gene.

A segment of DNA responsible for producing proteins that regulate the expression of other genes.

b. Structural gene.

A segment of DNA that will produce proteins responsible for a functional or structural component in a cell or organism.

c. Repressor protein.

A protein produced by a regulatory gene that prevents gene expression by binding to its operator.

d. Activator protein.

A protein produced by a regulatory gene that increases gene expression.

e. Operon.

A cluster of structural genes that all share the same regulatory framework (i.e., the same promotor and operator)

Question 20 (1 mark)

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

A. Promotor.

B. Repressor.

C. Operator.

D. Regulator.

Question 21 (1 mark)

Repressor proteins regulate the production of protein by binding to the:

A. Promotor region, preventing RNA polymerase from functioning.

B. Operator region, preventing RNA polymerase from functioning.

C. RNA polymerase, preventing it from binding to the promotor region.

D. DNA polymerase, preventing it from binding to the promotor region.

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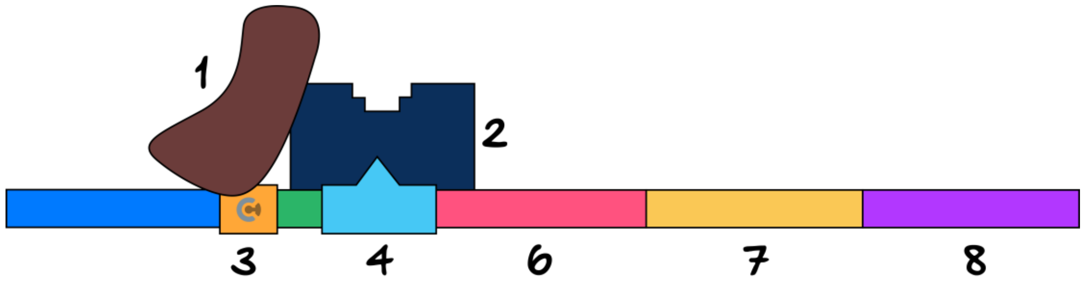
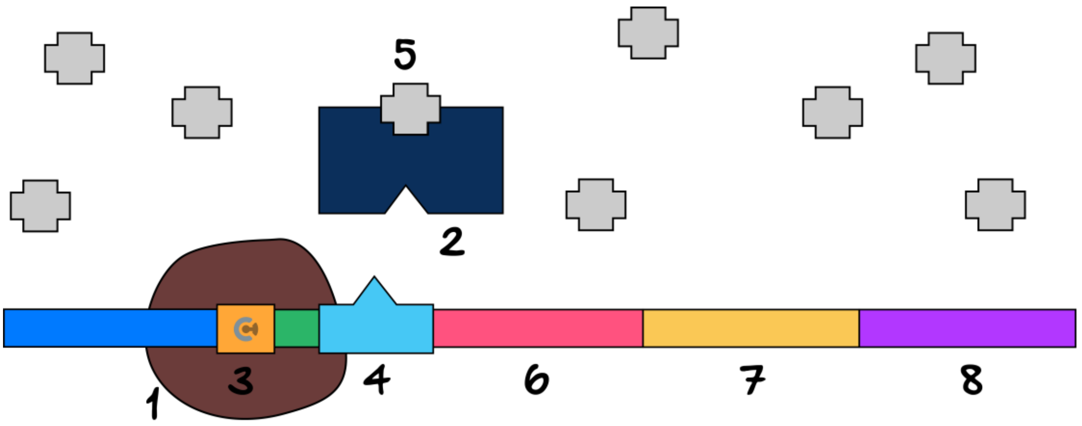
Question 22 (5 marks)

The trp operon is a method of gene regulation in some species of bacteria. It contains a series of three genes that code for the production of enzymes that facilitate the ability of the bacteria to metabolise tryptophan. These genes are switched on or off depending on whether tryptophan is present or absent.

a. Draw a labelled diagram to illustrate how the trp operon regulates the expression of the structural genes in the presence and absence of tryptophan. (2 marks)



In the absence of tryptophan, the repressor protein binds to the operator, upstream of the three structural genes. The presence of the repressor protein prevents RNA polymerase from binding to the operator region of the operon and prevent transcription from occurring.



When tryptophan is present it binds to the repressor protein, causing it to change shape and release the operator. RNA polymerase is now able to bind to the promoter region and transcription of the structural genes occurs.

Note: In the diagram, structures are as follows: **1 :** RNA polymerase; **2 :** repressor protein; **3 :** promoter region; **4 :** operator; **5 :** tryptophan; **6, 7 and 8 :** structural genes lacZ, lacY and lacA.

Mark allocation:

- 1 mark is awarded for providing a diagram that shows the repressor protein bound to the operator region in the absence of tryptophan.
- 1 mark is awarded for providing a diagram that shows the repressor protein changing shape and releasing the operator region in the presence of tryptophan.

Note: Annotations must be provided to be awarded each mark.

b. The trp operon is an example of gene regulation.

Explain how the bacterium benefits by being able to regulate the expression of the three genes that code for the production of the enzymes that facilitate the metabolism of tryptophan. (1 mark)

Protein synthesis is an endergonic process. Prevention of the expression of the structural genes in the absence of tryptophan enables the bacterium to conserve energy that can be used for other life-sustaining processes.

Mark allocation:

- 1 mark is awarded for providing an answer that demonstrates that protein synthesis is a process that uses energy and for explaining an advantage, such as enabling energy conservation.

c. Outline the role played by structural and regulatory genes in the trp operon system.

