CAMBRIDGE INTERNATIONAL AS & A LEVEL BIOLOGY · 9700

BIOLOGY



MARK SCHEME

6 NUCLEIC ACIDS AND PROTEIN SYNTHESIS

SCORE	PERCENTAGE
/	%

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Paper 1 Multiple Choice Answers: Nucleic Acids and Protein Synthesis

Question	Paper	Q. No.	Answer
800	9700_m20_qp_12	22	A
801	9700_m20_qp_12	23	D
802	9700_s20_qp_11	20	B
803	9700_s20_qp_11	21	A
804	9700_s20_qp_11	22	B
805	9700_s20_qp_12	22	C
806	9700_s20_qp_12	23	B
807	9700_s20_qp_13	20	B
808	9700_s20_qp_13	21	C
809	9700_w20_qp_11	21	A
810	9700_w20_qp_11	22	A
811	9700_w20_qp_12	20	C
812	9700_w20_qp_13	22	C
813	9700_w20_qp_13	23	C
814	9700_m19_qp_12	21	B
815	9700_s19_qp_11	22	B
816	9700_s19_qp_11	23	C
817	9700_s19_qp_12	18	A
818	9700_s19_qp_12	19	B
819	9700_s19_qp_12	20	C
820	9700_s19_qp_12	21	D
821	9700_s19_qp_13	24	B
822	9700_s19_qp_13	25	C
823	9700_s19_qp_13	26	B
824	9700_s19_qp_13	27	B
825	9700_s19_qp_13	28	B
826	9700_w19_qp_11	21	B
827	9700_w19_qp_11	22	B
828	9700_w19_qp_12	22	B
829	9700_w19_qp_12	23	B
830	9700_w19_qp_13	20	A
831	9700_w19_qp_13	22	C
832	9700_m18_qp_12	23	C
833	9700_m18_qp_12	24	D
834	9700_m18_qp_12	25	B
835	9700_s18_qp_11	22	C
836	9700_s18_qp_11	23	C
837	9700_s18_qp_12	23	B
838	9700_s18_qp_12	24	A
839	9700_s18_qp_13	22	A
840	9700_s18_qp_13	23	C
841	9700_w18_qp_12	23	D
842	9700_w18_qp_12	24	C
843	9700_w18_qp_13	22	B
844	9700_m17_qp_12	24	D
845	9700_s17_qp_11	13	B

Paper 1 Multiple Choice Answers: Nucleic Acids and Protein Synthesis (

Question	Paper	Q. No.	Answer
846	9700_s17_qp_11	24	D
847	9700_s17_qp_11	26	D
848	9700_s17_qp_11	27	D
849	9700_s17_qp_12	18	C
850	9700_s17_qp_12	21	C
851	9700_s17_qp_13	18	B
852	9700_s17_qp_13	19	D
853	9700_s17_qp_13	20	A
854	9700_w17_qp_11	19	C
855	9700_w17_qp_11	20	C
856	9700_w17_qp_12	22	C
857	9700_w17_qp_12	23	C
858	9700_w17_qp_12	24	D
859	9700_w17_qp_12	25	C
860	9700_w17_qp_13	25	B
861	9700_w17_qp_13	26	C
862	9700_m16_qp_12	20	B
863	9700_s16_qp_11	20	C
864	9700_s16_qp_12	19	A
865	9700_s16_qp_12	20	B
866	9700_s16_qp_12	22	B
867	9700_s16_qp_13	19	D
868	9700_s16_qp_13	20	D
869	9700_s16_qp_13	21	A
870	9700_w16_qp_11	19	B
871	9700_w16_qp_11	20	A
872	9700_w16_qp_12	22	B
873	9700_w16_qp_12	23	C
874	9700_w16_qp_13	20	C
875	9700_s15_qp_11	20	B
876	9700_s15_qp_11	21	A
877	9700_s15_qp_11	22	C
878	9700_s15_qp_12	22	A
879	9700_s15_qp_13	20	A
880	9700_w15_qp_11	22	C
881	9700_w15_qp_12	22	B
882	9700_w15_qp_13	22	C
883	9700_m20_qp_12	24	D
884	9700_s20_qp_11	23	C
885	9700_s20_qp_12	24	D
886	9700_s20_qp_13	22	C
887	9700_s20_qp_13	23	B
888	9700_w20_qp_12	21	B
889	9700_w20_qp_12	22	C
890	9700_w20_qp_13	24	C
891	9700_m19_qp_12	22	D

Paper 1 Multiple Choice Answers: Nucleic Acids and Protein Synthesis (

Question	Paper	Q. No.	Answer
892	9700_s19_qp_11	24	B
893	9700_s19_qp_11	25	C
894	9700_w19_qp_11	23	A
895	9700_w19_qp_13	21	A
896	9700_w19_qp_13	23	B
897	9700_s18_qp_12	25	C
898	9700_s18_qp_13	24	A
899	9700_s18_qp_13	25	C
900	9700_w18_qp_11	23	D
901	9700_w18_qp_13	23	A
902	9700_m17_qp_12	25	C
903	9700_m17_qp_12	26	B
904	9700_m17_qp_12	27	A
905	9700_s17_qp_11	25	A
906	9700_s17_qp_12	19	C
907	9700_s17_qp_12	20	D
908	9700_s17_qp_13	21	D
909	9700_w17_qp_11	18	B
910	9700_w17_qp_11	21	C
911	9700_w17_qp_13	23	C
912	9700_w17_qp_13	24	B
913	9700_m16_qp_12	19	C
914	9700_m16_qp_12	21	D
915	9700_m16_qp_12	22	B
916	9700_s16_qp_11	22	B
917	9700_s16_qp_12	6	C
918	9700_s16_qp_12	21	A
919	9700_w16_qp_11	21	A
920	9700_w16_qp_13	18	D
921	9700_w16_qp_13	22	D
922	9700_s15_qp_12	20	D
923	9700_s15_qp_12	21	D
924	9700_s15_qp_13	4	C
925	9700_s15_qp_13	11	D
926	9700_s15_qp_13	21	C
927	9700_s15_qp_13	22	A
928	9700_w15_qp_11	20	D
929	9700_w15_qp_11	21	B
930	9700_w15_qp_12	19	B
931	9700_w15_qp_12	20	A
932	9700_w15_qp_12	21	C
933	9700_w15_qp_13	21	B

65. 9700_w15_ms_22 Q: 3

(a) **A** = interphase **I** *ref. to early / late*
C = metaphase **;**
both needed for one mark [1]

(b) (**C**) **L**, **N**, **M**, **K ;** [1]

