**Q1.**

In a eukaryotic cell, transcription results in a molecule of pre-mRNA that is modified to produce mRNA. In a prokaryotic cell transcription produces mRNA directly.

(a)     Explain this difference.

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**(2)**

(b)     Give **two** differences between the structure of mRNA and the structure of tRNA.

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**(2)**

**(Total 4 marks)**

**Q2.**

(a)     Describe how a phosphodiester bond is formed between two nucleotides within a DNA molecule.

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**(2)**

(b)     The two DNA strands of a particular gene contain 168 guanine bases between them. The relationship between the numbers of guanine bases (G), adenine bases (A), thymine bases (T) and cytosine bases (C) in these two strands of DNA is shown in the following equation.

G = 4(A + T) – C

Use this information and your understanding of DNA structure to calculate the maximum number of amino acids coded by this gene.

Show your working.

Answer \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**(2)**

(c)     Name the protein associated with DNA in a chromosome.

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**(1)**

(d)     In the process of semi-conservative DNA replication, the two strands within a DNA molecule are separated. Each then acts as a template for the formation of a new complementary strand.

Describe how the separation of strands occurs.

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**(2)**

**(Total 7 marks)**

**Q3.**

(a)     Describe how mRNA is formed by transcription in eukaryotes.

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**(5)**

(b)     Describe how a polypeptide is formed by translation of mRNA.

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**(6)**

(c)     Define ‘gene mutation’ and explain how a gene mutation can have:

•        no effect on an individual

•        a positive effect on an individual.

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**(4)**

**(Total 15 marks)**

**Q4.**

**Figure 1** shows all the chromosomes present in one human cell during mitosis. A scientist stained and photographed the chromosomes. In **Figure 2**, the scientist has arranged the images of these chromosomes in homologous pairs.

|  |  |
| --- | --- |
| **Figure 1** | **Figure 2** |
|  |  |

(a)     Give **two** pieces of evidence from **Figure 1** that this cell was undergoing mitosis. Explain your answers.

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**(2)**

(b)     Tick (**✓**) **one** box that gives the name of the stage of mitosis shown in **Figure 1**.

|  |  |  |
| --- | --- | --- |
| **A** | Anaphase |  |
| **B** | Interphase |  |
| **C** | Prophase |  |
| **D** | Telophase |  |

**(1)**

(c)     When preparing the cells for observation the scientist placed them in a solution that had a slightly higher (less negative) water potential than the cytoplasm. This did not cause the cells to burst but moved the chromosomes further apart in order to reduce the overlapping of the chromosomes when observed with an optical microscope.

Suggest how this procedure moved the chromosomes apart.

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**(2)**

(d)     The dark stain used on the chromosomes binds more to some areas of the chromosomes than others, giving the chromosomes a striped appearance.

Suggest **one** way the structure of the chromosome could differ along its length to result in the stain binding more in some areas.

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**(1)**

(e)     In **Figure 2** the chromosomes are arranged in homologous pairs.

What is a homologous pair of chromosomes?

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**(1)**

(f)      Give **two** ways in which the arrangement of prokaryotic DNA is different from the arrangement of the human DNA in **Figure 1**.

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**(2)**

**(Total 9 marks)**

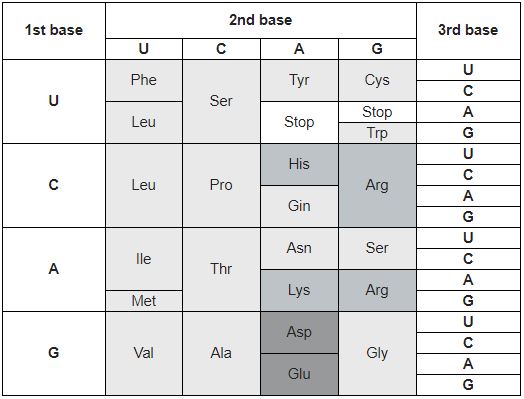
**Q5.**

(a)     Draw the general structure of an amino acid.

