

Structured Questions: Paper 2

7.2 Transcription & Gene Expression

7.2.1 Regulation of Gene Expression by Proteins / 7.2.2 Environment & Gene Expression / 7.2.3 Transcription / 7.2.4 Post-transcriptional Modification / 7.2.5 Skills: Analysing DNA Methylation Patterns

Easy (5 questions)	/45
Medium (5 questions)	/47
Hard (5 questions)	/56
Total Marks	/148

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Easy Questions

- 1 (a) Genes are not expressed equally in every cell of an organism. While essential genes needed for survival are continually expressed, other genes are regulated so that they are only expressed in specific cells, at specific times to produce specific amounts of protein.

Suggest why the regulation of gene expression is beneficial for an organism.

(1 mark)

- (b) Scientists have calculated that roughly 1.3% of a mouse genome is made up of coding sequences. Non-coding DNA sequences can produce functional RNA molecules called transfer RNA. Other non-coding sequences act as specific regions that interact with transcription factors to regulate gene expression.

(i) Define the term "coding sequence".

[1]

(ii) Name the type of non-coding region that decreases or blocks transcription when a repressor protein binds.

[1]

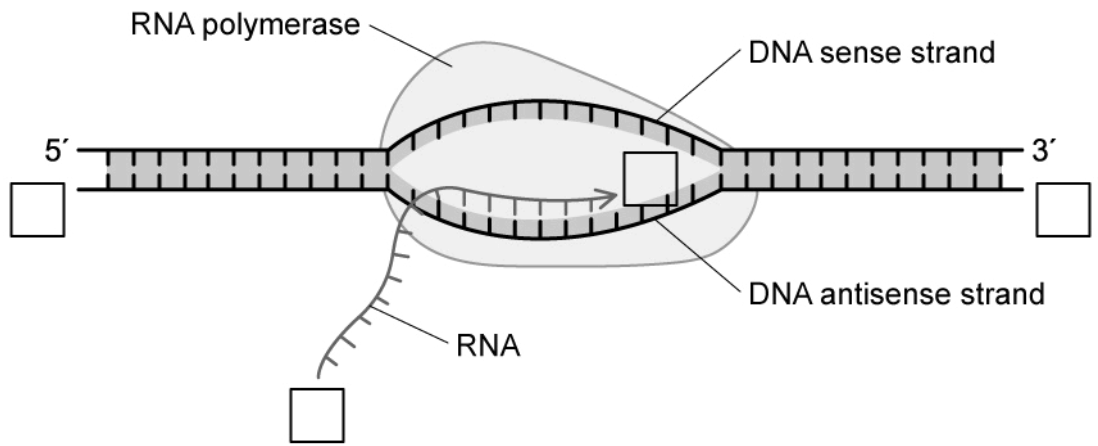
(2 marks)

- (c) When a gene is expressed, transcription occurs.

List the **three** stages of transcription in chronological order.

(1 mark)

- (d) The diagram below illustrates the action of RNA polymerase as it binds free RNA nucleotides to a growing RNA molecule.



Label the 5' and 3' ends of the DNA antisense strand and mRNA strand.

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(2 marks)

2 (a) Over 20,000 people died during the Dutch famine of 1944-1945. The "Dutch Hunger Winter" was unusual in that it started and ended very abruptly, allowing it to be analysed like an experiment to understand the effects of starvation and malnutrition on human health.

When investigating the short-term and long-term effects of the famine scientists found that pregnant women were particularly vulnerable. The children they gave birth to suffered from long-term health issues. As these children became adults they experienced significantly higher rates of obesity, diabetes and schizophrenia. Scientists also found that the Dutch Hunger Winter cohort had a 10% higher mortality rate after reaching 68 years old compared to those born before or after the famine. One study suggested that the conditions of the Dutch Hunger Winter silenced specific genes in unborn children and that they remained silenced through methylation.

(i) Define the term methylation.

[1]

(ii) Explain how methylation suppresses the transcription of a gene.

[1]

(2 marks)

(b) Methylation of DNA is an example of epigenetic modification which controls the expression of genes.

List **two** other types of epigenetic modification.

(2 marks)

(c) Both epigenetics and mutations lead to changes in the expressed characteristics of genes.

