**3.4 The Genetic code and Protein Synthesis question pack mark scheme 2016**

**M1.**          (a)     (i)      Deoxyribose;

*pentose / 5C sugar = neutral*

**1**

(ii)     Phosphate / Phosphoric acid;

*phosphorus / P = neutral*

**1**

(b)     Hydrogen (bonds);

**1**

(c)     381 / 384 / 387;

**1**

(d)     (Gln) Met Met Arg Arg Arg Asn;

**1**

(e)     Change in (sequence of) amino acids / primary structure;

Change in hydrogen / ionic / disulfide bonds leads to change in tertiary structure / active site (of enzyme);

Substrate cannot bind / no enzyme-substrate complexes form;

***Q*** *Reject = different amino acids are formed*

**3**

**[8]**

**M2.**          (a)     GCAAUG; ;

*Allow one mark if T instead of U, i.e. GCAATG*

**2**

(b)     (i)      DNA is edited / introns present in DNA;

*Allow reference to ‘junk’ or non-coding DNA*

**1**

(ii)     220; allow 218 or 219-allow 2

Three bases / nucleotides code for one amino acid;

Correct explanation for 218 or 219;

**2**

(c)     mRNA has no base-pairing, tRNA has base-pairing / mRNA linear,  
tRNA cloverleaf shape; mRNA has no binding site for amino acids,  
tRNA has; mRNA different for each gene / many kinds, only few / 20 / 64  
kinds of tRNA; accept mRNA longer / larger / more nucleotides than tRNA

**max 2**

**[7]**

**M3.**          (a)     (i)      C → B → E → F → A → D

*Mark links: 5 correct = 2, 4 correct = 1, <4 correct = 0*

**2**

(iii)     nucleus;

**1**

(iii)     A, D, F;    *(ignore E if evident)*

**1**

(b)     (i)      Isoleucine;

**1**

(ii)     TGG;

**1**

**[6]**

**M4.**          (a)     (i)      ACG;

**1**

(ii)     serine;

**1**

(b)     idea that DNA contains introns / mRNA is only exons / mRNA is “edited’;  
*(allow junk / non-sense DNA)*

**1**

(c)     binds to / blocks codon / triplet on mRNA so anticodon / tRNA will not fit in / base-pair;  
amino acids not delivered / joined;

*Accept translation will not occur for 1 mark*

**2**

**[5]**

**M5.**          (a)     Protein made of (chain of) amino acids;  
Each amino acid has its own base / triplet code;

**2**

(b)     UCA = 2 marks  
TCA – 1 mark;

**2**

(c)     CCG;  
GGG GGG;

**2**

(d)     (i)      Changes base sequence;  
Of later triplets / amino acid codes;

**2**

(ii)     S-phase / interphase;

**1**

(e)     1.      mRNA leaves (nucleus) through nuclear pore;

2.      To ribosome;

3.      tRNA molecules bring amino acids (to ribosome);

4.      Specific tRNA molecule for specific amino acid;

5.      Anticodon of tRNA corresponds / complementary to codon on mRNA;

6.      Peptide bonds form between amino acids;

7.      tRNA detaches and collects another amino acid;

8.      Ribosome moves along mRNA;

**max 6**

**[15]**

**M6.**          (a)     AGC; TTC;

**2**

(b)     anticodon complementary to codon / reads message on mRNA;

specific amino acid;

carried / transferred (to ribosome);

correct sequence of amino acids along polypeptide;

**3 max**

(c)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| (Met) | Phe | Gln | Gln | Lys | Gln | Phe |

**2**

*(three / four / five correct 1 mark; six correct 2 marks)*

**[7]**

**M7.**(a)     Translation;

**1**

(b)     Transfer RNA / tRNA;

**1**

(c)     TAC;

UAC;

**2**

(d)     Have different R group;

*Accept in diagram*

**1**

(e)     1.      Substitution would result in CCA / CCC / CCU;

2.      (All) code for same amino acid / proline;

3.      Deletion would cause frame shift / change in all following codons / change next codon from UAC to ACC;

**3**

**[8]**

**M8.**          (a)     (i)      9;

*Accept: nine*

**1**

(ii)     Introns / non-coding DNA / junk DNA;

Start / stop code / triplet;

*Neutral: Repeats.*

*Accept: ‘Introns and exons present’.*

*Reject: ‘Due to exons’.*

**1 max**

(b)     Change in amino acid / s / primary structure;

Change in hydrogen / ionic / disulfide bonds;

Alters tertiary structure;

*Reject: ‘Different amino acid is formed’ – negates first marking point.*

*Neutral: Reference to active site.*

**3**

(c)     Number of bases

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Number of bases | | | |
| C | G | A | T |
| Strand A | 26 | **19** | **20** | **9** |
| Strand B | 19 | **26** | 9 | **20** |