(c) **1** *idea that* centromere, has divided / divides (separating, sister / identical, chromatids) **;**
2 centromere attached to spindle fibre; **A** spindle
3 shortening / contraction, of spindle fibres (pulling centromeres) **;** **A** spindle, contracts / shortens
4 (so) sister / identical, chromatids, move to opposite poles **;** *need idea of separated, so* **A** ends / sides / halves **A** sister / identical, chromatids, will end up, at separate poles / in separate cells

[max 3]

[Total: 5]

66. 9700_s20_ms_22 Q: 1

(a)	*any two from* protein coat / capsid **;** **A** capsomeres nucleic acid core / DNA or RNA **;** acellular / AW **;**	**2**
(b)	*any three from* *no, because* resolution of light microscope, too low / not high enough **;** only able to distinguish points 200nm or more apart *or* size of virus / 30 nm, too small for resolution of (light microscope) of 200 nm **;** **A** range 100-300 nm wavelength of light too long **;** *idea that* virus too small to interfere with light waves **;**	**3**
(c)	*any three from* virus binds to receptors (on host cell surface membrane) **;** *ref. to* specificity / complementary shapes / complementary binding **;** endocytosis **;** description **;** e.g. membrane infolds / pinches in vesicle formed **;** **A** vacuole	**3**

67. 9700_m19_ms_22 Q: 6

(a)	*any **two** from:* asexual reproduction ; growth by increase in number of cells ; (tissue) repair ; regeneration of body parts ; replacement of, dead / worn out, cells ;	**2**
(b)	*any **one** from:* spindle / spindle fibre ; kinetochore ;	**1**
(c)	**A** phosphate ; pentose ; **B** pyrimidine ; **C** ribose ; **D** transcription ;	**5**
(d)(i)	non-cellular / acellular / not made of cells ; protein coat / capsid ; nucleic acid core / DNA or RNA ; AVP ; ; ; e.g. only replicate inside host cells ref. to no characteristics of living organisms (sensitivity, growth, etc.) ref. to size, e.g. most are smaller than bacteria ref. to capsomeres	**3**
(d)(ii)	500 (nm) ;	**1**

68. 9700_s19_ms_23 Q: 1

(a)	one nucleotide circled ;	**1**
(b)	cytosine and guanine ; three hydrogen bonds between the base pairs ;	**2**
(c)	(3) 5,4,1,2 ;	**1**
(d)	**I** maintains length of chromosomes / prevents chromosome shortening *any two from:* permit continued replication ; prevent loss of genes ; **I** prevents gene damage **A** genetic / coded, information **A** protein coding regions of DNA protect ends of chromosomes from being, degraded / AW ; AVP ; e.g. prevents ends of chromosomes from being attached to each other not mistaken for a break in DNA that needs repairing	**2**

69. 9700_w19_ms_22 Q: 4

<table>
<tr>
<td>(a)</td>
<td>
<table>
<tr><th>polymer</th><th>constituent monomer</th><th>type of bond between monomers</th></tr>
<tr><td>amylose</td><td>glucose</td><td rowspan="2">glycosidic
glycosidic ;
A glucosidic

I details of bond</td></tr>
<tr><td>cellulose</td><td>glucose</td></tr>
<tr><td>collagen</td><td>amino acid ;
R protein (amino acid)</td><td>peptide</td></tr>
<tr><td>DNA</td><td>DNA nucleotide</td><td>phosphodiester ;</td></tr>
<tr><td>glycogen</td><td>(α-)glucose ;
R β-glucose</td><td>glycosidic</td></tr>
</table>
</td>
<td>4</td>
</tr>
<tr>
<td>(b)</td>
<td>two from

1 amylose composed of α-glucose (monomers) and cellulose composed of β-glucose (monomers) ;

2 (amylose) α-1,4 v. (cellulose) β-1,4 (glycosidic) bonds ;
R if amylose stated to have α-1,6 bonds
I ref. to cellulose also has hydrogen bonds
If mp 1 and 2 not stated allow one mark for amylose has α-glycosidic bond and cellulose has β-glycosidic bond

3 (cellulose) adjacent, monomers / glucose(s), rotated through 180° ; AW
R ref. to heads / tails

4 amylose has an (energy) storage function v. cellulose has structural function / description relating to cell wall ;</td>
<td>2</td>
</tr>
</table>

(c)	*max 2 from mp 1 and 2 if transcription described or mix and match transcription and replication* *any five from:* **1** DNA (double helix / molecule) unwinds ; **I** unzips **R** DNA, strand / α helix, unwinds **2** hydrogen bonds break between, base pairs / bases / strands ; **A** hydrogen bonds break between nucleotides *only if clear that two strands are separated* **3** both strands used as templates ; *concise statement* **4** DNA polymerase, qualified ; e.g. involved in polynucleotide formation / phosphodiester bond formation / catalyses synthesis **R** joins phosphates **5** *ref. to* (free) activated (DNA) nucleotides / AW ; **A** phosphorylated nucleotides **R** RNA nucleotides **6** complementary (DNA) nucleotides added ; **R** RNA nucleotides **A** described in terms of complementary base pairing **A** A pairs with T and C pairs with G **7** *idea that* process, occurs / continues, along whole DNA molecule ; **8** *ref. to* Okazaki fragments / movement of polymerase in one direction / nucleotides added in one direction ; **A** correct ref. to leading and lagging strands **9** each newly formed molecule contains one original and one newly synthesised strand ; **10** AVP ; e.g. replication bubbles form / described *ref. to* repair / proofreading *ref. to* helicase (unwinding) / ligase (joining Okazaki fragments) *in correct context* **R** ligase joining phosphates process occurs, step-by-step / sequentially / AW *ref. to* RNA primers	**5**

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70. 9700_m18_ms_22 Q: 6

(a)	**1** adenine, thymine, cytosine, guanine ; **2** DNA polymerase ; **3** nucleotides ; **4** complementary base pairing ; **5** (DNA) ligase ; **6** semi-conservative (replication) ;	**6**
(b)(i)	**J** metaphase ; **K** prophase ; **L** telophase ; **A** anaphase	**3**
(b)(ii)	large size / same size as cells in mitosis / ora ;	**1**
(b)(iii)	1 chromosomes, orientated / arranged / AW, at, (spindle) equator / metaphase plate ; *plus any **one** from:* 2 chromosomes attached to, spindle / spindle fibres, at centromere / kinetochore ; 3 spindle fully formed ; 4 nucleolus has disappeared ; 5 nuclear envelope, has disassembled / broken down / AW ;	**2**