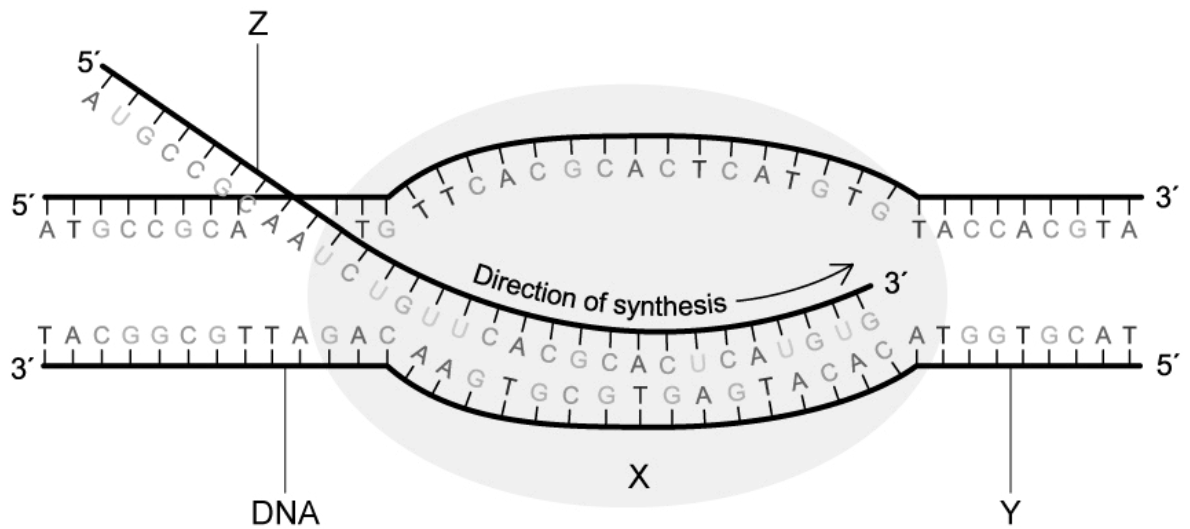
State the main way in which epigenetics differs from mutations.

(1 mark)

- (d)** Name another environmental factor aside from starvation, that can cause an organism's epigenome to change.

(1 mark)

3 (a) The process of transcription is illustrated in the diagram below.



(i) Identify molecule **X**.

[1]

(ii) Describe its role during transcription.

[2]

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(3 marks)

(b) From the image in part (a):

(i) Identify strand **Y**.

[1]

(ii) State the significance of strand **Y** in the process of transcription.

[1]

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(2 marks)

- (c)** After the process of transcription is completed, molecule **Z** must undergo splicing before it can move to the cytoplasm.

Describe the changes that are made to molecule **Z** before it leaves the nucleus.

(2 marks)

- (d)** The genetic code is universal across most forms of life.

Explain the importance of this statement.

(2 marks)

4 (a) Gene expression can be regulated after an mRNA transcript has been produced through post-transcriptional modification. There are several advantages of post-transcriptional modification, one of them being that it helps prevent the degradation of mRNA.

(i) Explain why mRNA is an inherently unstable molecule.

[1]

(ii) Suggest **two** other advantages of post-transcriptional modification in eukaryotic organisms.

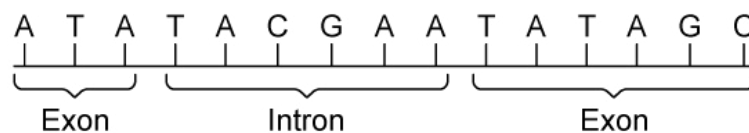
[2]

(3 marks)

(b) List **three** post-transcriptional events that must occur for pre-mRNA to become mature mRNA.

(3 marks)

(c) The diagram below shows the base sequence on part of a DNA sense strand.



Deduce, with a reason, the sequence of bases on the mRNA transcribed from this strand.

(2 marks)

(d) Explain why the proteome is bigger than the genome in eukaryotic organisms.

(1 mark)

5 (a) One mark is available for clarity of communication in this question.

Describe the structure and functions of nucleosomes.

(4 marks)

(b) A transcription factor binds to the promoter region of a gene which allows RNA polymerase to bind and for transcription to occur.

Draw a simple diagram to illustrate this process.

(3 marks)

(c) Outline how the lac operon functions to regulate gene expression in *Escherichia coli* when lactose is absent and when lactose is present.

(8 marks)

Medium Questions

- 1 (a) The compact structure of a nucleosome makes it impossible for transcription of DNA to occur.

Describe the mechanism that needs to occur in order to initiate transcription.

