Exampro A-level Biology (7401/7402)

Name:

Class:

DNA, Genes and Chromosomes

Author:

Date:

Time: 63

Marks: 50

Comments: **These questions mix the different styles of questions. Short answers, practical techniques, experimental data analysis, extended answer and comprehension Work through these, the more you do the better you will become with your exam technique.**

M1.(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]

M2.(a) (i) 4;

1

(ii) 1. Change in amino acid / (sequence of) amino acids / primary structure;

1. Reject = different amino acids are 'formed'

2. Change in hydrogen / ionic / disulphide bonds alters tertiary structure / active site (of enzyme);

2. Alters 3D structure on its own is not enough for this marking point.

3. Substrate not complementary / cannot bind (to enzyme / active

site) / no enzyme- substrate complexes form;

3

(b) 1. Lack of skin pigment / pale / light skin / albino;

2. Lack of coordination / muscles action affected;

2 max

(c) Founder effect / colonies split off / migration / interbreeding;

Allow description of interbreeding e.g. reproduction between individuals from different populations

1

[7]

M3. (a)

DNA	✓	2
mRNA	✗	1
tRNA	✓	1

One mark for each correct column
Regard blank as incorrect in the context of this question
Accept numbers written out: two, one, one

2

(b) (i) Marking principles
1 mark for complete piece transcribed;

Correct answer
UGU CAU GAA UGC UAG

1 mark for complementary bases from sequence transcribed;

but allow 1 mark for complementary bases from section transcribed, providing all four bases are involved

2

(ii) Marking principle
1 mark for bases corresponding to exons taken from (b)(i)

Correct answer
UGU UGC UAG
If sequence is incorrect in (b)(i), award mark if section is from exons. Ignore gaps.

1

[5]

M4.(a)

Statement	Vertical	Horizontal
Gene is replicated	✓	✓
Gene can be passed to other species of bacteria		✓
Involves conjugation		✓

*One mark for each correct **column***

2

(b) (i) 1. Prevents protein synthesis;

Accept: ribosomes produce proteins / chains of amino acids / polypeptides

Reject: ribosomes produce amino acids

2. (So) enzymes not produced / any named process involving proteins / enzymes is inhibited;

Accept: no (DNA) replication

Accept: cannot form a cell wall

Reject: no mitosis

Neutral: no growth / repair

2

(ii) **ACC GGA ACC ACG;**

1

(iii) **C;**

Accept: 'cytosine'

1

(iv) 1. Different tertiary structure / tertiary shape;

Neutral: 3D structure

2. (So tetracycline) does not fit / bind / is not complementary / does not enter / pass through (protein / into cell);

Q *Reject: any reference to 'active site', 'enzyme-substrate complex' or (tetracycline) not fitting / binding to an enzyme*

Accept: (so) more tetracycline pumped out of cell

2

[8]

M5.(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 <u>and</u> 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]

M6. (a) Phosphate;

Deoxyribose;

Q *Candidates must specify deoxyribose. This term is a specification requirement.*
Ignore anything that is not incorrect.

2

(b) 4;

1

(c) (i) 14;

1

(ii) 36;

If (c)(i) incorrect accept [50 – (c)(i)]

1

(d) Different genes;

Different (DNA) base sequences;

2

[7]