71. 9700_s17_ms_23 Q: 5

(a)	**1** DNA (double helix) unwinds ; **A** uncoils **I** unzips **R** DNA strand unwinds **2** hydrogen bonds break between, base pairs / bases / strands ; **3** both strands used as templates ; **4** catalysed by / AW, DNA polymerase ; **5** *ref. to* (free) activated nucleotides / AW ; **6** complementary (DNA) nucleotides added ; **R** RNA nucleotides **A** described in terms of complementary base pairing **7** step-by-step / sequentially / AW ; **8** *idea that* process continues, along whole DNA molecule ; **9** replication bubbles / described **or** *ref. to* Okazaki fragments ; **10** replication is semi-conservative / each newly formed molecule contains one original and one newly synthesised strand **11** AVP ; e.g. *ref. to* repair / proofreading *ref. to*, helicase / ligase *in correct context*	**max 5**
(b)	telomere(s) ;	**1**
(c)(i)	adenine and guanine ;	**1**
(c)(ii)	*idea that* purines and pyrimidines are different sizes / two rings and one ring ; purine normally bonds with pyrimidine (to maintain DNA double strand width) ; *idea that* two purines or two pyrimidines will distort the double helix width (in a transversion event) ; **ora** AVP ; e.g. (transversion event) more likely to be detected by the repair mechanism **ora**	**max 2**
(d)	*idea that* mutation occurs for a gene controlling cell division ; detail ; e.g. proto-oncogene to oncogene tumour suppressor gene switched off ; *ref. to* disruption of cell cycle / shortened interphase ; (results in) uncontrolled cell division ; **I** uncontrolled growth other detail of result of mutation ; e.g. divide indefinitely / no programmed cell death do not respond to signals to stop dividing loss of, specialisation / function	**max 3**
	Total:	**12**

72. 9700_w16_ms_22 Q: 3

(a) *two from*

fructose		*sucrose*
no glycosidic bond ;	(v	glycosidic bond) *look for ora*
monosaccharide / one sugar unit **A** monomer *('sugar', is in question)*	v	disaccharide / two sugar units / fructose and glucose ; **A** two monomers / dimer **I** polysaccharide

R if a disaccharides is stated as one of the two monomers

A sucrose is a disaccharide made from the monosaccharides glucose and fructose

one ring (structure)	v	two rings ; **A** *sketch to show one ring v two rings*
$C_6H_{12}O_6$ **A** fewer / less, C and H and O atoms	v ora	$C_{12}H_{22}O_{11}$;

additional points accepted

powder	v	crystalline
linear or ring structure	v	two rings / only ring(s)
reducing, end / AW	v	(no reducing ends)

I reducing sugar **I** non-reducing sugar [2]

(b) *look for ora throughout if describing the other enzyme with low optimum*

three from

1 *idea of* can use high(er) temperatures for process ;

2 increased temperature increases, number of collisions (between enzyme and substrate) / number of ES complexes (formed) ;

3 more product / high(er) rate of reaction ; AW

4 less prone to denaturation ; **A** won't denature
A described in terms of loss of active site

5 more stable / lasts longer ; **A** thermostable **A** reused over and over
I temperature resistant [3]

(c) *accept 'glucose isomerase' for 'enzyme'*
accept '100 percent activity' for 'maximum activity'
accept (initial) rate of reaction for activity

penalise once if 'pH' and/or percentage activity (or %) not stated

three from

1 maximum / peak of, activity, at lower pH for free enzyme ora
or
free enzyme lower optimum pH ora
or
free enzyme pH 7.4 / 7.5 / 7.6 v immobilised pH 8.5 ;

2 free enzyme has higher / AW activity, at pH, 6 / 6.5 / 7 / 7.5 ; **A** up to pH 8
ora for immobilised (lower up to pH 8) *
or
free enzyme has higher activity over greater range of pH** (between pH 6–9) ;

3 data to support mp 2 ; **any one pH and comparative activity*
*** needs two pHs and comparative activities*
A manipulated data

4 free enzyme has lower activity, pH 8 to pH 9 ; **A** after pH 8.0
ora for immobilised (higher after pH 8)

5 data to support mp 4 ; *any one pH and comparative activity / manipulated data*
increase to max activity

6 free enzyme has (slightly) steeper increase in activity as pH increases to pH 7 ; ora

7 data to support mp 6 ;

allow ecf to 2 max if free and immobilised the wrong way round but all statements are correct [3]

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(d) (i)

amino acid sequence	met	tyr	glu	pro	lys
student's nucleotide sequence	AUG	UAU	GAC	CCU	UGU
correct = ✓ incorrect = ×	✓	✓	×	✓	×

one mark if bottom row correct ; [1]

(d) (ii) *three from*

1 genetic code is, degenerate ; **A** redundant

2 64 codons and 20 amino acids ;
A 61 codons for 20 amino acids (*3 STOP codons)*

3 *idea that* more than one, codon / triplet, specifies an amino acid ;

specific to the first five amino acids of glucose isomerase

4 example of choice of codons to specify the same amino acid ;
(must use Table 3.2 to find codons for the amino acids from Table 3.1)
tyr UAU UAC
glu GAA GAG
pro CCU CCC CCA CCG
lys AAA AAG
use of another example from Table 3.2 may be used to support mp3

5 AVP ; e.g.
start codon always AUG / met has only one codon, so only sequence for amino acids 2-5 may be different
start codon, may be different / may not always be AUG $_{met}$ [3]

[Total: 12]

73. 9700_w15_ms_21 Q: 3

(a) (late) anaphase / (early) telophase ; **R** early anaphase [1]

(b) produce more genetically identical cells / AW ;
for growth (of the root) ;
asexual reproduction ;
replace (old / worn out) cells ;
repair (damaged tissue) ; **A** *ref. to* wounds **R** repair cells [max 2]

(c) **(i)** 8 ; [1]

(ii) for sexual reproduction ;
to form gametes ; **A** pollen and, egg / ovum **R** sperm

ref. to diploid number must be restored (in zygote)
or
fusion / fertilisation, of two haploid cells results in, diploid cell / zygote ;

prevents chromosome number doubling each generation ; [max 3]

(d) **1** DNA double helix unwinds ; **I** unzips **R** DNA strand unwinds
2 hydrogen bonds break between, base pairs / bases / strands ;
3 both strands used as templates ;
4 catalysed by / AW, DNA polymerase ;
5 *ref. to* (free) activated nucleotides / AW ;
6 complementary DNA nucleotides added ;
A described in terms of complementary base pairing
7 step-by-step / sequentially / AW ;
8 *idea that* process, occurs / continues, along whole DNA molecule ;
9 replication bubbles / described
or
ref. to Okazaki fragments ;
10 replication is semi-conservative / each newly formed molecule contains one original and one newly synthesised strand
11 AVP ; e.g. *ref. to* repair / proofreading
ref. to, helicase / ligase *in correct context* [max 5]

[Total: 12]

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74. 9700_s20_ms_21 Q: 6

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

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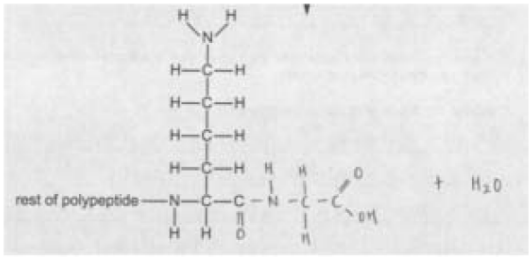
75. 9700_s20_ms_23 Q: 5

