

Mark schemes

(a) (i) Deoxyribose;

1 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] (a) Phosphate;

2

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]

3

(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]

(a)

(i)

ACG;

4

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] (a) antibiotic has diffused / spread / moved into agar;

5

k
i
l
l
e
d
/
i
n
h
i
b
i
t
e

- (b) largest clear area / inhibition zone / killed the most bacteria; 1
- (c) disrupts cell wall / prevents cell wall synthesis; stops DNA replication; 2
- [5] (a) Protein made of (chain of) amino acids;

6

- 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] (a) (i) C → B → E → F → A → D

7

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

- (iii) nucleus; 1
- (iii) A, D, F; (*ignore E if evident*) 1
- (b) (i) Isoleucine; 1
- (ii) TGG; 1
- 1 (a) (i) join / attach nucleotides, to form a strand / along backbone / phosphodiester bonds; [6

8

- (*reject reference to H bonds, complementary base pairing*) 1
- (ii) ribosome / RER; 1
- (b) (i) CGTTACCAA; 1
- (ii) CGU UAC CAA; 1
- (c) substitution; 1
- (d) (i) alanine; 1
- (ii) (mutation 1) no change(to sequence of amino acids);
codon for alanine / degenerate codon / same amino acid coded for; 2
- (mutation 2)
(change in sequence) valine replaced by alanine / codon for alanine;
folding / shape / tertiary structure / position of bonds may change;
(*reject peptide bonds*) 2

[10] (a) side effects / allergic reactions / low toxicity to cells;

9

interaction with other drugs / effective in conditions of use / reasonably stable; should only act on the problem bacteria / narrow spectrum; how much resistance the bacteria have built up;

2 max

- (b) (i) tetracycline

prevents tRNA binding to ribosomes / amino acid / mRNA;

1

amino acids not available / brought / picked up;

1

chloramphenicol

prevents amino acids being joined / prevents primary structure forming;

1

no enzymes / no structural proteins formed;

(accept cell wall formation if qualified) (prevents protein synthesis gains one mark in either section, once only)

1

- (ii) only prevents tRNA binding to 70S / prokaryotic / bacterial ribosomes / human ribosomes are different sizes / shapes / structure;

1

[7] (a) AGC; TTC;

10

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
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2

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

[7] (a) high energy radiation / ionising particles;

11

named particles / α , β , γ ;
colchicine; x rays /
cosmic rays; uv (light);
carcinogen / named carcinogen;
mustard gas / phenols / tar (qualified);

1 max

- (b) (i) removal of one or more bases / nucleotide;
frameshift / (from point of mutation) base sequence change;

2

- (ii) sequence of bases in mRNA would change;
(sequence of) amino acids different / different primary structure;
(active site / enzyme 1) changed tertiary shape / changed active sites; white pigment does not bind; lilac pigment not produced / white pigment remains unchanged / enzyme 1 does not function;

(iii) blue and lilac; white;

<i>colour of petal</i>
<i>(white)</i>
blue
lilac;
white;

2

[9] (a) chloroplast, so cell photosynthesises and moves to optimum / best light intensity for

12

photosynthesis;
avoids damage due to bright light;

2

(b) (i) 2700

1

$$\frac{242 \times 7500 \times 900}{60} \quad (\text{ii}) \quad \begin{matrix} {}^6 = 2 \text{ marks} \\ = 27\,225\,000 / 27 \times 10 \end{matrix}$$

(allow 1 mark for principle:

$$\frac{\text{amino acids} \times \text{proteins}}{\text{time}}$$

)

2

(c) (i) rate slightly slower / not affected in first 20 / 30 minutes / lower peak than control; then decreases / much lower (than control);

(allow 1 mark for increase in first 20 / 30 minutes, then decreased, if not compared with control / normal)

(disqualify flagellum grows longer)

2

(ii)

1. actinomycin has no effect (on growth of flagella); even though mRNA production / transcription prevented;

(accept references to 'expt 1')

2. (re)growth little affected by puromycin at first; protein synthesis inhibited, so likely to be using proteins present;

4

[11] (a) 387;

13

- (b) (i) CCAG; 1
- (ii) 5; 1
- (c) high energy radiation / X rays / ultraviolet light / gamma rays; high energy particles / alpha particles / beta particles; named chemical mutagens e.g. benzene / caffeine / pesticide / mustard gas / tobacco tar / free radicals;
(two named examples of any of the above = 2 marks)
length of time of exposure (to a mutagen); dosage
(of mutagen); 2 max
- (d) (i) UAC UUA UGG; 1
- (ii) addition and deletion (of bases / nucleotides); thymine added;
adenine deleted;
(addition of thymine and deletion of adenine = 3 marks)
(allow addition of adenine (RNA) and deletion of uracil (RNA)
= 2 marks) 3

