6. Nucleic Acids and Protein Synthesis

6.2 Protein Synthesis

Paper 2

Marking Scheme

Q1.

(b)	*any **two** from:* **1** removal of introns (from primary transcript) ; **2** (after removal of introns) exons, are joined together, in different, sequences / combination(s) ; **A** alternative splicing **3** not all the exons are used (in making the polypeptides) ; **I** capping and poly-A tails	**2**

Q2.

(d)(i)	(a gene mutation is a) change in the sequence of base pairs in a DNA molecule ; **A** change in the DNA, base / nucleotide, sequence **I** change in RNA base sequence **I** names of mutations codes for / may result in / results in / AW, an altered / a different / a changed, polypeptide ; **A** protein / amino acid sequence / primary structure, *for polypeptide*	**2**
(d)(ii)	*any **two** from:* differences owing to, RNA / gene, splicing ; **A** primary transcript for RNA **A** *ref. to* alternative splicing **R** DNA splicing **R** mutation occurring during gene splicing (differences occur during) removal of, introns / non-coding sequences ; **R** if introns described as bases / nucleotides / codons **R** different number of introns removed / some introns remain exons / coding sequences, detail ; e.g. joined differently / in a different combination in middle (of transcript), removed / not included for repeating sequence, removed / not included (so) messenger RNA / mRNA, formed is different ;	**2**

Q3.

(b)(i)	*any **one** from:* increases rate of translation of, enzyme / nitrate reductase ; increases, enzyme / nitrate reductase, synthesis / concentration ; **A** more nitrate reductase produced *idea of* more metabolically efficient ; e.g. enzyme only produced when needed AVP ; e.g. more nitrate is reduced to nitrite / more nitrite is formed leads to increased supply of nitrite for amino acids / amino acid synthesis	**1**

Q4.

(c)	*any **four** from:* *max 3* **1** example of structural change to sucrase ; e.g. translation stops prematurely / truncated polypeptide / AW change in the primary structure / different amino acid(s) polypeptide does not, fold into / form, (correct) tertiary structure **2** suggestion of why sucrase is non-functional ; e.g. active site, not complementary / changed shape binding site changed shape, sucrose does not bind to active site catalytic site changed shape, glycosidic bond cannot be broken **3** polypeptide not produced as mRNA does not attach to ribosome ; **4** polypeptide recognised as abnormal and degraded ; *max 3* **5** deletion mutation is loss of one or more nucleotides (in the gene coding for sucrase) ; **6** (causes a) change in the sequence of, nucleotides / bases / base pairs, (in the, gene coding for sucrase / DNA molecule) ; **7** (causes a) change in the sequence of, nucleotides / bases, in, mRNA / an mRNA molecule ; **8** consequence to codons ; *(if not a deletion of, three / multiples of three)* all the codons after the deletion mutation are altered causes a frameshift *(deletion, of three / multiples of three)* one or more codons absent, then same sequence **9** mutation may, form a premature stop codon / introduce a stop codon ;	**4**

Q5.

(a)	sequence of, nucleotides / bases, that is part of DNA ; **A** sequence of DNA nucleotides (that) codes for a polypeptide ; **A** protein / enzyme / amino acid chain	**2**

Q6.

(d)(i)	**X**: transcription ; **Y**: translation ;	**2**

(d)(ii)	*any **three** from:* *allow ecf if introns and exons consistently the wrong way round* 1 introns, are non-coding / do not code for amino acids / are not involved in polypeptide synthesis ; **R** introns are triplets / codons, that are non-coding **I** exons are coding 2 introns are removed, after transcription / from primary transcript / before mRNA is formed ; **R** introns removed from, mRNA / primary mRNA 3 (only) exons (join to) form mRNA ; **A** mRNA, contains / AW, exons **A** only exons are translated *if mp 2 and 3 not awarded, allow one mark for:* gene splicing / RNA splicing / mRNA does not contain introns **or** splicing *if RNA noted within response – this includes the **A** for mp4 (*UAA *etc because these are RNA codons)* ; **R** DNA splicing 4 some (DNA) triplet(s) / (mRNA) codon(s) are STOP codons ; **A** UAA / UAG / UGA, is a STOP codon **or** STOP, codons / triplets, do not code for an amino acid / terminate translation **A** some, triplets / codons, terminate translation so do not code for amino acids **I** *ref. to* premature STOP codons 5 *ref. to* met / first amino acid / amino acid coded for by START codon, (may be) removed after translation ; 6 AVP ; e.g. *ref. to* (non-coding) regulatory sequences	**3**

Q7.