Second column correct;

Columns three and four correct;

**2**

**[7]**

**M9.**(a)     1.      Helicase;

2.      Breaks hydrogen bonds;

3.      Only one DNA strand acts as template;

4.      RNA nucleotides attracted to exposed bases;

5.      (Attraction) according to base pairing rule;

6.      RNA polymerase joins (RNA) nucleotides together;

7.      Pre-mRNA spliced to remove introns;

**6 max**

(b)     1.      Polymer of amino acids;

2.      Joined by peptide bonds;

3.      Formed by condensation;

4.      Primary structure is order of amino acids;

5.      Secondary structure is folding of polypeptide chain due to hydrogen bonding;

*Accept alpha helix / pleated sheet*

6.      Tertiary structure is 3-D folding due to hydrogen bonding and ionic / disulfide bonds;

7.      Quaternary structure is two or more polypeptide chains;

**5 max**

(c)     1.      Hydrolysis of peptide bonds;

2.      Endopeptidases break polypeptides into smaller peptide chains;

3.      Exopeptidases remove terminal amino acids;

4.      Dipeptidases hydrolyse / break down dipeptides into amino acids;

**4**

**[15]**

**E1.**          (a)     (i)      Most candidates correctly named part **R** as deoxyribose. Answers identifying part **R** as pentose or as a five carbon sugar were considered too imprecise due to the question clearly identifying the molecule as being DNA.

(ii)     Most candidates correctly named part **Q** as a phosphate group or as phosphoric acid. Unfortunately, some candidates incorrectly named parts **R** and **Q** the wrong way round.

(b)     Almost every candidate correctly stated ‘hydrogen bonds’.

(c)     Approximately fifty percent of candidates obtained this mark. Although there was a wide range of incorrect answers, the most common error was to divide, rather than multiply the number of amino acids by three.

(d)     Over 90 % of candidates were able to correctly work out the sequence of amino acids.

(e)     This question proved to be an effective discriminator. Most candidates gained at least one mark, often by mentioning a change in the sequence in amino acids. However, a significant number of candidates incorrectly referred to ‘different amino acids being formed’. Many of these candidates gained a second mark for describing that the active site or tertiary structure would be altered. Better candidates gained maximum marks either by linking this to enzyme-substrate complexes not being formed or to changes in hydrogen/disulfide bonds.

**E2.**          **Unit 2**

          (a)     Two marks were scored regularly. Confusion between T and A does exist in a significant number however, giving rise to the incorrect responses of GCAAUG and GCUUTG.

(b)     In (i) the idea of editing of mRNA was well understood, although some did remove the exons and therefore retained the introns. Poor expression was in evidence here. A few thought that stop and start codons could account for the large difference in number of nucleotides. In (ii) some extremely good answers were seen. Once again many candidates failed to gain marks through poor quality of expression. Amino acids are not made from three bases and, unless qualified by referring to code, the mark was not allowed. Some believed there to be 290 amino acids, but for the correct reason. A significant number believed there to be two amino acids because they went back to the DNA sequence at the beginning of the question rather than the piece of mRNA 660 nucleotides long. This was, however, given credit.

(c)     The examiners were very surprised to find this was badly answered, even by many of the best candidates. Candidates do not appreciate the difference between structure and function. Equally they were unable to provide pairs of matching statements. Successful candidates discussed linear and clover-leafed structure or length of molecules. A major error in a significant number of responses was to imply that tRNA was only three nucleotides long. Amino acid binding sites were discussed in terms of carrying amino acids. It was obvious that many candidates mis-read the question and discussed differences between DNA and RNA, as they referred to the bases present in the molecules.

**Unit 3**

(a)     This was a straightforward application question and most candidates gave the correct response.

(b)     Part (i) was reasonably well answered. The most common incorrect response was to explain the difference in length in terms of the start/stop codons. Responses to part (ii) showed candidates often chose to refer to the original sequence for part (a) rather than the section in part (b) to which the question actually referred. The examiners credited a correct response regardless of which section of mRNA was being used.

(c)     Only the most able candidates were able to give two structural differences. The vast majority of candidates gave a mixture of structural and functional differences.

**E3.**          **BYA2**

Most candidates were able to give the correct sequence in (a) (i). In (a) (ii), almost everybody gave the correct answer of nucleus, though there were some references to cytoplasm. There were fewer correct answers to (a) (iii), however, as many candidates assumed that only one stage had to be chosen. Part (b) was well answered by most. A small number of candidates gave the complementary sequence for the tRNA anticodon, UAA, rather than the name of an amino acid in (b) (i). The commonest error in (b) (ii) was to include uracil in the base sequence.