**(1)**

**Table 1** shows mRNA codons and the amino acids coded for by each codon. It also shows some properties of the R group of each amino acid.

**Table 1**



**Key** to the properties of the R group of each amino acid

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | No overall change |  | Positively charged |  | Negatively charged |

(b)     The genetic code is described as degenerate.

What is meant by this? Use an example from **Table 1** to illustrate your answer.

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**(2)**

A scientist investigated changes in the amino acid sequence of a human enzyme resulting from mutations. All these amino acid changes result from single base substitution mutations.

This enzyme is a polypeptide 465 amino acids long.

**Table 2** shows the result of three of the base substitutions.

|  |  |  |
| --- | --- | --- |
| **Table 2** | | |
| **Amino acid number** | **Correct amino acid** | **Amino acid inserted as a result of mutation** |
| 203 | Val | Ala |
| 279 | Glu | Lys |
| 300 | Glu | Lys |

(c)     What is the minimum number of bases in the gene coding for this polypeptide?

Answer = \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**(1)**

(d)     Use information from **Table 1** to tick (✔) one box that shows a single base substitution mutation in DNA that would result in a change from Val to Ala at amino acid number 203

|  |  |
| --- | --- |
| CAA → CGA |  |
| GUU → GCA |  |
| GUU → GUC |  |
| CAC → CGG |  |

**(1)**

(e)     A change from Glu to Lys at amino acid 300 had no effect on the rate of reaction catalysed by the enzyme. The same change at amino acid 279 significantly reduced the rate of reaction catalysed by the enzyme.

Use all the information and your knowledge of protein structure to suggest reasons for the differences between the effects of these two changes.

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**(3)**

**(Total 8 marks)**

**Q6.**

(a)     Give the **two** types of molecule from which a ribosome is made.

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**(1)**

(b)     Describe the role of a ribosome in the production of a polypeptide. Do **not** include transcription in your answer.

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**(3)**

(c)     The table below shows the base sequence of part of a pre-mRNA molecule from a eukaryotic cell.

Complete the table with the base sequence of the DNA strand from which this pre-mRNA was transcribed.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  | DNA |
| **A** | **C** | **G** | **C** | **A** | **U** | **U** | **A** | **U** | pre-mRNA |

**(1)**

(d)     In a eukaryotic cell, the base sequence of the mRNA might be different from the sequence of the pre-mRNA.

Explain why.

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**(2)**

**(Total 7 marks)**

Mark schemes

**Q1.**

(a)     1.      DNA of eukaryotic cell has non-coding regions / introns within gene

*Allow converse: (But) a prokaryotic cell does not have non-coding regions / introns in DNA;*

**OR**

pre-mRNA contains non-coding regions / introns;

2.      (After transcription / during modification) these regions are removed from (pre-)mRNA;

*Ignore references to 'cells need / bacteria do not need’*

**2**

(b)     1.      mRNA longer

**OR**

Has more nucleotides than tRNA;

2.      mRNA is a straight molecule but tRNA is a folded molecule / clover-leaf shaped molecule;

3.      mRNA contains no paired bases / hydrogen bonds but tRNA has some paired bases / hydrogen bonds.

**2 max**

**[4]**

**Q2.**

(a)  1.      Condensation (reaction)/loss of water;

2.      (Between) phosphate **and** deoxyribose;

3.      (Catalysed by) DNA polymerase;

*Reject if DNA polymerase joins AT/GC OR complementary nucleotides/bases OR forms hydrogen bonds*

**2 max**

(b)     Correct answer for 2 marks = 70;;

Accept for 1 mark,

A = 42 **and** T = 42

**OR**

420 (total bases in gene)

**OR**

210 (bases in template strand)

**2**

(c)     Histone;

**1**

(d)     1.      DNA helicase;

2.      Breaks hydrogen bonds between base pairs/ AT and GC/complementary bases

OR

Breaks hydrogen bonds between polynucleotide strands;