Include a reference to the functional distinction between structural and regulatory genes in your answer. (2 marks)

Regulatory genes code for the production of proteins that regulate the expression of other genes. Structural genes code for the production of any protein that plays a structural or functional role in an organism. In the trp operon, regulatory genes code for the production of the repressor protein, which regulates transcription. The three genes (lacZ, lacY and lacA) are structural genes because they code for the production of the enzymes that facilitate the metabolism of tryptophan.

Mark allocation:

- 1 mark is awarded for explaining the distinction between structural and regulatory genes.
- 1 mark is awarded for identifying examples of structural and regulatory genes in the trp operon.

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Sub-Section: Describe the Regulation of the trp Operon Through the Action of the Repressor Protein

Question 23

Definition: Repression.

The process by which the trp operon is regulated through the action of a repressor protein.

Question 24 (1 mark)

In reference to the trp operon, the gene is expressed when trp is not present because:

A. RNA polymerase is able to bind to the promotor.

B. trp is able to bind to the repressor.

C. The trp is able to block the action of RNA polymerase.

D. There is the formation of an attenuation loop due to the pause in translation at the leader sequence.

Question 25 (1 mark)

When trp is present in $E.coli$:

A. It binds directly to the trp repressor, causing a conformational shape change.

B. It binds directly to the operator, preventing RNA polymerase from binding.

C. It causes the formation of hairpin loops disabling the process of attenuation.

D. It does nothing.

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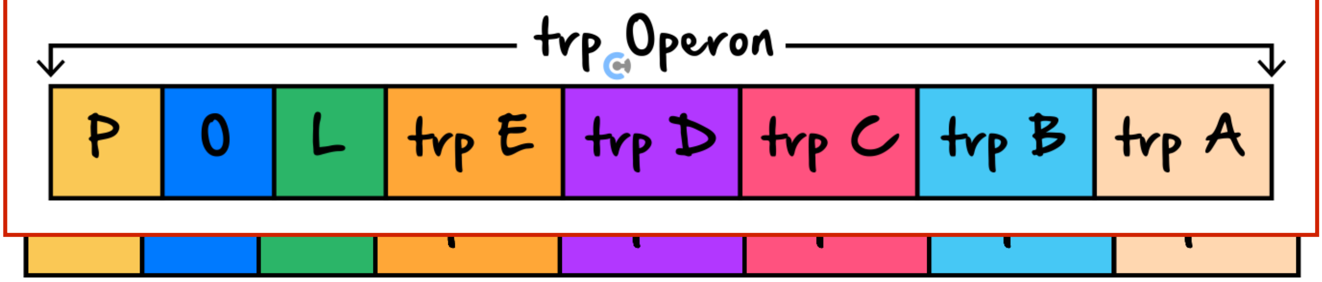
Question 26 (8 marks)

Repression is used by *E.coli* in order to regulate the levels of tryptophan that is present in the cell.

a. In the figure below, draw where a repressor protein would bind when tryptophan levels are high in the bacterial cell. (2 marks)

For correct position of repressor:



b. Explain why bacteria regulate the gene expression of enzymes involved in the synthesis of tryptophan. (1 mark)

Regulation of gene expression of enzymes involved in tryptophan synthesis enables the bacteria to conserve energy/ATP when tryptophan levels in the environment are high.

c. Explain the role of the trpR gene in the regulation of the trp operon. (3 marks)

As it says solution pending, the answer can be:

The trpR gene codes for the trp repressor protein, which plays a key role in regulating the trp operon.

1. Production of the trp repressor: The trpR gene is transcribed into mRNA and then translated to produce the trp repressor protein, which is inactive on its own.
2. Activation by tryptophan: When tryptophan levels are high, tryptophan molecules bind to the trp repressor. This binding causes a conformational change in the repressor protein, activating it.
3. Repression of the operon: The active repressor, now bound to tryptophan, attaches to the operator region of the trp operon. This prevents RNA polymerase from binding to the promoter and transcribing the genes needed for the synthesis of tryptophan. This ensures that the genes involved in tryptophan production are not expressed when tryptophan is abundant in the cell.

Thus, the trpR gene helps regulate the trp operon by controlling the activity of the repressor protein in response to tryptophan levels.

d. Andy thinks that once the trp production has stopped, it cannot be restarted. Is this true? (2 marks)

No, the repressor will dissociate after a while to “check” if trp levels have changed and then a new repressor will respond accordingly.

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Sub-Section: [1.3.6] Describe the Regulation of the trp Operon Through Attenuation in High trp Environments

Question 27

Definition: Attenuation.

The process by which the trp operon is regulated after transcription of the leader sequence has begun.

Question 28 (1 mark)

In the process of attenuation in the trp operon, which of the following determines whether the attenuator loop or anti-terminator loop forms?

A. The presence of the trp repressor protein bound to the operator.

B. The availability of tryptophan affecting ribosome stalling during translation.

C. The rate at which RNA polymerase binds to the promoter region.

D. The interaction between the leader sequence and the structural genes.

Question 29 (1 mark)

What happens during attenuation in the trp operon when tryptophan levels are high?

A. The ribosome stalls at the leader sequence, allowing the anti-terminator loop to form.

B. The ribosome moves quickly through the leader sequence, causing the attenuator loop to form.

C. The trp repressor protein binds to the operator, stopping transcription completely.

D. RNA polymerase skips over the leader sequence, allowing the transcription of structural genes.

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Question 30 (5 marks)

Describe the process of attenuation of the trp operon.

Take sample response from 1.3 workbook!

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