(a)	*any two from* sequence of DNA nucleotides ; forms part of a DNA molecule / length of DNA / AW ; coding for a polypeptide ; **A** protein	**2**
(b)	interphase ; **I** phases of interphase	**1**
(c)(i)	two phosphates added to existing phosphate ; *base* = adenine ; *sugar* = ribose ;	**3**
(c)(ii)	purine ;	**1**
(d)	*any three from* to produce, many / AW, new blood cells ; *idea that* large numbers are required to, transport oxygen / maintain immune system ; produce genetically identical cells ; loss of genetic material may not allow function / cells maintain function / cells are able to function ; replacement of, old / damaged / dead, cells ; AVP ; e.g. to maintain healthy numbers of cells red blood cells have short life	**3**

76. 9700_w20_ms_21 Q: 6

(a)(i)	*in context of mutations in genes* *any **two** from:* uncontrolled, (cell) division / mitosis ; cell cycle not regulated ; programmed cell death does not occur / cell becomes immortal ; uncontrolled growth not suppressed ; *ref. to* mass of abnormal cells ; AVP ; e.g. cell cycle checkpoints impaired proto-oncogenes become oncogenes tumour suppressor genes switched off	**2**
(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**
(b)(i)	*any **three** from:* vaccination stimulates an immune response ; antigen presentation, qualified ; e.g. TSA engulfed by, phagocyte / named phagocyte antigen binds to, specific / complementary, receptor, on, T-lymphocyte / cytotoxic T cell / killer T cell ; clonal expansion ; **A** described e.g. divides by mitosis to form a clone (receptor on) cytotoxic T cell / killer T cell, binds to TSA on tumour cell ; release of, perforin / hydrogen peroxide (to kill tumour cell) ; **A** other named e.g. granzymes AVP ; e.g. causes lysis of the cell	**3**
(b)(ii)	*advantage any **one** relevant e.g.* tumour cells may have more than one TSA ; stimulate a specific immune response to each TSA ; *idea that* TSA on patient's tumour cells has the appropriate antigen *idea that* personalised treatment so more effective *disadvantage any **one** relevant e.g.* high cost of personalised treatment ; immune system may not recognise TSA on own body cell as, foreign / non-self , the cells in the tumour may not have the TSA in the vaccine ; patient's tumour may not be large enough to obtain enough cells for treatment ; patient needs surgery to obtain (large quantity of) cells ; AVP ; e.g. *suggestion that* tumour cell may settle in a part of the body and not be destroyed	**2**

77. 9700_w20_ms_23 Q: 5

(a)(i)	**I** *presence or absence of water* diagram shows bond between C (of lysine) and N (of glycine) **and** double bond to O shown correctly ; glycine drawn correctly ; **R** if R is used instead of H on glycine  	**2**
(a)(ii)	condensation ; **A** dehydration (reaction)	**1**
(a)(iii)	**I** high tensile strength *any **two** from:* allows close packing of, triple helix / three polypeptides ; **A** chains **I** tight coiling **A** 'binds more tightly' glycine, has smallest R group / R group of glycine is H / is smallest amino acid ; **A** glycine is small glycine, is every third amino acid in the, polypeptide / chain ;	**2**
(b)	**I** collagen is insoluble / collagen is strong *any **four** from:* **1** collagen, has high tensile strength / does not stretch / AW ; **A** withstands large pulling forces **2** *any ref. to* use of collagen in the body ; e.g. (walls of) arteries or veins / tendons / cartilage / skin / basement membranes / around alveoli / bones / teeth **I** hair / **R** if any *ref. to* elastic(icity) *three from* **3** triple helix has many hydrogen bonds between, polypeptides / chains ; *mp4, 5, 6 and 7 – must be clear that answers are about molecules, but accept triple helix for molecule* **4** collagen molecules form, fibrils / fibres ; **5** strong / covalent, (cross) links between molecules ; **6** (ends of) molecules (in fibril / fibre) are staggered ; **7** AVP ; e.g. (many) collagen molecules lie parallel	**4**
(c)	*induced fit* **1** active site changes shape ; **A** active site moulds round substrate **A** 'active site changes to fit the substrate (more closely)' **2** (so) active site becomes (fully) complementary shape to collagen ; *any four from* **3** formation of, enzyme-substrate complex / ESC ; **4** lowering of activation energy ; **5** breakage of peptide bond ; **6** active site returns to, pre-ESC / original, shape **and** can be reused ; **7** AVP ; e.g. *ref. to*, binding site / catalytic site (of active site) e.g. suggestion of how activation energy lowered, e.g. strain put on bond / alternative pathway	**5**

(d)	*description* **1** general description of effect of pH on activity ; e.g. as pH increases the activity increases and then decreases e.g. as pH increases activity reaches a peak e.g. use of data with unit for relative activity to describe increase and decrease (see next page) **2** **2** optimum pH is 7 ; *explanation* *any **three** from:* **3** partial denaturation in, acid **and** alkaline conditions / AW ; **A** 'starts to denature' as alternative to partial denaturation *small changes either side of optimum* **4** (ionisable) R-groups in, active / catalytic, site affected ; *large changes either side of optimum* **5** hydrogen bonds / ionic bonds, break / disrupted ; **6** active site (shape) / (enzyme) tertiary structure, changes, so substrate / collagen, no longer fits into active site / fewer ESC complexes formed ; **A** fits less well *in context of partial denaturation* **7** AVP ; e.g. detail of R groups	**4**

78. 9700_s19_ms_21 Q: 6

(a)(i)	30% ; **A** anywhere in the answer bases, are paired / are complementary ; **A** with *ref. to* binding **A** hydrogen bonds between, A and T / C and G **A** thymine *or* T pairs with adenine *or* A / cytosine or C pairs with guanine or G calculation / explanation for 30% ; e.g. A□T = 40%, C□G = 60%, half of 60% = 30%	**3**
(a)(ii)	mitochondria / mitochondrion (in cytoplasm) ; **R** whole answer if anything else is first or second in answer **R** 'mitochondria and / or cytoplasm'	**1**
(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**