(c)(i)	1.8% ; working ; $\frac{30 \times 3}{5000} \times 100$ *codons for 29 amino acids (including start met) and a stop codon* *allow 1 mark if only 28 or 29 instead of 30, so 1.7% answer obtained*	**2**

(c)(ii)	*any **two** from:* introns / non-coding regions, removed / AW ; exons / coding regions, are joined together ; gene splicing / RNA splicing ; **R** DNA splicing AVP ; e.g. guanine (cap) added (to 5′ end) poly A tail / many As, added (to 3′ end)	**2**

Q8.

(c) — 3

allow pre-RNA for primary transcript

*either exon **or** intron statement required for mp2 to 7, one mark each row*
*any **three** from:*

exons	introns
1 both, are (nucleotide sequences that are) transcribed / form part of the primary transcript ;	
2 (DNA/RNA) coding (sequences) **R** coding genes **I** exons have the genetic code	(DNA/RNA) non-coding (sequences) **R** non-coding genes
3 (RNA exons) needed / involved / AW, in translation **or** for formation of, polypeptides / proteins / carbonic anhydrase	not involved in translation / AW
if mps 2 and 3 not gained 'exons code for proteins' or ora 1 mark	
4 not removed, from primary transcript / from RNA / during gene splicing / during RNA splicing	removed, from primary transcript / from RNA /during gene splicing / during RNA splicing
5 (join to) form mRNA / contain mRNA codons **A** remain in mRNA	not part of mRNA / in primary transcript only
6 not involved in regulating activity of genes / AW	may have regulatory roles **A** other suggestions for role
7 AVP e.g. (as part of mRNA) leave the nucleus / go to cytoplasm / go to ribosomes	AVP e.g. remain in nucleus

if all are differences and all statements are reversed (i.e. introns for exons and vice versa) max 2 marks

Q9.

(b)(i) — 1

transcription ;

(b)(ii) — 2

*can award either mp1 with mp2 ,**or** mp3 with mp4*

1 removal of introns (from primary transcript / RNA) ;
2 exons joined together ;

or

3 splicing ;
4 of, primary transcript / RNA ;

(c)(i) — 4

*any **four** from:*
1 *ref. to* amino acid activation / charging amino acids before attachment to tRNA / AW ; **A** aminoacylation
2 tRNA attached to, specific amino acid / glycine ; **R** 'picks up'
3 *idea that* anticodon / CCG, identifies specific amino acid ;

4 tRNA transports / AW, amino acid to ribosome ;
5 *ref. to* (tRNA) entering the A (aminoacyl) site in ribosome ;

6 tRNA, anticodon / CCG, binds to mRNA, codon / GGC ;
A correct ref. to, complementary pairing / base pairing / H bond formation *as AW for binding*
7 (specific) amino acid / glycine, in correct position in the polypeptide chain / AW ;
A helps to form / AW, primary structure of cotransporter protein
8 AVP ;
e.g. tRNA, recycled / reused
forms aminoacyl tRNA / amino acid-tRNA complex
tRNA-ligase / aminoacyl-tRNA synthetase

Q10.

(c)(i)	**1** correct use of examples ; *two of gene, gene mutation, protein, altered protein* *gene = kelch13* *gene mutation = kelch13* mutation **or** F446I **or** (mutation has) adenine / A, not, thymine / T *protein/polypeptide* = PfK13 *altered protein* isoleucine / ile, instead of, phenylalanine / phe **2** (mutation has), changed / altered / AW, sequence / arrangement / order, of nucleotides / bases, (in DNA) ; *ref. A replacing T still needs stated idea of a changed sequence* **R** *if gene explanation also given and stated as sequence of amino acids* **3** (gene) codes for the production of a, polypeptide / protein AW **or** (gene mutation) produces / results in, altered / changed / non-functioning / reduced function, polypeptide / protein ; AW **A** produces changed sequence of amino acids **R** *if gene and gene mutation explanations given and one is incorrect*	**3**

Q11.

(b)(ii)	*any **four** from:* three bases / triplet of bases / codon, code(s) for one amino acid ; frameshift mutation ; change in, triplet of bases / codon ; *ref. to* every, triplet / codon, after deletion will be different ; may introduce a stop codon ; primary structure / sequence of amino acids / AW, will be altered ; (stop codon results in) formation of, shortened / truncated, polypeptide ; AVP ; e.g. *ref. to* errors in RNA splicing *ref. to* affects post-translational modification bonds that form between R groups, will / may, be altered tertiary structure of protein will be altered non-functional protein formed altered function of the protein	**4**
(b)(iii)	*any **one** valid suggestion e.g.:* no effect on protein structure (because introns are non-coding) ; non-functional / reduced function of, protein (as intron not spliced after transcription) ; may affect regulation of gene expression ; **A** example e.g. reduction in the rate of transcription RNA polymerase does not bind *ref. to* errors in RNA splicing ; *ref. to* formation of an oncogene ;	**1**

Q12.

