

- | | | | | |
|----|-----|---|-------|------------|
| 1. | (a) | (i) 8; | 1 | |
| | | (ii) 6; | 1 | |
| | | (iii) TACCG; | 1 | |
| | (b) | transcription; | 1 | |
| | (c) | tRNA 'clover leaf' shape;
tRNA standard length, mRNA is variable;
tRNA has an amino acid binding site;
tRNA has anticodon available/ mRNA has codons;
tRNA has hydrogen bonds between base pairs; | max 2 | [6] |
| | | | | |
| 2. | (a) | G and GATCC or CTAG and GATC;
CCTAG G | 1 | |
| | (b) | hydrogen bonds;
between bases; | 2 | |
| | (c) | to form same sticky ends/same exposed base sequence;
as pairing of bases must occur; | 2 | [5] |
| | | | | |
| 3. | (a) | (i) pro; | 1 | |
| | | (ii) AUA/AUG; | 1 | |
| | (b) | DNA uncoils/two strands separate/unzips;
nucleotides of mRNA align with one strand;
according to specific base pairing;
RNA polymerase joins up nucleotides;
mRNA moves out of nucleus/into cytoplasm/attaches to ribosomes;
tRNA takes specific amino acid to mRNA;
anticodon of tRNA pairs with codon of mRNA/
3 bases on tRNA pair with 3 bases on mRNA; peptide bond between amino acids;
codons read sequentially/ribosome moves along mRNA;
tRNA collects another amino acid from cytoplasm;
polypeptide/protein released from ribosome/
polypeptide complete when stop codon reached; | 7 | |

- (c) changes in base sequence will not necessarily affect amino acid coded for/most amino acids have more than one code; these codes differ only in the third base; so changes in the third base are likely to cause no change in the amino acid sequence/ protein; changes in first/second base result in an incorrect amino acid in the sequence/ formation of the incorrect protein/example of mutation causing this type of change; change in amino acid present may have no effect on functioning of protein/some amino acids more important in tertiary structure than others; 3

[12]

4. (a) mutation results in incorrect sequence of bases/nucleotides in DNA/frame shift of nucleotides; incorrect codons/base triplets on mRNA; so incorrect amino acids brought to ribosome/incorrect tRNA bring amino acids; wrong sequence of amino acids changes tertiary structure or active site (of enzyme)/no longer functions as enzyme/no or different enzyme formed/protein non-functional; 4

- (b) strain 2 cannot make Z because enzyme 2 is missing; strain 2 has enzyme 3 present; so Z can be converted to arginine; 2

- (c) haploid fungi have one set of chromosomes, diploid have two sets of chromosomes; in haploid fungi all alleles are expressed; in diploid fungi recessive alleles often hidden; only expressed in homozygous individuals; 3

[9]

5. (a) change in code / base sequence; detail e.g. substitution / addition / deletion; of base(s); different amino acid(s) inserted into protein /polypeptide; role of tRNA 4

- (b) protein has different shape; tyrosine no longer fits into active site 2
(allow (b) points in (a))

[6]

6. (a) ribose, phosphate and base all labelled;
base and phosphate both joined to ribose 2
- (b) (i) $123 \times 3 = 369$ 1
(ii) CGA AAT TCA CTC 1
- (c) **Quality of written communication.**
The answer to this part of the question requires continuous prose.
To gain one mark for Quality of Written Communication these answers should be presented in clear, scientific English. Technical terminology should have been used effectively and should usually be accurate.
- (i) ribosome / rough -endoplasmic reticulum 1
- (ii) codons on mRNA;
anticodons on tRNA;
20 types tRNA molecule
specific amino acid attached to tRNA;
peptide bonds formed max 3
- (d) sugar - phosphate backbone gives strength;
(coiling gives) compact shape;
sequence of bases allows information to be stored;
long molecule stores large amount of information;
information can be replicated / complementary base pairing;
(double helix protects) weak hydrogen bonds / double helix makes
molecule stable prevents code being corrupted;
chains held together by weak hydrogen bonds;
chains can split for replication / transcription max 6

[14]

7. (a) Ribosome / rough ER 1
- (b) (i) Amino acid 1
(ii) Group of bases complementary to 3 bases / codon on mRNA 1
(iii) tRNA short chain versus mRNA long chain
OR tRNA clover leaf shape versus mRNA straight chain
OR tRNA folded versus mRNA straight;
OR tRNA fixed length versus mRNA variable length 1

[4]

8. (a) (i) Cells disrupted to remove DNA;
Endonuclease / restriction enzyme cuts DNA;
Reference to specificity;
Reference to sticky ends;
Plasmid cut;
With (same) endonuclease;
Use of ligase;
Treatment of recipient bacteria to make them
accept plasmid e.g. heat shock. max 5
- (ii) Fermenter;
Detail; e.g. supplied with appropriate food / oxygen / suitable
temperature 2
- (b) (i) Addition / deletion / substitution;
Of nucleotide / base 2
- (ii) mRNA formed;
Detail e.g. RNA polymerase / complementary base pairing /
transcription (linked to mRNA formation);
mRNA attaches to ribosomes / rough ER;
tRNA molecules bring amino acids;
Anticodons on tRNA complementary to mRNA codon / translation;
Amino acids joined together / peptide bonds. 5
- (iii) Only liver cells have (membrane) proteins /
receptors correct shape for virus to bind onto 1
9. (a) (i) Codon; 1
- (ii) Tyrosine; 1
- (b) (i) Base sequence / codon (of DNA) is changed;
Different (sequence of bases in) mRNA;
Attracts different tRNA / anticodon;
Different amino acid inserted into protein / polypeptide; 3 max
- (ii) More than one base triplet / codon codes for one type of amino acid;
Suitable example / true for the third base of the codon; 2
- (c) Endonuclease / restriction enzyme cuts DNA;
Reference to specificity sticky ends / use the same restriction
enzyme on fragment and plasmid;
Ligase used to fix ends; 3