79. 9700_s18_ms_22 Q: 2

(a)(i)	A = adenine T = thymine **R** thiamine / thyamine G = guanine C = cytosine *all correct = 2 marks* *one, two or three correct = 1 mark*	**2**
(a)(ii)	*three from:* 1 complementary base pairing / complementary bases / base pairing / base pairs / complementary pairing ; 2 A with T and G with C ; 3 hydrogen bonding / hydrogen bonds ; *in context of between base pairs / holding strands together* 4 ref. to purines with pyrimidines ; 5 double ring (bases) with single ring (bases) ; **A** *idea of* longer base with shorter base 6 two (DNA), strands / polynucleotides ; **A** two chains **A** double helix (as double implies two strands) **7** strands (anti)parallel / distance between strands always the same ;	**3**
(b)	deoxyribose ; **A** 2-deoxyribose / 2-deoxy-D-ribose	**1**
(c)	*two from:* (information could be) sequence of amino acids ; **A** idea that a polypeptide/protein has amino acids arranged in an order / AW **I** primary structure / chains of amino acids (different) proteins have, different / specific, sequences (of amino acids) ; (up to) 20 different amino acids in proteins ; **A** approximately 20 *idea that* there is a great variety in protein structure ; **I** have many functions	**2**

80. 9700_w18_ms_22 Q: 5

(a)	*polymer – context of a chain / strand* (similar) repeating, smaller molecules / subunits **or** repeating / many, monomers / (RNA) nucleotides ; **R** branching **A** *idea of* nucleotides joined together to form a chain **A** made of nucleotides to form polynucleotide *'made of nucleotides' 'made of monomers' not enough* *macromolecule (in context of RNA)* large (biological) molecules / 1000 or more atoms / high molecular mass ; **A** giant / huge, structure **I** long	**2**
(b)	add Benedict's (solution / reagent) and, boil / heat to 95 °C ; **A** temperature 80 °C and above precipitate / (change from clear blue to) green / yellow / orange / red / brown ; **R** if a wrong colour included e.g. black / purple	**2**
(c)	<table><tr><th>feature</th><th>DNA nucleotide</th><th>RNA nucleotide</th></tr><tr><td>sugar component</td><td>deoxyribose</td><td>ribose ;</td></tr><tr><td>purine bases</td><td>adenine / A guanine / G</td><td>adenine / A guanine / G } ;</td></tr><tr><td>pyrimidine bases</td><td>cytosine / C thymine / T</td><td>cytosine / C uracil / U } ;</td></tr></table> **R** *thiamine for thymine*	**3**

81. 9700_w18_ms_23 Q: 3

(a)(i)	**D** (nitrogenous organic / nucleotide) base ; **A** pyrimidine / uracil / cytosine **R** purine **E** ribose ; **I** pentose **F** phosphate (group) ;	**3**
(a)(ii)	*any one from* two, strands / polynucleotides (not one) ; **A** two chains **R** polypeptides deoxyribose (not ribose) ; **A** correct ref. to –OH (on C2) instead of –H group on the pentose / sugar thymine (not uracil) ; **R** thiamine have base pairs ; (double) helix / helical (not straight chain) ; longer ;	**1**
(b)	*any four from* **1** template RNA binds to (part of) region **X** ; **2** in active site of, telomerase / enzyme ; **3** DNA / free, nucleotides, pair with / bind to / align with, RNA ; **4** ref. to complementary, bases / base pairs ; **5** A–T and C–G and U–A ; **6** phosphodiester bonds form, between (DNA) nucleotides / AW ; treat as neutral any *refs.* to likely enzymes, e.g. ligase, etc. **7** telomerase moves, in the direction of the arrow / to the right ; **8** AVP ; e.g. hydrogen bonds between bases telomerase acts as a reverse transcriptase	**4**
(c)	*prokaryotes* have, circular DNA ; **A** 'loop of DNA' **I** plasmid(s) do not have telomeres ; do not have chromosomes ; AVP ; e.g. 'DNA has no ends'	**1**
(d)	*any two from* cancer cells divide, uncontrollable / continuously ; **ORA** **A** cancer cells divide but do not undergo cell death telomerase is required to ensure, chromosomes, do not shorten ; telomerase is, synthesised / produced / found, in cancer cells ; **ORA** high levels of telomerase indicate cells that are cancerous / AW ; AVP ; e.g. *idea that* gene for telomerase switched on	**2**

82. 9700_s17_ms_21 Q: 4

<table>
<tr><td>(a)</td><td>mRNA

1 single-stranded ;
2 no hydrogen bonding / only DNA has hydrogen bonding ;
3 no base pairs / only DNA has base pairs ;
4 uracil and not thymine / DNA has thymine instead of uracil ;
treat as neutral T and U, look for complete term
5 ribose not deoxyribose ;
6 detail, e.g. –H and not –OH on C2 ;
7 short(er) / DNA is longer ; A smaller / bigger
8 not a helix ;</td><td>max 4</td></tr>
<tr><td>(b)(i)</td><td>third triplet is a stop codon so
only two amino acids are joined by peptide bonds / chain only 2 amino acids long ;
A will still have Val-His as the first two amino acids
very short molecule is produced / chain stops after His(tidine) ;
R frameshift / description of frameshift</td><td>max 1</td></tr>
<tr><td>(b)(ii)</td><td>a triplet is deleted so
(polypeptide / sequence / β chain) has one less amino acid ;
polypeptide does not have Leu (as the third amino acid) ;
I Leu is not, produced / made / synthesised</td><td>max 1</td></tr>
<tr><td>(c)</td><td><table>
<tr><th>feature</th><th>DNA replication</th><th>transcription</th></tr>
<tr><td>a single-stranded molecule is produced</td><td>×</td><td>✓</td></tr>
<tr><td>hydrogen bonds are broken</td><td>✓</td><td>✓ ;</td></tr>
<tr><td>both strands of DNA act as templates</td><td>✓</td><td>× ;</td></tr>
<tr><td>phosphodiester bonds are formed</td><td>✓</td><td>✓ ;</td></tr>
<tr><td>DNA polymerase is used</td><td>✓</td><td>× ;</td></tr>
</table></td><td>4</td></tr>
<tr><td>(d)</td><td>I functions of telomerase
permits continued replication (in stem cells / meristematic cells) ; A ora
prevents loss of, genes / genetic material / DNA ; A ora
A prevents shortening of, chromosomes / DNA
length of telomere determines lifespan of, cells / cell lineage ;
AVP ; e.g. prevents ends of chromosomes attaching to each other prevents apoptosis / cell death / cell destruction</td><td>max 2</td></tr>
<tr><td>(e)</td><td>1 translation / construction of <u>polypeptide</u>(s) ;
2 provide binding site for mRNA / mRNA attaches to ribosome / AW ;
A entering ribosome
3 provides binding sites for (two) tRNA molecules ;
A entering ribosome
4 two amino acids are held close together ;
5 formation of <u>peptide bond</u>(s) ; R dipeptide / polypeptide, bond
6 (allows) assembly of amino acids into, sequence / primary structure ;
7 AVP ; e.g.
P and A site (and E site)
bond between amino acids catalysed by peptidyl transferase</td><td>max 4</td></tr>
</table>