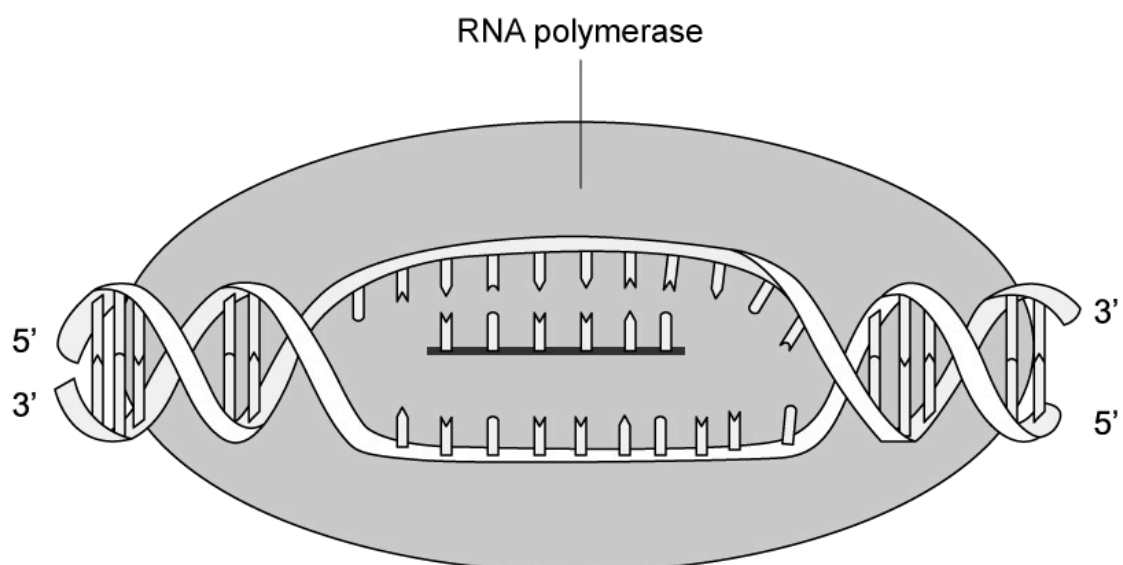
(3 marks)

- (b) During transcription, the DNA strand unwinds into two strands. One is named the sense strand and the other one the antisense strand.

Distinguish between the sense and antisense strands of DNA during transcription.

(1 mark)

- (c) The diagram below shows the process of transcription.



- i. Label the sense and antisense strands.
- ii. Draw an arrow on the diagram to show where the promoter region is located.

(2 marks)

(d) Transcription occurs in three stages: initiation, elongation and termination.

Describe what events occur during the elongation stage of transcription.

(1 mark)

2 (a) Nucleosomes help regulate transcription in eukaryotic cells.

State three chemical modifications of a nucleosome that could alter gene expression.

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(3 marks)

(b) Regulation of gene expression occurs in both eukaryotes and prokaryotes.

Describe two differences of this process in eukaryotes and prokaryotes.

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(2 marks)

(c) The following sections of a gene are important in regulating gene expression and transcription: promoter, coding sequence, terminator.

State the role of each of these components.