[15]

- (d) Details of taking a replica:
 ef filter paper / felt / nylon membrane;
 To obtain an exact copy;
 Bacteria spread on agar to obtain separate colonies;
 Grown on agar containing ampicillin;
 Bacteria containing plasmid survive;

For principles and detail of replica plating:

Placed on agar containing tetracycline;

Bacteria growing on ampicillin, but not tetracycline contain
 the recombinant plasmids;

Because foreign DNA has been inserted into the tetracycline gene;

5 max

[15]

10. (a) (DNA) polymerase; 1

(b) different lengths;
 because different numbers of nucleotides/strand synthesis stops at modified
 nucleotide; (*allow references to base*) 2

(c) lay (gel) close to photographic/X ray film;
 develop film/dark areas/fogging/bands/autoradiogram; 2

[5]

11. (a) (i) high energy ionized particles/X-rays/ultraviolet light/high energy
 radiation/uranium/plutonium/gamma rays/tobacco tar/
 caffeine/pesticides/mustard gas/base analogues/free radicals;
 (*reject radiation*) 1

(ii) mutation;
 change in the sequence of nucleotides/bases/addition/deletion/
 substitution;
 changed order of amino acids/different protein/different tertiary;
 structure;
 inactive enzyme if shape of active site is changed/enzyme-substrate
 complex does not form; 3 max

- (b) mutation in gene 1;
 enzyme e_1 inactive/faulty; (*disqualify if both e_1 and e_2 inactive*)
 ornithine not converted to citrulline/citrulline not produced
 /unable to grow on ornithine;
 gene 2 not mutated/not affected;
 enzyme e_2 active;
 arginine produced from citrulline;
 arginine produced from citrulline;
- 4 max

[8]

12. (a) DNA uncoils;
 strands separate;
 formation of mRNA;
 complementary base pairing/RNA nucleotides pair with DNA nucleotides;
 RNA polymerase joins nucleotides together/forms mRNA;
 mRNA moves to ribosomes/rough ER;
 tRNA brings amino acids;
 anticodons on tRNA pair with mRNA codon;
 amino acids joined together by peptide bonds;
 ribosome moves along to next codon;
- 6 max

- (b) (i) high energy radiation/ionising radiation/named chemical/gamma rays/
 X-rays/UV rays/high energy particles;
- 1

- (ii) substitution;
- 1

- (c) three bases code for one amino acid;
 one codon in sequence changed/no frame shift;
 all other codons unaffected;
- 2 max

- (d) normal – glutamic acid;
 sickle cell – valine;
- 2
- (*allow one mark for correct two amino acids the wrong way round*)

- (e) sequence of amino acids affects shape of protein;
 as bonding changed;
 shape of molecule determines properties/ability to combine with oxygen;
- 3

[15]

13. (a) change in base/nucleotide; 1
- (b) change in base sequence in mRNA / different mRNA codons;
different tRNA molecules pair with mRNA;
with different amino acids / change in primary structure;
(reject produces different amino acids)
change in tertiary structure of protein;
change in shape of active site; 3 max
- (c) (i) no accumulation of phenylalanine; 1
- (ii) phenylalanine needed to form proteins or named protein /
impossible to get diet with none present / essential amino acid /
form other amino acids; 1

[6]

14. (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 haemophiliac's blood contains (active) Factor IX;
the mixture has both Factors and so the pathway can
complete/blood clots; 2 max

[6]

15. (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]
QWC 1

16. (a) (i) number of bases = 4440 (*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) (i) 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
- (ii) (loss of amino acid) changes tertiary structures/3D shape;
so sugar molecules cannot be attached (to form glycoprotein/
functional protein);
so (defective) unable to bind to chloride ions/use ATP; 2 max
17. (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

[10]

	(ii) addition and deletion (of bases/nucleotides); thymine added; adenine deleted; <i>(addition of thymine and deletion of adenine = 3 marks)</i> <i>(allow addition of adenine (RNA) and deletion of uracil (RNA)</i> <i>= 2 marks)</i>	3	
			[9]
18.	(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]
19.	(a) different form of a gene;	1	
	(b) hydrogen bonds broken; semi-conservative replication / both strands used (as templates); <u>nucleotides</u> line up; complementary / specific base pairing / A and T / C and G; <u>DNA</u> 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]
20.	(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) $\frac{242 \times 7500 \times 900}{60} = 27\,225\,000 / 27 \times 10^6 = 2 \text{ marks}$ 2

(allow 1 mark for principle: $\frac{\text{aminoacids} \times \text{proteins}}{\text{time}}$)

- (c) (i) rate slightly slower / not affected in first 20/30 minutes / lower peak than control; then decreases/ much lower (than control); 2

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

(disqualify flagellum grows longer)

- (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]

21. (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]

22. (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]

23. (a) (i) join/attach nucleotides, to form a strand/along backbone/
 phosphodiester bonds; 1
(reject reference to H bonds, complementary base pairing)
- (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; 2
 folding/shape/tertiary structure/position of bonds may change;
(reject peptide bonds)

[10]