*Reject hydrolysis of hydrogen bonds*

**2**

**[7]**

**Q3.**

(a)  1.      Hydrogen bonds (between DNA bases) break;

*Ignore DNA helicase.*

*Reject hydrolysing hydrogen bonds.*

2.      (Only) one DNA strand acts as a template;

3.      (Free) RNA nucleotides align by complementary base pairing;

*For ‘align by complementary base pairing’, accept ‘align to complementary bases’ or ‘align by base pairing’.*

4.      (In RNA) Uracil base pairs with adenine (on DNA)

OR

(In RNA) Uracil is used in place of thymine;

*Do not credit use of letters alone for bases.*

5.      RNA polymerase joins (adjacent RNA) nucleotides;

*Reject suggestions that RNA polymerase forms hydrogen bonds or joins complementary bases.*

6.      (By) phosphodiester bonds (between adjacent nucleotides);

7.      Pre-mRNA is spliced (to form mRNA)

OR

Introns are removed (to form mRNA);

**5 max**

(b)     1.      (mRNA attaches) to ribosomes

OR

(mRNA attaches) to rough endoplasmic reticulum;

2.      (tRNA) anticodons (bind to) complementary (mRNA) codons;

3.      tRNA brings a specific amino acid;

4.      Amino acids join by peptide bonds;

5.      (Amino acids join together) with the use of ATP;

6.      tRNA released (after amino acid joined to polypeptide);

7.      The ribosome moves along the mRNA to form the polypeptide;

**6 max**

(c)     (Definition of gene mutation)

1.      Change in the base/nucleotide (sequence of chromosomes/DNA);

*For 4 marks at least one mark must be scored in each section of the answer.*

*Accept named mutation for ‘change’.*

2.      Results in the formation of new allele;

(Has no effect because)

3.      Genetic code is degenerate (so amino acid sequence may not change);

OR

Mutation is in an intron (so amino acid sequence may not change);

*Accept description of ‘degenerate’, eg some amino acids have more than one triplet/codon.*

4.      Does change amino acid but no effect on tertiary structure;

5.      (New allele) is recessive so does not influence phenotype;

(Has positive effect because)

6.      Results in change in polypeptide that positively changes the properties (of the protein)

OR

Results in change in polypeptide that positively changes a named protein;

*For ‘polypeptide’ accept ‘amino acid sequence’ or ‘protein’.*

7.      May result in increased reproductive success

OR

May result in increased survival (chances);

**4 max**

**[15]**

**Q4.**

(a)     1.      The (individual) chromosomes are visible because they have condensed;

*Both parts of each answer are required – evidence and explanation.*

*For ‘they’ accept ‘chromosomes/chromatin/DNA’*

*Accept ‘tightly coiled’ or ‘short and thick’ for condensed but do not accept ‘contracted’.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

2.      (Each) chromosome is made up of two chromatids because DNA has replicated;

*Both parts of each answer are required – evidence and explanation.*

*Accept ‘sister chromatids’ for ‘two chromatids’.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

3.      The chromosomes are not arranged in homologous pairs, which they would be if it was meiosis;

*Both parts of each answer are required – evidence and explanation.*

*Accept not meiosis because bivalents/chiasmata/crossing over not seen.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

**2 max**

(b)     Automarked q – ✔ prophase

**1**

(c)     1.      Water moves into the cells/cytoplasm by osmosis;

*Reject water moving into chromosomes/nucleus.*

2.      Cell/cytoplasm gets bigger;

*Accept idea of cell/cytoplasm has greater volume/swells/expands.*

*Ignore references to pressure changes, turgidity and chromosomes being more dilute.*

*Ignore references to changing water/fluid contents of the cell.*

*Allow ECF for ‘nucleus expands’ but not for ‘chromosomes expand’.*

**2**

(d)     Differences in base sequences

**OR**

Differences in histones/interaction with histones

**OR**

Differences in condensation/(super)coiling;