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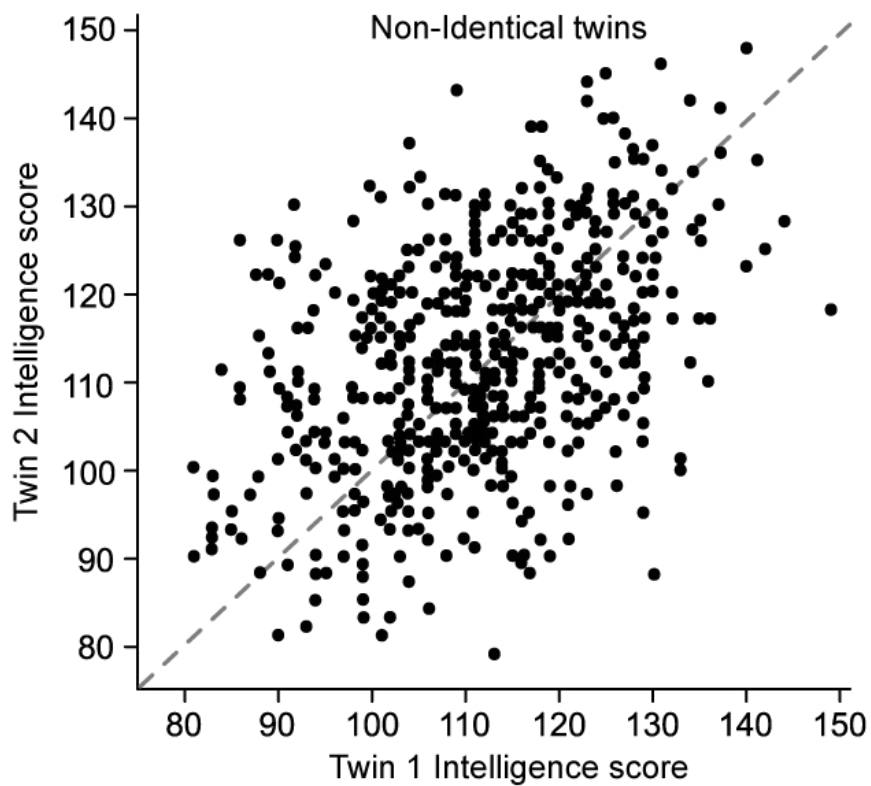
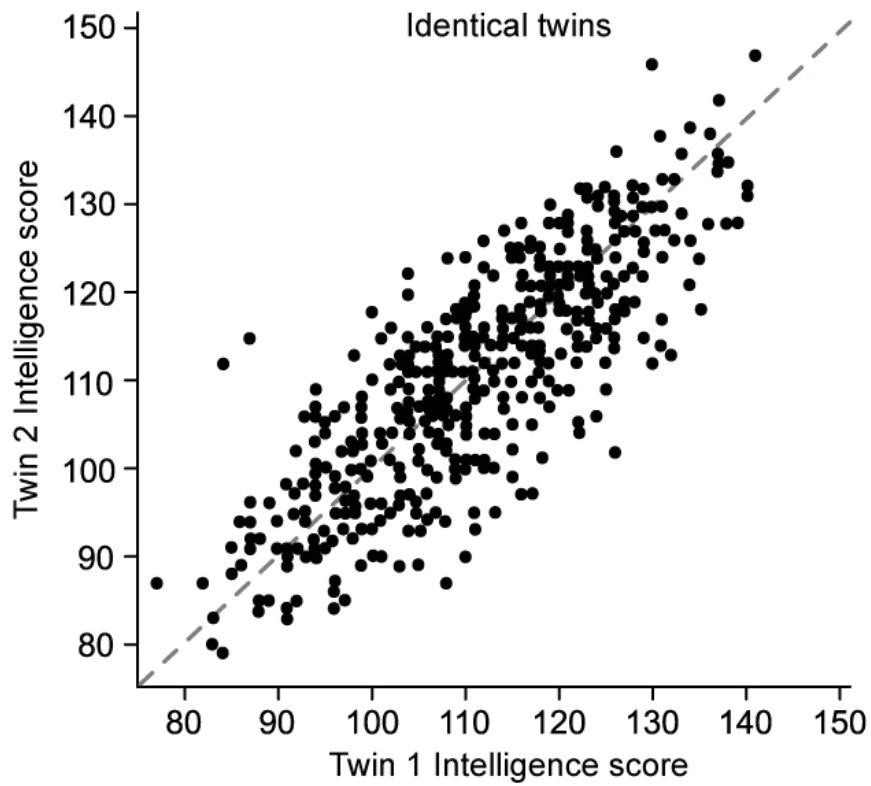
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(3 marks)

- 3 (a)** Environmental factors, internal and external, can influence gene expression by affecting levels of regulatory proteins or transcription factors. Environmental factors explain the differences observed between identical twins, even though they have the same DNA.

Scientists have investigated a range of phenotypic traits, such as intelligence, in twins. Data has been compared between identical and non-identical twins to help determine whether these characteristics are genetic or more greatly influenced by the environment. The graphs below shows data comparing identical and non-identical twins and their IQ.