83. 9700_s17_ms_23 Q: 2

(a)	*one mark for the formula and two marks for the correct answer* (magnification =) $\frac{\text{image / scale bar (length)}}{\text{actual / object (length)}}$; **A** triangle / letters only 3000 ;; 30 000 ÷ 10 ; *using 30 mm as measured length* **A** calculated values for measured lengths of 29 mm or 31 mm *allow one mark if correct answer given with units* *allow one mark if incorrect answer and* *correct measurement and correct working* *correct measurement and formula but incorrect conversion* *measurement ± 2 mm and correct working*	**3**
(b)	*name* (large permanent) vacuole ; *function* *one from* store of / holds / AW, cell sap ; **R** if contains organelles store of / holds / AW, water / ions / named ion(s) / minerals / salts / pigments / sugars / named sugars ; **A** nutrients **I** substances / molecules / food **I** storage unqualified pushes chloroplast to edge of cell ; gives, turgidity / turgor pressure / hydrostatic pressure / support / AW ; **A** makes, firm / rigid **A** controls / maintains, turgidity **I** gives shape / strengthen / provides structure store of / holds, waste (products) ; **A** breakdown of (large) waste products **I** reactions occur in vacuole, unqualified *allow function mark even if name of organelle left blank or incorrect*	**2**
(c)	nucleus ; chloroplast(s) ; mitochondrion ; **A** mitochondria	**max 2**
(d)	***A*** nucleic acid / DNA / RNA ; **A** genetic material **I** strand **R** circular DNA ***B*** protein coat / capsid / capsomere / protein subunit ;	**2**
(e)(i)	gene coding for systemin is (a length of) DNA ; **A** *idea that* a length of DNA codes for systemin transcription / production of mRNA ;	**2**
(e)(ii)	herbivore proteases and plant proteases have different (shaped) active sites ; serpin / competitive inhibitor, only complementary to (shape of) active site of herbivore proteases ; **ora** **A** can only fit serpin is specific to (active sites of) herbivore proteases ; AW proteases act on different, substrates / (parts of) proteins ; **A** similar shape only to herbivore substrates AVP ; e.g herbivore proteases cut at different amino acid sequences *allow other acceptable suggestions e.g.* *suggestion that* serpin physically separated from plant proteases ; detail, e.g. in vesicle / plant proteases in vacuole ; cannot bind to active site of plant proteases ; serpin released when plant parts ingested by herbivores ;	**max 3**
(e)(iii)	affinity for substrate has decreased ; needs a higher concentration of substrate to saturate active sites / AW ; **A** needs a higher concentration to reach, ½ Vmax / Vmax *idea that* inhibitor prevents substrate from binding (to active site) so more substrate required (to compete) ;	**1**
	Total:	**15**

84. 9700_w16_ms_23 Q: 4

(a) hydrogen (bond) ; [1]

(b) *three from*

1 tRNA carries an amino acid to ribosomes ;
2 (each type of) tRNA carries a specific amino acid ;
3 anticodon (on tRNA) binds to codon on mRNA ; *anticodon may be labelled on Fig. 4.1*
4 tRNA molecules hold amino acids, in place / in P and A sites (of ribosome), for peptide bond formation ;
5 tRNA molecules, reused / described ; **I** tRNA leaves ribosome unqualified
6 AVP ; e.g. amino acid is attached to ACC region **I** examples of complementary base pairing between codon and anticodon [max 3]

(c) *max 2 if in context of making mRNA*

1 gene for each tRNA (molecule) is transcribed ;
2 hydrogen bonds in DNA are broken ;
I unwinding / unzipping
3 one strand of DNA is the template ;
4 RNA polymerase ;
5 (free RNA) nucleotides joined together / formation of phosphodiester bonds ;
I complementary base pairing
6 AVP ; e.g. correct ref. to helicase in breaking hydrogen bonds [max 3]

[Total: 7]

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85. 9700_s15_ms_21 Q: 6

(a) **P** – thymine ; **R** thiamine / thiamin / thyamine
Q – cytosine ;
R – guanine ;
S – uracil ; [4]

(b) **1** copy of the, DNA / gene, (coding) for a, polypeptide / globin ; **A** protein

2 travels from, DNA / nucleus / chromosome, to ribosome ;
A mRNA made in nucleus, attached to ribosome *so movement is implied*

3 for translation / for (haemo)globin production ;

4 mRNA codes for, sequence / order, of amino acids ; **A** for primary structure

5 *idea that* (nucleotide / base) sequence is a series of codons ;

6 base pairing / AW, between codon on mRNA and anticodon on tRNA ;
e.g. of AW
hydrogen bonds between bases
examples of base pairing: A–U / C–G
R binding between bases [max 3]

[Total: 7]

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86. 9700_s15_ms_23 Q: 2

(a) (late) interphase / phase / after G1 phase / before G2 phase ;
A after first growth phase / before prophase / before mitosis / after cytokinesis [max 1]

(b) (i) hydrogen / H, (bonds) ; [1]

(ii) Y, single ring structure ; **A** smaller molecule compared to **X** [1]

(c) (i) change in, nucleotide / base, sequence of DNA ;
any one from
new allele fomed ;
deletion / substitution / addition / frame shift , (mutation) ;
change to / altered, mRNA ; **A** altered codon(s)
(causing) change in, primary structure / amino acid sequence, of, polypeptide / protein ;
A different protein / altered function of protein / non-functional protein [max 2]

(ii) cell cycle shorter / interphase shorter / division more frequent ;
(cell cycle) checkpoints not controlled ;
uncontrolled (growth / division) / AW ;
AVP ; e.g. no differentiation (into epithelial cell)
A no cell death / apoptosis [max 2]

[Total: 7]

87. 9700_s20_ms_22 Q: 5

(a)	presence of sucrose (in sieve tube) lowers water potential (of phloem sap) ; **A** makes water potential more negative water enters (sieve tube), by osmosis / down water potential gradient ; increases volume (in sieve tube) ; increases hydrostatic pressure (in sieve tube at source) ; **A** turgor pressure *ref. to* lower hydrostatic pressure (in sieve tube at sink) ; *allow ecf for no ref. to, hydrostatic / turgor* detail ; e.g. sucrose removed at sink water follows sucrose that exits sink movement of, (phloem) sap / sucrose, down pressure gradient / from high to low hydrostatic pressure ; mass flow ;	**4**
(b)(i)	glycosidic ;	**1**
(b)(ii)	nucleotide components are base, pentose sugar, phosphate ; UDP has, uracil and ribose and two phosphates / one extra phosphate ;	**2**
(b)(iii)	*max three if describing breakdown of sucrose* *allow points from diagrams* *any four from* *induced fit* shape of, substrates / UDP and glucose, not (fully) complementary to shape of active site (of sucrose synthase) ; *lock and key* shape of, substrates / UDP and glucose, complementary to shape of active site (of sucrose synthase) ; *allow ecf if no ref. to shape* *induced fit* active site flexible / moulds around, substrates / UDP and glucose ; AW *lock and key* active site does not change shape / is not flexible / AW ; *induced fit* (active site moulds around so) *idea of* provides better fit / fully complementary ; *lock and key* substrate fits into active site ;	**4**
(c)	α-glucose ; **A** glucose **R** β-glucose α, 1-4 ; α, 1-6 ; *bond types either way round* glycogen ;	**4**

