

- M1.** (a) 387; 1
- (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
- M2.** (a) (i) join/attach nucleotides, to form a strand/along backbone/
 phosphodiester bonds;
(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

[9]

- (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]
- M3.** (a) (i) UGC; 1
- (ii) TGCTAC; 1
- (b) (DNA) contains introns / non-coding bases / mRNA only contains exons / coding bases;
Assume that 'it' refers to DNA
Neutral: DNA contains introns and exons
Neutral: 'splicing'
Neutral: pre-mRNA contains introns
Ignore refs. to start and stop codons 1
- (c) Different primary structure / amino acid sequence / amino acid coded for;
Reject: different amino acids produced / formed
Neutral: refs. to bonds 1
- (d) 1. Acetylcholine not broken down / stays bound to receptor;
2. Na⁺ ions (continue to) enter / (continued) depolarisation / Na⁺ channels (kept) open / action potentials / impulses fired (continuously);
3. (Intercostal) muscles stay contracted / cannot relax;
3. *'Muscles contract' is not enough*
Accept: diaphragm stays contracted / cannot relax 3
- [7]

- M4.** (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]
- M5.** (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) translation cannot occur; binds to/blocks codon/ triplet on mRNA;
 anticodon/tRNA will not fit in/base-pair; amino acids not
 delivered/ joined; 2 max [5]
- M6.** (a) chloroplast, so cell photosynthesises;
 moves to optimum/best light intensity for photosynthesis;
 avoids damage due to bright light; 2 max
- (b) (i) 2700 1
- (ii) $\frac{242 \times 7500 \times 900}{60} = 27\,225\,000 / 27 \times 10^6 = 2 \text{ marks}$
(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]

- M7.** (a) (i) $C \rightarrow B \rightarrow E \rightarrow F \rightarrow A \rightarrow D$
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]

- M8.** (a) (i) ACG;

1

- (ii) Serine;

1

- (b) DNA contains introns / (pre) mRNA is edited; 1
- (c) (Tetracycline) binds to/blocks mRNA triplet;
Anticodon/tRNA triplet cannot pair with mRNA triplet;
Amino acid not added to polypeptide chain;
Translation prevented; 2 max

[5]

- M9.** (a) (i) Phosphate and ribose;
Accept in either order. Both correct for one mark.
For phosphate accept PO_4 / Pi / \textcircled{P} but not P.
Do not accept phosphorus.
Ignore references to pentose / sugar. 1
- (ii) TAGGCA; 1
- (b) (i) Does not contain hydrogen bonds/base pairs /contains
codons / does not contain anticodon / straight/not folded / no
amino acid binding site/longer;
Assume that "it" refers to mRNA.
Do not accept double stranded. 1
- (ii) (pre-mRNA) contains introns / mRNA contains only exons;
Assume that "it" refers to pre-mRNA.
Accept non-coding as equivalent to intron. 1
- (c) (i)

Part of chromosome	U
Middle	18
End	21

One mark for both figures correct

1

- (ii) 1. Different genes;
 2. Have different (base) sequences / combinations of (bases);
 3. (Pre-mRNA) transcribed from different DNA/codes for different proteins;
Note this question is not about the position of bases on genes.
 1. *Telomere on end is equivalent.*

2 max

[7]

M10. (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
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2

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

[7]

M11. (a) different form of a gene;

1

- (b) hydrogen bonds broken;
 semi-conservative replication / both strands used (as templates);
nucleotides line up;
 complementary / specific base pairing / A and T / C and G;
DNA polymerase;

4 max

- (c) deletion causes frame shift / alters base sequence (from point of mutation);
 changes many amino acids / sequence of amino acids (from this point);
 substitution alters one codon / triplet;
 one amino acid altered / code degenerate / same amino acid coded for;

3 max

[8]

- M12.** (a) 1. Hydrolysis breaks proteins / hydrolyses proteins / produces amino acids (from proteins);
2. Protein synthesis involves condensation;
3. Hydrolysis of polysaccharides/lipids linked to energy source (for synthesising proteins);
- Do not award any credit if hydrolysis and condensation confused.*
- 3. Accept hydrolysis of other molecules if related to protein synthesis.*
- 2 max
- (b) Amino acids (from calliphorin) can be joined in different sequences/ rearranged;
- 1
- (c) 1. Fall, rise and fall;
2. Rise after 40 and fall after 80;
- Ignore concentration values.*
- 2
- (d) (i) Fall / increase then fall;
- Lysosomes associated with tissue breakdown;
- 2
- (ii) 1. Tissues/cells are being broken down;
2. RNA is digested/hydrolysed/broken down;
3. By enzymes from lysosomes;
4. New proteins not made / no new RNA made;
- 2 max
- (e) 1. (RNA) associated with making protein;
2. New / adult tissues are forming;
- 2
- (f) 1. In the first 6 days no/little oxygen supplied / with breakdown of tracheae, no/little oxygen supplied;
2. (Without tracheae) respire anaerobically;
3. Anaerobic respiration involves reactions catalysed by enzyme **B** / conversion of pyruvate to lactate/involves lactate production;
4. Enzyme **A**/Krebs cycle is part of aerobic respiration;
- Or, with emphasis on aerobic respiration:*
- 1. Tracheae supply oxygen / after 6 days oxygen supplied;*
- 2. (With tracheae) tissues can respire aerobically.*
- 4

[15]

M13.	(a) (i) ATA;	1	
	(ii) AUA;	1	
	(b) tRNA 'clover leaf' shape; (allow reference to loop / folded structure) tRNA standard length; tRNA has an amino acid binding site; tRNA has anticodon available / three exposed bases; tRNA has hydrogen bonds (between base pairs);	2 max	[4]
M14.	(a) Protein made of (chain of) amino acids; Each amino acid has its own base code/code; Triplet codes;	max 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]
M15.	(a) mutation changes the amino acid sequence/primary structure of Factor VIII protein; 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 haemophilic's blood contains (active) Factor IX;
the mixture has both Factors and so the pathway can
complete/blood clots; 2 max [6]
- M16.** (i) mRNA attaches to ribosome;
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]
- M17.** (a) RNA polymerase;
DNA polymerase is incorrect
Ignore references to RNA dependent or DNA dependent
Allow phonetic spelling 1
- (b) (i) (Receptor/transcription factor) binds to promoter;
Stimulates RNA polymerase/enzyme X;
Transcribes gene/increase transcription; 2 max
- (ii) Other cells do not have the/oestrogen/ER α receptors;
But do not accept receptors in general. 1

(c) Similar shape to oestrogen;

Binds receptor/prevents oestrogen binding;

Receptor not activated/will not attach to promoter/no transcription;

Accept alternative

Complementary to oestrogen;

Binds to oestrogen;

Will not fit receptor;

2 max

[6]

M18. (a) high energy radiation /ionising particles;
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;

4 max

(iii) blue and lilac; white;

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

2

[9]

M19. (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]