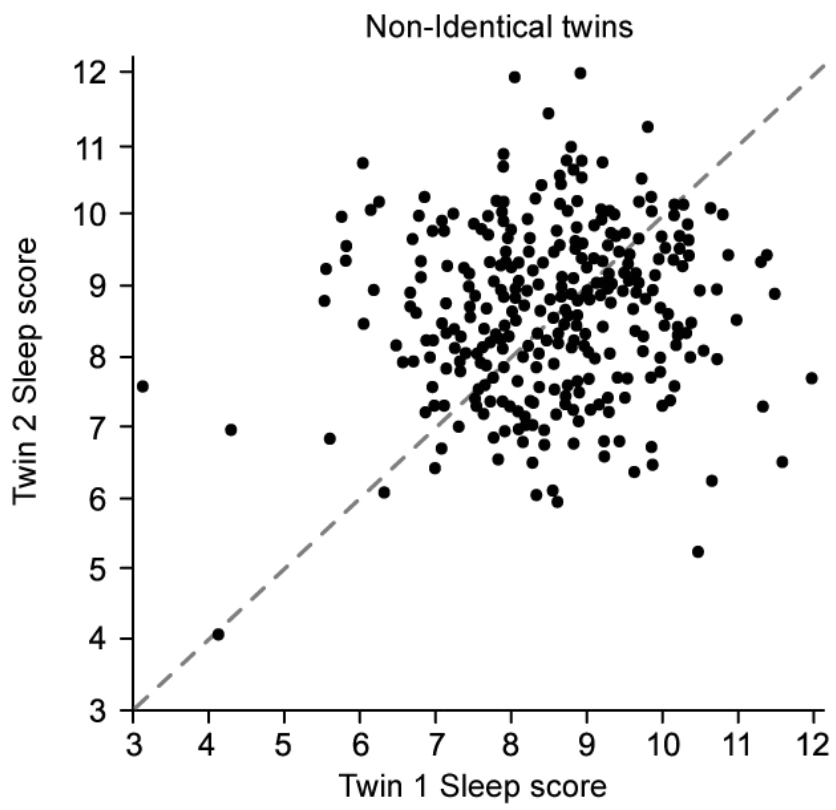
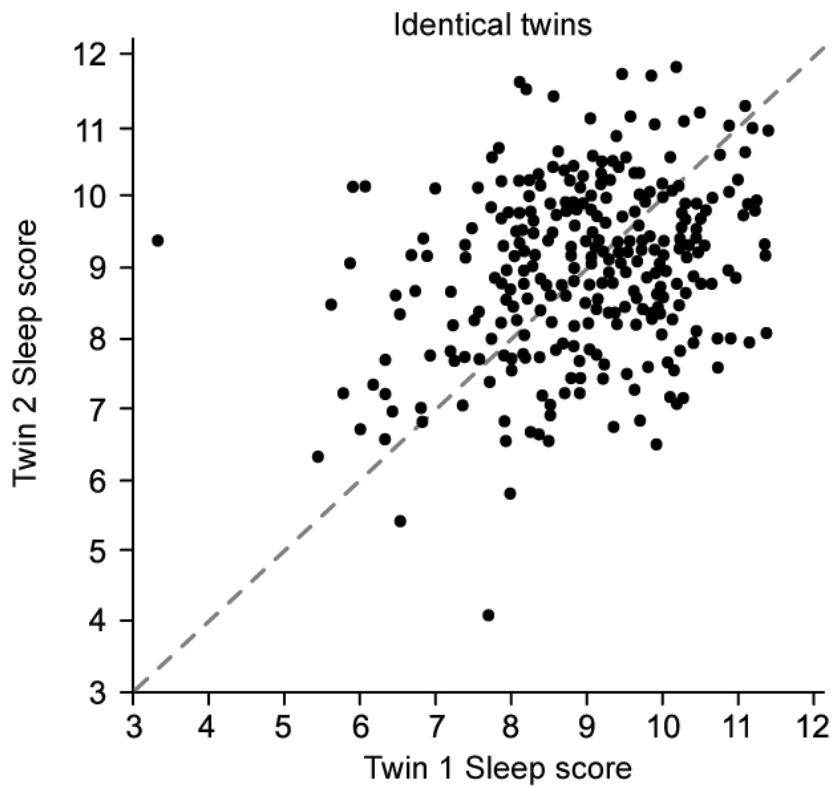


Suggest conclusions that could be drawn from the data shown in the graphs.

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(3 marks)

- (b)** The scientists also investigated how many hours per night identical and non-identical twins typically sleep. The results are shown in the graph below. The scientists concluded that sleep was not a heritable factor and environmental factors caused differences in sleep time.



Evaluate the scientists' conclusion.

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(2 marks)

- (c)** The environment has been shown to contribute to heritable changes in gene function. One such factor is epigenetics.

Outline what is meant by the epigenome.

(3 marks)

- (d)** DNA methylation involves the direct addition of a methyl group (-CH₃) to cytosine bases which can influence gene expression.

Explain the impact of methylation of DNA bases on gene expression.

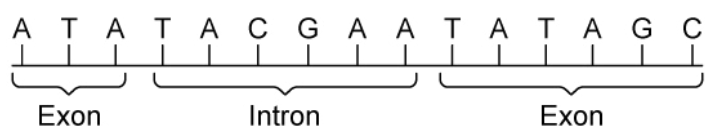
(2 marks)

- 4 (a) Gene expression can be regulated after an mRNA transcript has been produced, this is called post-transcriptional modification of mRNA.

Outline the mechanisms involved in post- transcriptional modification.

(3 marks)

- (b) The diagram below shows the base sequence on part of a template DNA strand.



Deduce, with a reason, the sequence of bases on the mRNA transcribed from this strand.

(2 marks)

- (c) Mature mRNA is transcribed from a gene and then translated into a protein. One single gene can give rise to different polypeptide chains.

Explain how a single gene can give rise to different amino acid sequences.

(1 mark)

- (d) A piece of mRNA is 972 nucleotides long but the DNA coding strand from which it was transcribed is 1215 nucleotides long.

Explain why there is a difference in the number of nucleotides.

(1 mark)

5 (a) *One mark is available for clarity of communication throughout this question.*

Messenger RNA (mRNA) is used during translation to form polypeptides. Describe how mRNA is produced in the nucleus of a cell.

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(7 marks)

(b) Explain the events of mRNA splicing.