CHAPTER 5

1.	D
2.	A
3.	C
4.	C
5.	D
6.	B
7.	C
8.	B
9.	C
10.	A
11.	A
12.	C
13.	B
14.	B
15.	C
16.	A
17.	A
18.	B
19.	A
20.	C
21.	D
22.	A
23.	D
24.	C
25.	A
26.	C
27.	C
28.	A
29.	C
30.	A
31.	A
32.	C
33.	D
34.	A
35.	C
36.	C
37.	C
38.	A
39.	
40.	
41.	
42.	
43.	C
44.	A

CHAPTER 5

45.	B
46.	A
47.	D
48.	B
49.	A
50.	B
51.	D
52.	B
53.	B
54.	C
55.	A
56.	D
57.	D
58.	D
59.	B
60.	C
61.	A
62.	C
63.	A
64.	C
65.	A
66.	B
67.	C
68.	B
69.	D
70.	C
71.	A
72.	C
73.	C
74.	B
75.	A
76.	A
77.	B
78.	A
79.	C
80.	C
81.	C
82.	C
83.	A
84.	B
85.	B
86.	B

Q1.

Question			Expected Answers		Marks
5	(a)	(i)	U - phosphate / PO_4; **R** phosphoric acid / phosphorus / P W - deoxyribose; **R** pentose X - cytosine; **R** nitrogenous base / pyrimidine / C		3
		(ii)	Z - hydrogen; **R** H		1
	(b)		*Assume answer is about polypeptide unless indicated otherwise. A comparison is not required. Information given below is for either polypeptide or DNA features. **A** ideas from either column. Do not penalise if points are not corresponding on one line / sentence. Mark all points on line. Only **R** if biologically incorrect.*		
			polypeptide	*DNA*	
			amino acids	nucleotides ;	
			one / single strand / chain	two / double strand / chains ;	
			peptide bonds **R** between peptides / polypeptides	phosphodiester ;	
			20 monomers / sub units **A** > 4 monomers / sub units	only 4 monomers / sub units ; **R** 4 bases	
			no phosphate / PO_4	has phosphate / PO_4 ;	
			2^o / 3^o structure	double helix ;	**3 max**

Q2.

Question			Expected Answers	Marks
1	(a)	**W**	cytosine;	
		X	deoxyribose;	
		Y	nucleotide (triphosphate);	**[3]**
	(b)		base pairing/A-T and C-G; **A** purine - pyrimidine	
			ref to complementary/explained with ref to H bonds; **R** complementary in wrong context	
			(free) nucleotides pair with both, strands/each strand/polynucleotides/sides;	
			both strands act as templates;	
			to produce two DNA molecules that are identical to one another;	**[max 3]**

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(c) (all nuclei/cells) are genetically identical; **A** genetic stability, same genetic information, exact genetic material, genetic material does not vary, same genotype;

no mutation;

any consequence of mutation;

e.g. cells not recognised, cells divide uncontrollably, substitution of 1 amino acid results in disease e.g. sickle cell anaemia, enzyme's active site altered, forms different protein with different function. **[max 2]**

[Total: 8]

Q3.

3 **(a)** *one mark per row*

statement	protein	DNA	messenger RNA	cellulose
hydrogen bonds stabilise the molecule	✓	✓	x	✓ ;
glucose is the subunit molecule	x	x	x	✓ ;
subunits are joined by peptide bonds	✓	x	x	x ;
may be hydrolysed to amino acids	✓	x	x	x ;
contains uracil	x	x	✓	x ;

[5]

(b) CAG; **[1]**

(c) tRNA, combines with amino acid / carries amino acid to ribosome;
idea of specificity; e.g. each type of tRNA is specific to an amino acid
anticodon matches amino acid idea;
example from Fig. 3.1;
codon on messenger RNA pairs with anticodon on tRNA;
example from Fig. 3.1;
two sites on ribosome;
further detail; e.g. P and A site (and E)
leave ribosome after amino acid joins polypeptide;
continually reused; **[max 5]**

Q4.

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4 (a) (i) **A** transcription ;
B tRNA / transfer RNA ;
C ribosome ; **A** subunit of ribosome / ribosomal subunit
treat 70S / 80S or small / large as neutral
D anticodon ; [4]

Q5.

5 **(a)** interphase / S phase / synthesis phase ; **R** G1/G2 unqualified by interphase [1]

(b) **(i)** hydrogen ; [1]

(ii) **M** = adenine and **O** = cytosine ; [1]

(c) each strand, of DNA acts as a template (for the synthesis of a complementary strand) ;
A described in terms of base pairing
new DNA (molecule) has one, old / parental / original, strand and one, new / daughter strand ;
R 'half old and half new' unless clearly referring to two strands [2]

(d) *accept ora*
(errors are) mutations / named type of mutation ;
ora if corrected there are no mutations
(may lead to) production of altered proteins, so, impaired / loss, of function ;
A altered amino acid in, protein / primary structure
(may lead to) different antigens, so cells are rejected (by immune system) ;
idea that cells cannot function together / impaired coordination ;
ref. to cancerous cells / cancer(s) / tumours / sickle cell anaemia or other named monogenic condition ;
further detail ;
e.g. uncontrolled, division / mitosis / cell replication / cell growth
e.g. lack of contact inhibition / no apoptosis *or* described / (proto)oncogene(s) [2 max]

[Total: 7]

Q6.