(d)(i)	nuclear pore ; **A** nuclear pores	**1**
(d)(ii)	**B** = transcription ; **C** = translation ;	**2**
(d)(iii)	(80S) ribosome ; **I** 70S	**1**

Q13.

(d)	*any **three** from:* *ref. to* genetic code ; *in correct context* amino acids coded for by more than one codon / two or more codons for (most) amino acids ; **A** triplet (of, bases / nucleotides) 64 codons and 20 amino acids ; third base in codon can be different / only first two bases in codon are same ; AVP ; *idea that* amino acid sequence is only the result of exons / gives information only about introns only sure of sequence for, two amino acids / met and trp degenerate code / degeneracy of code **R** degenerative *ref. to* control sequences STOP codons (also) have more than one triplet (of bases) STOP codons do not specify amino acids	**3**

Q14.

(b)(iii)	*any **three** from:* DNA binds to (complementary section of) mRNA / hydrogen bonds form between the complementary bases (of DNA and RNA) ; mRNA cannot bind to the ribosome ; ribosome cannot, move along the mRNA ; consequence e.g. no sites for tRNA to bind / tRNA cannot bring attached amino acid ; tRNA anticodons cannot form hydrogen bonds with mRNA codons ; AVP ; e.g. *idea that* DNA enters nucleus to bind and mRNA then too large to leave via nuclear pores	**3**

Q15.

(b)	anticodon ;	**1**
(c)	CAG / cytosine, adenine, guanine ; **A** GAC	**1**
(d)	hydrogen bonds form (between complementary bases) ;	**1**

Q16.

(a)(ii)	*any **two** from:* *ref. to* change of a single, nucleotide / base (in sequence of DNA) **or** one base substitution (mutation) ; change in one, DNA triplet / mRNA codon ; *ref. to* tRNA with a different anticodon / tRNA brings a different amino acid ; idea that different primary structure leads to different tertiary structure ;	**2**

Q17.

(b)(i)	transcription ;	1

(c)(i)	Phe Tyr ; *one mark for both correct*	1
(c)(ii)	**B D F G** ; *in any order*	1

(c)(iii)	*resistance* **1** shape / tertiary structure, of, β-subunit / enzyme, altered / AW ; **I** active site changes shape **A** quaternary structure of enzyme altered **2** rifampicin / antibiotic, cannot / does not, bind (as well) ; AW **R** *if context is binding to active site* *different levels of resistances* *any **two** from:* **3** (because) other mutations are involved ; AW **A** described from Table 2.1 e.g. **C** has 2 (other) mutations and **D** and **E** have 3 **4** mutations may result in different changes to, structure / shape of, β-subunit / enzyme, and result in different, effects / levels of resistance ; **5** data from Table 2.2 to support mp 4 ; *must be linked to concept of mp4* **6** AVP ; e.g. *ref. to* different binding abilities (of rifampicin to enzyme) some (of the other) mutations may cause more of a change to binding site for rifampicin mutation(s) may make it harder to bind lower resistance = binds, more strongly / for longer time lower resistance = higher proportion of transcription events hindered e.g. idea that mutations still, produce functioning enzyme / allow catalysis to occur	3

Q18.

(b)(ii)	thymine only present in DNA / no thymine in RNA ; uracil (nucleotide) replaces thymine (nucleotide) in transcription ;	1

Q19.

(c)(i) — **3**

3 structures correct and involvement, incorrect / not stated, allow 1 mark
three correct rows
I *extra rows added with additional structures*

nucleus / chromosome	(has) gene / DNA, coding for protein ***or*** (for) transcription / mRNA synthesis ; **A** produces ribosomes *if stated as made in nucleolus*
nucleolus	produces, rRNA / ribosomes / ribosomal subunits ;
ribosome **A** ribosomal subunit	(site of) polypeptide / protein, synthesis **A** described **I** makes amino acids **A** to synthesise enzymes **or** (for) translation **or** binding of, mRNA / tRNA ;
rough endoplasmic reticulum **A** rough ER / RER **R** wrong word for 'rough' if RER also stated	site of, polypeptide / protein, synthesis **A** described **A** to synthesise enzymes **or** (for) translation **or** (for) attachment of ribosomes **or** protein / post-translational, modification **A** examples **or** protein transport ; **I** packaging proteins
transport vesicle	to move protein from RER to Golgi (body / apparatus / complex) ;
Golgi (body / apparatus / complex)	for, protein / post-translational, modification / AW ; **A** examples **I** packaging proteins
mitochondrion	provides / produces, ATP for, tRNA aminoacylation / charging amino acids before attachment to tRNA ;

Q20.