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(4 marks)

(c) Outline the role of protein-protein interactions in the regulation of transcription.

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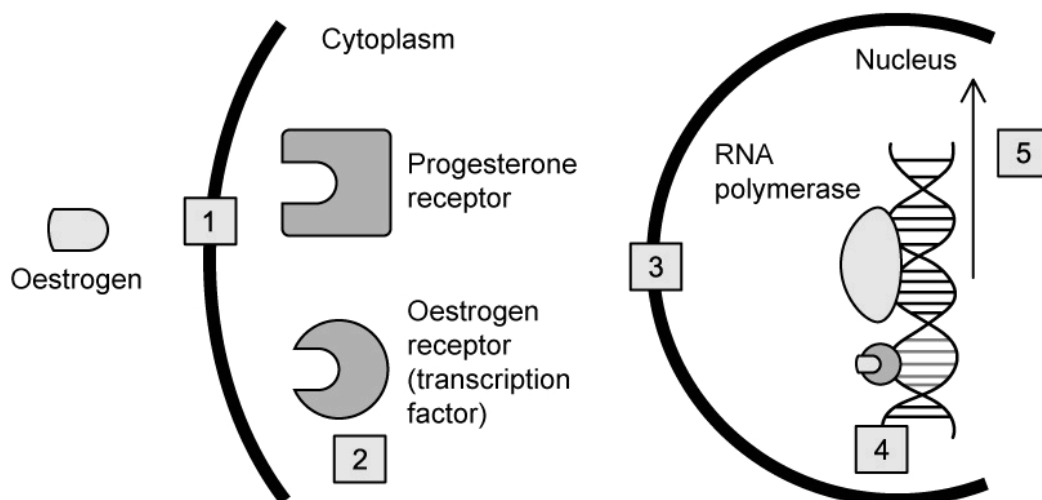
(4 marks)

Hard Questions

1 (a) Explain how transcription factors stimulate the expression of a gene.

(3 marks)

(b) The diagram below shows the mechanism by which oestrogen initiates gene expression.

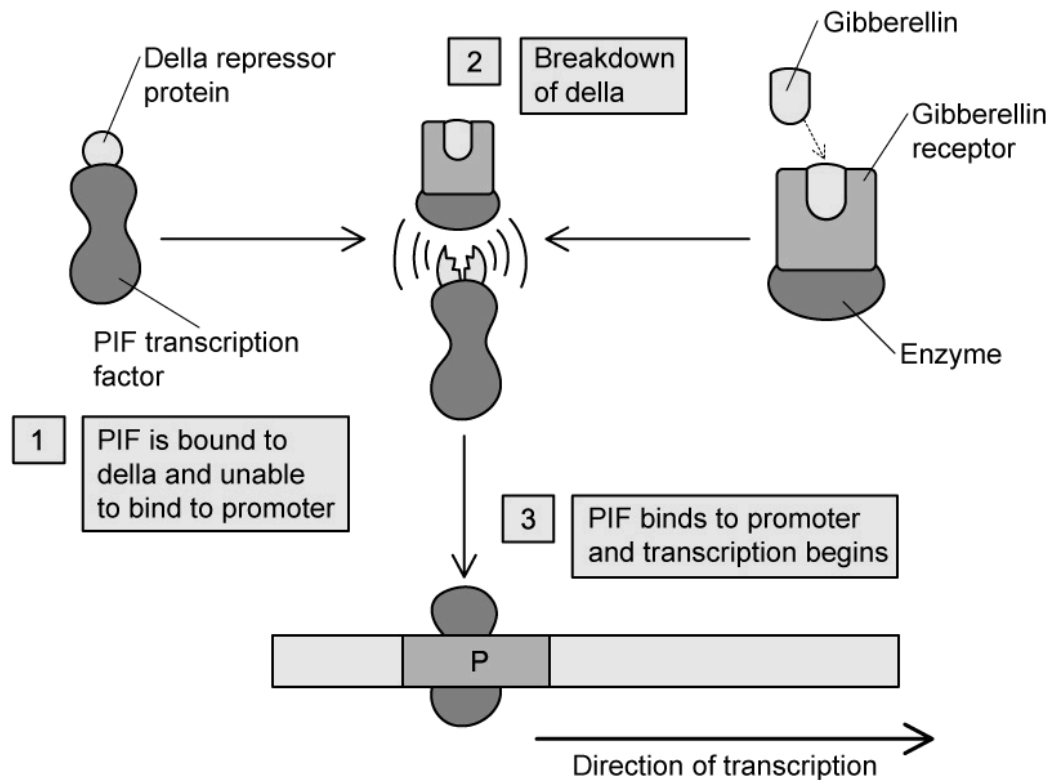


Compare and contrast the mechanism of action shown in the diagram with the process of non-competitive enzyme inhibition.