[9] (a) (i) number of bases = 4440

14

allow 4446 if they refer to start / stop

- each amino acid coded for by triplet / three bases
(so three times more bases than amino acids); 2
- (ii) deletion;
(deletion) of three bases;
because substitution / addition would change amino acid(s); 2 max
- (b) codon on mRNA; specific / complementary
base pairing with; anti-codon on tRNA;
specific tRNA for each amino acid; protein
formed by condensation reactions /
peptide bonds formed; 4 max

[8] (a) memory B / T cells do not recognise (new antigens);

15

antibodies previously produced are not effective
as shape not complementary to new antigen;

2

(b) (i) antigen in membrane presented to lymphocytes /
produce cytokinins;

1

(ii) mitochondria provide (more) ATP / energy;
(more) RER / ribosomes synthesise proteins;
(more) Golgi body secretes / modifies or packages proteins /
produces glycoproteins;
(B lymphocytes) produces antibodies;

4

[7]

change in base / nucleotide (in DNA);

16

change in base sequence of mRNA / change in codons / idea of
frameshift following deletion or addition / incorrect tRNA /
anticodon; incorrect amino acids / different primary structure /
formation of new stop codon; different tertiary structure / different 3D
structure / different polypeptide / shortened polypeptide;
different shape of active site / no active site present;

[5] (a) mutation changes the amino acid sequence / primary structure of Factor VIII protein;

17 changes the tertiary structure / 3D shape;

2

(b) (mutant) Factor VIII protein is non-functional / does not work with Factor IX; so no
conversion of Factor X to active form and pathway blocked;

2

(c) boy's blood contains (active) Factor VIII;
Factor VIII haemophiliac's blood contains (active) Factor IX;
the mixture has both Factors and so the pathway can
complete / blood clots;

2 max

[6] (i) mRNA attaches to ribosome;

18

codon on mRNA; binds to an anti-codon on tRNA; each tRNA brings a
specific amino acid; sequence of codons / bases on mRNA determines
order of amino acids; formation of peptide bonds / amino acids joined
by condensation reactions;

4 max

(iii) inserted gene / mRNA complementary to normal gene / mRNA;
binds to it to prevent protein synthesis / form double strand /
prevents mRNA binding to ribosomes; will not stop all translation,
some mRNA reaches ribosomes / because not all mRNA is bound
by inserted gene mRNA;

2 max

[6]

19

- (a) (Gene 1) allele A makes enzyme converting J to K / colourless to red;

Allele a produces no / non-functional enzyme;
(Gene 2) allele B makes enzyme converting K to L / red to purple;
Allele b produces no / non-functional enzyme;
("Recessive alleles produce no / non-functional enzyme" = 2)
White flowers result from genotype aa;
... regardless if B or b / even if aaB_ ;
Colourless (substance) / J produces white;
Red flowers when A_ bb / enzyme 1 only;
Purple flowers when A_ B_ / enzymes 1 and 2;

6 max

- (b) (i) (1) (red parent) AAbb;

(2) (white parent) aaBB;

2

- (ii) F₁ are AaBb;

F₂ ratio of 9 : 3 : 4;

Purple : red : white;

Suitable working shown;

4

- (c) (i) aabb, aaBb, and aaBB; (allow aabb & aaB_)

1

- (ii) (Crush each type of white petal to make an extract, and) add some of the (red) pigment / K, to petal OR incubate with K;
(extract becoming) purple is identified as aaBB OR that staying red, after K is added, is aabb;

2

[15] (a) Two suitable differences between DNA and RNA;

20

1 mark per correct row to 2 max

e.g.

DNA is double stranded, RNA is single stranded;
DNA has thymine present, RNA has Uracil present;

Accept T and U

DNA is larger/heavier/longer, RNA is smaller/lighter/shorter;
DNA has a deoxyribose sugar, RNA has a ribose sugar;
DNA stays in the nucleus, RNA leaves the nucleus;

2 max

- (b) Three suitable examples;

e.g.

Carries coded information about the sequence of amino acids;
Copied from DNA/gene;
Code is in sequence of bases / triplet / three bases / a codon codes for one amino acid;
Moves out of nucleus/goes into cytoplasm;
To ribosomes;

Accept codons allow anticodons / tRNA to bind

Accept carries 'start' and 'stop' codes

Accept moves through ribosomes

3 max

[5]

(a) Any two of:

21

DNA	RNA
Large molecule	Smaller
Double stranded	Single stranded
Contains Thymine (T)	Contains Uracil (U)
Contains deoxyribose	Contains ribose

2 max

(b) Base sequence (on DNA/in gene);
Determines sequence of amino acids;
By determining base sequence on (messenger) RNA;
Code is a triplet code/three base code for an amino acid;

2 max

(c) Pairs of chromosomes/two chromosomes;
With genes for same features / with same genes;
At same loci / in same sequence;

Accept same alleles

2 max

[6]