**BYA3**

(a)     The sequence of events was familiar to most. One mistake tended to lead to others, however. Nearly everyone was able to identify the nucleus. Some appeared to think only one letter was required in part (iii), but many successfully produced all three.

(b)     This question was accessible to many although part (ii) offered more scope for errors and several did not work through all the steps needed.

**E4.**          (a)     (i)      Most correctly gave the coding sequence of ACG. The most common incorrect answer involved replacing A with T.

(ii)     Most identified serine correctly.

(b)     There was some good understanding of introns and many identified this correctly as the explanation for the different number of nucleotides. The main incorrect answer occurred when candidates concentrated solely on stop/start codons.

(c)     This was poorly answered by many candidates. Most had some understanding of what was happening but only the better candidates could express this in enough detail to achieve full marks.

Weak candidates failed to use terms like codon, anticodon or translation, and often simply restated the question. Many referred to tetracycline carrying a stop codon.

**E5.**          **Unit 2**

(a)     Much confusion was shown here between bases, amino acids, DNA and protein. Few were able to give a clear account and many discussed translation, mRNA and tRNA and stumbled on markworthy points almost incidentally.

(b)     This usually scored two marks.

(c)     Although many produced a correct 9-letter code, several gave CCC rather than CCG, and some listed every triplet mentioned in the question.

(d)     This part of the question was not answered well. General accounts of mutation were often provided or changes other than addition of bases were given. Even those who were moving in the right direction failed to explain that the amino acid chain would only differ from this point onward. Many correctly identified the stage as interphase or the S phase but some offered translation or transcription.

(e)     Examiners commented on the precise use of language here even in papers where it was lacking elsewhere. Many started with transcription but got into their stride and gained 6 marks easily. Not all mentioned nuclear pores or the tRNA collecting more of the same amino acid. Several made creditable attempts to say that the amino acid was specific to the anticodon. Problems arose in the location of peptide bonds which were thought to join codons to ‘matching’ anticodons and a few failed to mention amino acids at all.

**Unit 3**

In part (a), many candidates did not link the base code with different amino acids in the sequence. Weaker candidates were confused about DNA structure and referred to it containing amino acids. In (b), the correct base sequence was given by most candidates. In (c), many failed to give the correct answer, but produced a long list of triplet codes instead. In (d)(i), many did not link a change in the sequence of bases with a change in the amino acid sequence and, hence, a change in the protein. It was common to read that a change in base sequence gave a different protein without further detail. Most candidates gave the S-phase or interphase in (d)(ii) although some offered ‘transcription’ or ‘replication’. Part (e) was surprisingly badly done by many candidates. Many started with transcription, but when they reached the required part of the story, described the process erroneously. Many did not refer to mRNA leaving the nucleus via nuclear pores, nor to the fact that tRNA brings *specific* amino acids. The complementary codon/anticodon binding was well described, but many candidates described anticodons attaching to amino acids. Many referred to polypeptide bonds instead of peptide bonds. Weaker candidates confused protein synthesis with DNA replication.

**E6.**          The majority of candidates gained the marks for application of knowledge. Straightforward recall proved difficult for some, through lack of adequate preparation for the examination.

(a)     There was a very disappointing number of correct responses. The vast majority of candidates quoted ‘mRNA codons’ and gained no marks.

(b)     Candidates who had not thoroughly learnt the factual material necessary to understand protein synthesis gave confused accounts and failed to gain any marks. Many candidates gained two marks but common omissions were failure to mention the specific nature of the amino acid carried and also failure to complete the story by reference to the correct sequence on the completed polypeptide.

(c)     The vast majority of candidates gained both marks.

**E8.**          (a)     (i)      Almost ninety percent of candidates were able to determine the maximum number of amino acids which could be coded for by the sequence of DNA bases provided.

(ii)     There was almost an equal split here between candidates who correctly referred to introns or stop/start codons and those candidates who incorrectly provided an explanation in terms of the code being degenerate.

(b)     This question proved to be a very effective discriminator. Most candidates gained at least one mark, often by mentioning a change in the sequence of amino acids. However, a significant number of candidates incorrectly referred to ‘different amino acids being formed’. Many candidates gained a second mark for explaining that the tertiary structure would be altered. Better candidates gained maximum marks either by linking this to changes in hydrogen/ionic/disulfide bonds. Candidates were not penalised for references to ‘active sites’ even though the question did not indicate that the protein was an enzyme.

(c)     Rather surprisingly, only half of the candidates gained marks on this question. Those that did gain credit usually obtained both marks by realising that it was important to match the number of complementary base sequences between strand A and strand B.

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