(3 marks)

(c) Plant cells use transcription factors in a similar way to animal cells. One transcription factor found in plant cells is called PIF. When activated, PIF binds to the promoter region

which triggers transcription of the amylase gene. PIF is inhibited by the presence of a repressor protein called DELLA. The plant hormone gibberellin stimulates the breakdown of DELLA to activate PIF. This process is shown in the diagram below.



Using the information above, suggest how the application of gibberellin hormone could facilitate the germination of seeds.

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(4 marks)

(d) Totipotent cells from one organism are genetically identical, however, not all of these genes are ultimately expressed.

Explain how differential gene expression forms an organism with specialised cells.

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(4 marks)

2 (a) In the 1800s Jean Baptiste Lamarck published his theory of inheritance of acquired characteristics which suggested that an organism can inherit characteristics that had been acquired during its parent's lifetime. Lamarck's theory has been much debated in the scientific world over the years, but more recently, advances in the understanding of epigenetics have led scientists to reconsider Lamarck's ideas.

Outline how the field of epigenetics supports the theory of inheritance of acquired characteristics.

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(3 marks)

(b) Explain how changes to DNA methylation and acetylation can activate gene expression.

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(5 marks)

(c) Epigenetic therapy could be used to treat diseases resulting from epigenetic changes by reversing changes to the acetylation of histones and methylation of DNA.

Suggest how knowledge of epigenetics could lead to the development of more effective treatments for diseases such as cancer.

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(2 marks)

3 (a) Outline the mechanism by which interactions between the genome and epigenome determine the proteome of an organism.

(3 marks)

(b) Explain why the genome of a bacterium is more simple to determine than the genome of a human.

(2 marks)

(c) The human genome project established that the human genome is made up of 26 564 genes and these genes contain 233 785 exons and 207 344 introns.

Use this information to calculate the average ratio of exons to introns per gene in the human genome.

(2 marks)

4 (a) A scientist obtained the mitotic index for a tissue sample taken from a patient.

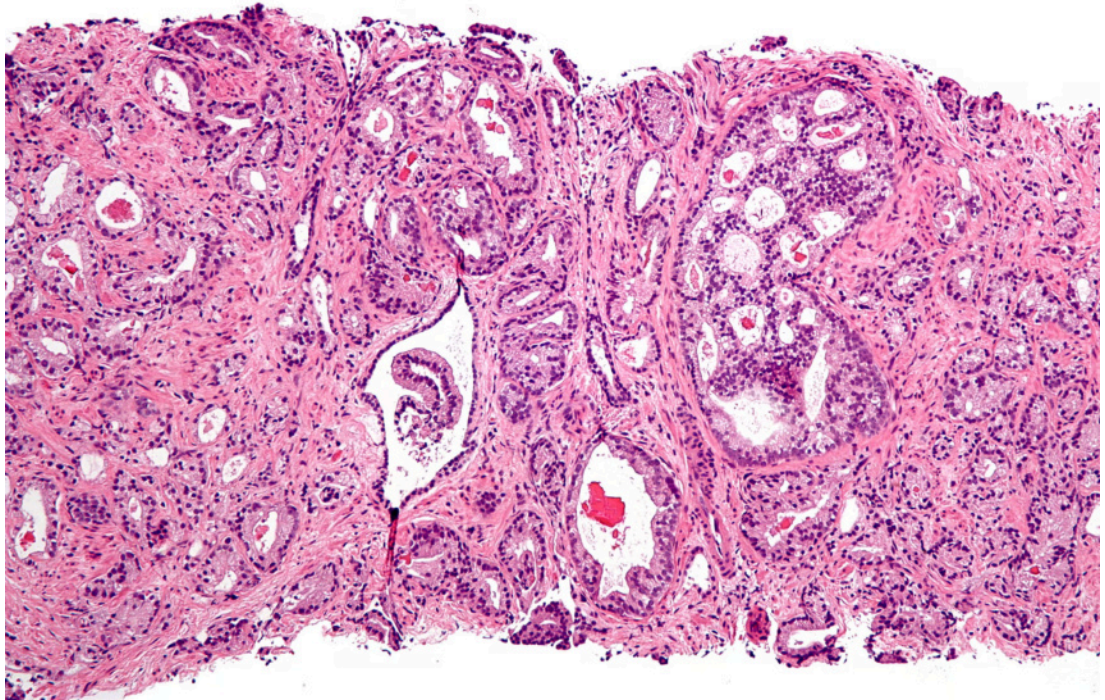


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- (i) Define the term mitotic index. [1]

- (ii) Suggest how the mitotic index could be used to indicate the presence of cancer in a tissue sample. [2]