*Answer must be in context of differences in arrangement of chromosomes not just related to the properties of the stain.*

*Accept spec section 8 ideas e.g. different methylation/acetylation*

*Accept different genes*

*Reject different alleles*

**1**

(e)     (Two chromosomes that) carry the same genes;

*Reject ‘same alleles’*

*Accept ‘same loci’ (plural) or ‘genes for the same characteristics’*

**1**

(f)      (Prokaryotic DNA) is

1.      Circular (as opposed to linear);

2.      Not associated with proteins/histones ;

3.      Only one molecule/piece of DNA

**OR**

present as plasmids;

*Max 1 if prokaryotic DNA only found as plasmids OR if prokaryotic DNA is single stranded.*

*Ignore references to nucleus, exons, introns or length of DNA. Do not credit converse statements.*

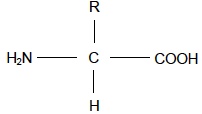
*Ignore descriptions of eukaryotic DNA alone.*

**2 max**

**[9]**

**Q5.**

(a)



*Accept other correct representations.*

**1**

(b)     1.      More than one codon codes for a single amino acid;

*Accept ‘triplet’ or ‘sequence of 3 bases/nucleotides’ for ‘codon’.*

*Reject ‘production/produces’ for ‘codes for’.*

*Do not infer mp1 from mp2.*

2.      Suitable example selected from Table 1;

**2**

(c)     1395;

*Accept 1398 and 1401 (for those that include start and/or stop codons)*

*Allow 2796 or 2802 or 2790*

*Ignore ‘bases/base pairs/bp/bps’ written after the numerical answer.*

**1**

(d)     ✔CAA → CGA

**1**

(e)     1.      (Both) negatively charged to positively charged change in amino acid;

2.      Change at amino acid 300 does not change the shape of the active site

**OR**

Change at amino acid 300 does not change the tertiary structure OR Change at amino acid 300 results in a similar tertiary structure;

*Reference to ‘shape’ of active site only needed once.*

3.      Amino acid 279 may have been involved in a (ionic, disulfide or hydrogen) bond **and** so the shape of the active site changes

**OR**

Amino acid 279 may have been involved in a (ionic, disulfide or hydrogen) bond **and** so the tertiary structure changed;

**OR**

Amino acid 279 may be in the active site **and** be required for binding the substrate;

*Reference to ‘shape’ of active site only needed once.*

*Both parts are required for each mark option.*

*For ‘a bond’ reject peptide bond.*

**3**

**[8]**

**Q6.**

(a)     1.      **One of** RNA / ribonucleic acid(s) / nucleotide(s)/nucleic acid(s) / rRNA / ribosomal RNA / ribosomal ribonucleic acid

**and**

**one of** protein(s) / polypeptide(s) / amino acid(s) / peptide(s) / ribosomal protein;

*Reject DNA, deoxyribonucleic acid, tRNA, transfer RNA, transfer ribonucleic acid, mRNA, messenger RNA, messenger ribonucleic acid.*

*Ignore enzyme(s), base(s).*

**1**

(b)     1.      mRNA binds to ribosome;

2.      Idea of two codons / binding sites;

3.      (Allows) tRNA with anticodons to bind / associate;

4.      (Catalyses) formation of peptide bond between **amino acids** (held by tRNA molecules);

5.      Moves along (mRNA to the next codon) / translocation described;

*Assume ‘it’ refers to ribosome.*

**3 max**

(c)     TGCGTAATA;

Any errors = 0 marks

**1**

(d)     1.      Introns (in pre-mRNA);

2.      Removal of sections of (pre-mRNA) / splicing;

*Introns removed’ scores 2 marks.*

*Reference to ‘introns present in mRNA’ disqualifies mp1 but allow ECF for mp2.*

*Accept for 1 mark mRNA contains only exons.*

**2**

**[7]**