(b)(i)	G G U C ;	**1**
(b)(ii)	anticodon ; *any two from:* **Q** / anticodon, binds / AW, to, codon on mRNA ; **I** *ref. to* complementary bases alone *idea that* specificity ensures correct primary structure (of polypeptide / protein) ; **A** correct amino acid sequence (of polypeptide / protein)	**3**
(b)(iii)	site of attachment of (specific) amino acid (to tRNA) / amino acid binding site ;	**1**

Q21.

(c)	*two marks to complete table* first process — transcription second process — translation third process — glycosylation fourth process — exocytosis *allow one mark if transcription first process and exocytosis last process but other two wrong way round* *allow one mark if transcription and translation wrong way round and other two correct*	**2**

Q22.

(d)	*any four from:* **1** (alleles have) different nucleotide sequences **; A** different base sequences **2** base substitution / substitution of a base **; A** T replaced by A **3** (alleles have) different mRNA codons **; A** altered mRNA codon **R** altered genetic code **4** (results in) one amino acid change **or** change from, glutamic acid / glutamate / glu, to, valine / val **or** changed primary structure **; A** changed sequence of amino acids **R** *if implies whole sequence changes* **5** AVP **;** e.g. Hb^A = CTC and Hb^S = CAC (on template strand) **A** Hb^A = GAG and Hb^S = GTG (on non-template strand) **or** Hb^A = CTT and Hb^S = CAT (on template strand) **A** Hb^A = GAA and Hb^S = GTA (on non-template strand) *this is **not** also mp2* *ref. to* amino acid substitution at position 6 (*this is **not** also mp4*) **A** 6th, codon / triplet, changed **6** changed, (β-globin / Hb) tertiary structure **; A** polypeptide / (Hb molecule) quaternary structure **R** β-globin / polypeptide **7** *ref. to* loss of globular structure / hydrophobic amino acid faces outside (instead of towards centre) **;** **A** described e.g. (val) amino acid with hydrophobic R-group instead of (glu) amino acid with hydrophilic R-group *accept hydrophilic / polar, amino acid* *accept hydrophobic / non polar, amino acid*	**4**

Q23.

(d)	*any four from:* **1** (alleles have) different nucleotide sequences **; A** different base sequences **2** base substitution / substitution of a base **; A** T replaced by A **3** (alleles have) different mRNA codons **; A** altered mRNA codon **R** altered genetic code **4** (results in) one amino acid change **or** change from, glutamic acid / glutamate / glu, to, valine / val **or** changed primary structure **; A** changed sequence of amino acids **R** *if implies whole sequence changes* **5** AVP **;** e.g. Hb^A = CTC and Hb^S = CAC (on template strand) **A** Hb^A = GAG and Hb^S = GTG (on non-template strand) **or** Hb^A = CTT and Hb^S = CAT (on template strand) **A** Hb^A = GAA and Hb^S = GTA (on non-template strand) *this is **not** also mp2* *ref. to* amino acid substitution at position 6 (*this is **not** also mp4*) **A** 6th, codon / triplet, changed **6** changed, (β-globin / Hb) tertiary structure **; A** polypeptide / (Hb molecule) quaternary structure **R** β-globin / polypeptide **7** *ref. to* loss of globular structure / hydrophobic amino acid faces outside (instead of towards centre) **;** **A** described e.g. (val) amino acid with hydrophobic R-group instead of (glu) amino acid with hydrophilic R-group *accept hydrophilic / polar, amino acid* *accept hydrophobic / non polar, amino acid*	**4**

Q24.

(b)(iii)	*two from:* translation, cannot / does not, begin / occur **or** polypeptide / protein, synthesis, cannot occur / decreases ; **I** ompF not made **A** chain of amino acids **R** transcription does not occur so translation does not occur **R** if in context of mutation or enzyme inhibition mRNA cannot attach to, ribosome / small subunit / ribosomal subunit ; (first) tRNA (with UAC anticodon) / tRNA carrying met, cannot bind (to START codon) ;	**2**