



# **A-Level Biology**

## **Protein Synthesis**

### **Mark Scheme**

**Time available: 67 minutes**

**Marks available: 53 marks**

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## Mark schemes

1.

(a) 1. Hydrogen (bonds);

2. Phosphodiester (bonds);  
*Accept ester/covalent bond*

2

(b) Correct answer for 2 marks = 1489/1489.2;;

Incorrect answer but for 1 mark accept:

876

**OR**

1861 - 1862

2

(c) 1. tRNA is 'clover leaf shape', mRNA is linear;

*Must be a comparison*

*Reject tRNA is double stranded*

*Accept tRNA is folded for tRNA is 'clover leaf shaped'*

2. tRNA has hydrogen bonds, mRNA does not;

3. tRNA has an amino acid binding site, mRNA does not;

*Accept 'CCA end' for amino acid binding site*

4. tRNA has anticodon, mRNA has codon;

2

(d) 1. mRNA fewer nucleotides

**OR**

Pre-mRNA more nucleotides

**OR**

mRNA has no introns/has (only) exons

**OR**

Pre-mRNA has (exons and) introns;

*Accept mRNA is shorter OR pre-mRNA is longer*

2. (Because of) splicing;

2

**[8]**

2.

- (a) 1. tRNA brings specific amino acid (to ribosome);
- 2. Anticodon (on tRNA) binds to codon (on mRNA);
- 3. Amino acids join by condensation reaction (using ATP)

**OR**

Amino acids join to form a peptide bond (using ATP);

3

- (b) 1. Hydrogen bonds form instead of ionic bonds;
- 2. Changes the tertiary structure (of the crystallin);  
*Ignore reference to active site*

2

- (c) 3 correct = 2 marks;;
- 2 correct = 1 mark;
- 0 or 1 correct = 0 marks

mRNA codon for the non-mutant triplet	AGG
Mutated mRNA codon	GGG
Mutated DNA triplet	CCC

2

[7]

3.

- (a) 1. (Free RNA) nucleotides form complementary base pairs;  
*Accept A-U, G-C **OR** combination of those pairs*
- 2. Phosphodiester bonds form;  
*Accept linkages for 'bonds'*
- 3. By (action of) RNA polymerase;

3

- (b) Base/nucleotide/triplet sequence coding for polypeptide/sequence of amino acids/primary structure;

1

- (c) Serine Alanine Glycine Proline;  
*Must be in this order Accept Ser Ala Gly Pro / S A G P*

1

(d) Mark as pairs. 1 and 2 **or** 3 and 4.

(No)

1. G to C (in the second codon/for Glycine)

**OR**

CGT to CCT (in second codon/for Glycine);

2. (So), substitution (not addition mutation);

*Reject if substitution of Glycine (for Alanine)*

**OR**

3. (If addition) frameshift / all triplets moved;

4. (So), affects more than one amino acid;

2

[7]

4.

(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]

5.

(a) (The proteome is the full) range of / number of different proteins that a cell is able to produce (at a given time);

OR

(The proteome is the full) range of / number of different proteins the genome / DNA is able to code for;

*Do not accept number of proteins unqualified*

1

- (b) 1. mRNA does not have hydrogen bonds / base pairing, tRNA does;  
**OR**  
mRNA is linear / straight chain, tRNA is cloverleaf;
2. mRNA does not have an amino acid binding site, tRNA does;  
*Accept mRNA cannot carry an amino acid, tRNA can*
3. mRNA has more nucleotides;  
*Accept mRNA is longer or converse*
4. (Different) mRNAs have different lengths, all tRNAs are similar / same length;
5. mRNA has codons, tRNA has an anticodon;  
*Statements must be comparative*

2 max

- (c) 1. mRNA associates with a ribosome / ribosome attaches to mRNA;  
*Idea of association is required*
2. Ribosome moves to / finds the start codon / AUG;
3. tRNA brings / carries (appropriate / specific) amino acid;  
*Must be explicitly stated and not inferred.*
4. Anticodon (on tRNA complementary) to codon (on mRNA);
5. Ribosome moves along to next codon;  
**OR**  
Ribosome 'fits' around two codons / can fit two tRNAs;  
*Must be explicitly stated and not inferred.*
6. (Process repeated and) amino acids join by peptide bonds / condensation reaction (to form polypeptide);  
**OR**  
(Process repeated and) amino acids joined using (energy from) ATP (to form polypeptide);

5

[8]

6.

(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]**