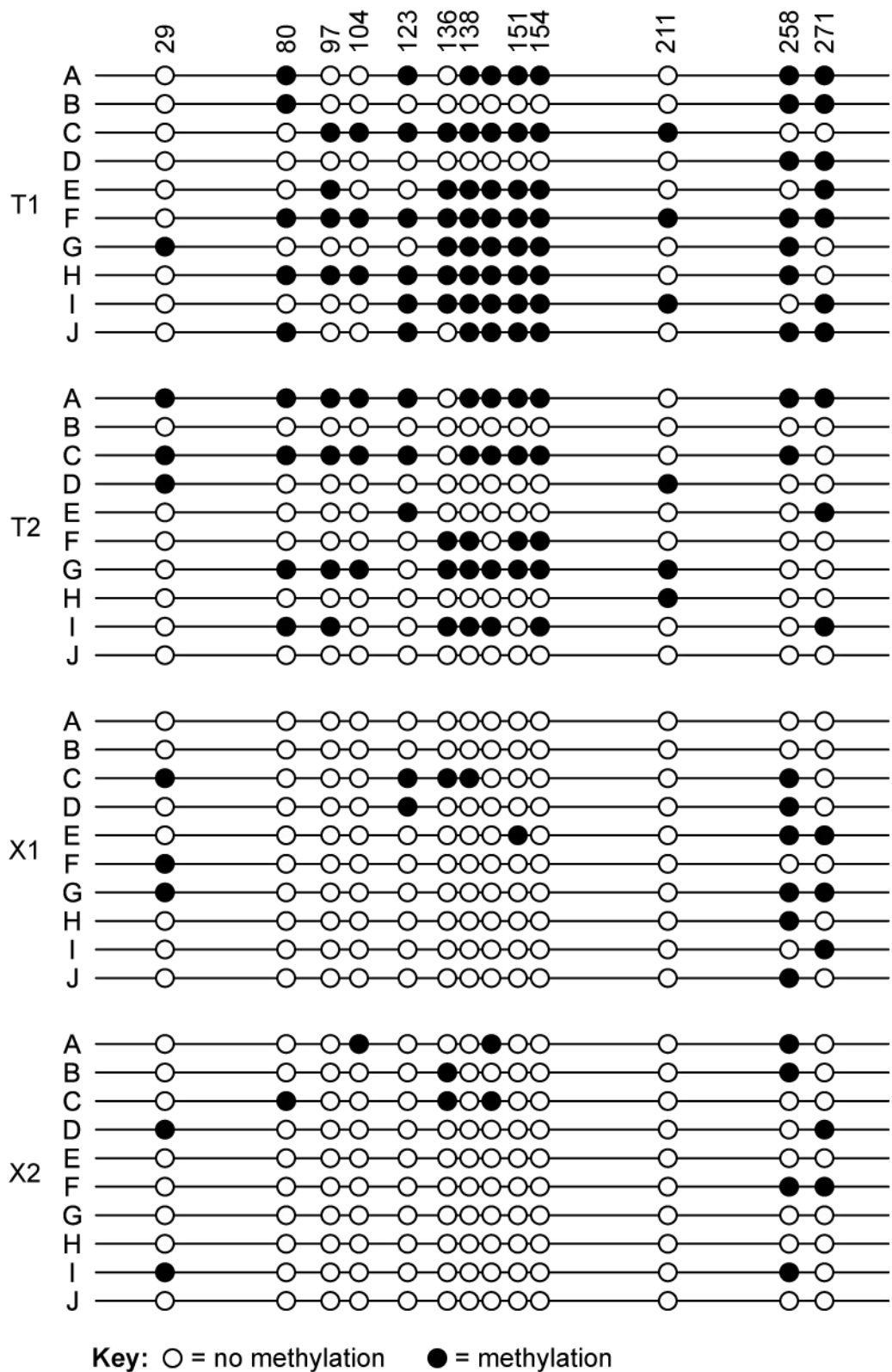
(3 marks)

(b) DNA contains several non-coding regions.

State **two** functions of these regions.

(2 marks)

- (c)** DNA methylation plays a vital role in gene regulation by affecting transcription. Tissue samples were obtained from two prostate cancer tumours (T1 and T2) and two normal prostate samples (X1 and X2). A specific gene was indicated as a plausible cause of cancer. The promoter of this specific gene was cloned several times (A-J). The data below shows the DNA methylation patterns from these samples. The numbers (29–271) represent different markers in the promoter region.



Use the information above to compare and contrast the methylation patterns in tumorous and normal tissue samples.

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(3 marks)

(d) Predict the effect DNA methylation could have on tumour cell genes.

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(2 marks)

(8 marks)