3 **(a)** **D** – uracil ;
E – adenine ;
F – ribose ; **I** pentose / sugar
G – phosphate ; **A** phosphate [4]

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(b) *answers must be in pairs*

mRNA	DNA
ribose	deoxyribose ;
differences between pentoses / sugar may be described in terms of OH on C2	
uracil / no thymine	thymine / no uracil ;
single, polynucleotide / strand / chain	two, polynucleotides / chains / strands ; **A** double
no hydrogen bonds	hydrogen bonding ;
not a helix / straight chain	(double) helix ;
ratio of A+G to C+T varies / AW	ratio of A+G to C+T = 1 / AW ;
no base pairing (within molecule)	base pairing ;
base pairing A-U with, tRNA / anticodon	base pairing is A-T
shorter	longer ;
found in cytoplasm / leaves nucleus	found in nucleus ;
attached to ribosome(s)	not attached to ribosome(s) ;
short-lived	long-lived ;
transfer of information (to ribosome)	information storage / AW ;
codes for one polypeptide	codes for more than one polypeptide ;
produced by transcription	produced by (semi-conservative) replication

[max 3]

(c) **1** translation ; **R** *if transcription given as well, unless in correct context*
A use of, nucleotide / base, sequence, to make, amino acid chain / polypeptide / protein
I protein / polypeptide, synthesis

2 moves towards / combines with, ribosome ;

3 ref to small and/or large sub-units ; **I** small / large ribosome

4 codon(s) ; *only accept in correct context*

5 transfer / t, RNA, bringing, amino acid(s), to mRNA / ribosome ;

6 anticodon(s) ; *only accept in correct context*

7 (complementary) base pairing ;

8 any e.g. of codon:anticodon base pairing ; *need six bases*

9 ref to polyribosome(s) / used by many ribosomes ;

10 (mRNA short-lived) ref to production of protein for short period of time ; [max 4]

[Total: 11]

Q7.

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2 **(a)** *one mark per complete correct row*

DNA	RNA	
two, polynucleotides / chains / strands **A** double	single, polynucleotide / strand / chain	;
(double) helix	not a helix / straight chain ;	;
deoxyribose	ribose *differences between pentoses / sugar may be described in terms of OH on C_2*	;
thymine / no uracil	uracil / no thymine	;
hydrogen bonding (between all bases)	hydrogen bonds between some bases **A** no hydrogen bonds	;
ratio of A+G to C+T = 1 / AW	ratio of A+G to C+T varies	;
longer	shorter	;
one type	more than one type / three types / mRNA + tRNA + rRNA	;

[max 3]

(b) *(GCG)* CGC ;
(ACA) UGU ; [2]

(c) 714 ;; **A** 717 / 720
if, no / incorrect, answer given, award one mark for correct working [2]

(d) 1 (tRNA) carries amino acid to ribosome ;
2 ref. to specificity of amino acid carried ; **A** role in ensuring correct primary structure
3 ref. anticodon (on tRNA): codon (on mRNA) binding ;
4 ref. complementary / base pairing ; **A** A-U, C-G
5 ref to tRNA binding sites within ribosome ;
6 two tRNAs bound to, mRNA / ribosome, at same time ;
7 amino acids held close to each other / AW ;
8 (for) peptide bond formation ;
9 (tRNA) can be reused / binds another amino acid ; [max 4]

[Total: 11]

Q8.

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6 (a) (i) *hydrogen bonds drawn onto Fig. 6.1*

lines must go between O-H, N-H as follows

two lines between A and T H — O and N — H ;
three lines between C and G H — O and N — H and O — H ; [2]

(ii) **1** hydrogen bonds hold (two), polynucleotides / strands / chains, together ;
A hold, (complementary) nucleotides / base pairs, together
A ora e.g. prevents, unwinding / strand separation
2 (many hydrogen bonds) give stability / DNA is stable molecule / DNA is long lasting / AW ; *ignore ref. to strength*
3 can be broken for, transcription / replication ;
4 ref. to (double) helix ; [2]

(b) **1** (named) base / nucleotide, pairing ;
2 purine – pyrimidine ;
3 percentage of A = percentage of T ; **A** very similar
4 percentage of C = percentage of G ; **A** very similar
5 data quote in support ; [max 3]

(c) (i) *idea that*

percentages of, A and T / C and G, are not the same / three percentages are similar; [1]

(ii) single-stranded DNA / not double-stranded / not a double helix ;
A may be other bases ; [1]

[Total: 9]

Q9.

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4 **(a)** **(i)** *DNA because*
RNA (has uracil) does not have thymine ; [1]

(ii) phosphodiester ; [1]

(iii) deoxyribose ; [1]

(b) collects / attaches to, specific amino acid
or
takes specific amino acid / activated tRNA, to ribosome ;

idea of, adjacent / two, amino acids and codon-anticodon binding ;
peptide bond formation / ref. elongation, (to form polypeptide) ; [max 2]

(c) *accept points from a diagram*

1 loss of a water molecule / condensation reaction ;

2 OH / O^-, from, carboxyl / -COOH / COO^- (group) of one amino acid ;
3 H / H^+, from, amine / NH_2 / NH_3^+ (group) of other amino acid ;
2/3 *allow one mark for ref. to involvement of carboxyl and amine group*

4 (peptide bond) links C–N ; [3]

[Total: 8]

Q10.

4 **(a)** 1 important in contributing to 3-D structure of molecule / AW ;
2 many hydrogen bonds so, gives stability / strands not easily separated / long lasting ; AW
3 (individual) hydrogen bonds (more) easily broken (than covalent bonds) ; **A** hydrogen bonds weak / hydrogen bonds can be broken

consequence
4 (so strands can be separated) for (DNA) replication ; **A** description
5 (so strands can be separated) for (DNA) transcription ; **A** description

6 hydrogen bonds only form between, specific bases / named base pairs, so, few mistakes / faithful replication / AW ;
7 *idea that* hydrogen bonds can easily re-form (without chemical reaction) ; [max 4]

(b) **P** = transcription
Q = translation ; [1]

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(c) (i) sequence will not (spontaneously) change / AW ; **A** decreases chance of mutation
(so) gene products / proteins, produced will always be functional ;
maintains all, genetic information / AW, throughout life of cell ;
same, genetic information / AW, passed on to, daughter cells / offspring ;
AVP ; e.g. maintains size so still enclosed within nucleus [max 2]

(ii) translation / protein synthesis, will stop when mRNA breaks down ;
allows re-use of nucleotides (for other mRNA) ;
ref. to control of gene expression ; **A** prevents too much product forming
ref. to control of cell activity / fast response to changing rquirements ;
ref. to efficiency in energy use ; [max 2]

[Total: 9]

Q11.

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4 (a) **J** thymine ;
K guanine ;
L hydrogen bond ;
ignore H / H_2 bond [max 3]

Q12.

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5 **(a)** *three from* ;;;
allow mps without naming DNA / RNA if already gained in previous point
must be comparison statement per row
mark first comparison per row unless one row left blank

	DNA replication	*DNA transcription*
1	DNA, formed / AW	mRNA / pre-mRNA (transcript) , (formed)
2	two (identical) DNA molecules formed	one mRNA molecule (formed)
3	product double-stranded DNA	product single stranded (m)RNA
4	all of DNA molecule, replicated / unwinds / involved	part of DNA molecule / gene, involved
5	both strands involved	one strand (involved) *treat ref. to sense / antisense strands as neutral*
6	(involves / uses) DNA polymerase	RNA polymerase
7	(free) DNA nucleotides, required / used	RNA nucleotides
8	(process involves complementary) base pairing A–T *ignore* C–G	(complementary) base pairing A–U
9	takes place in late interphase / S-phase / synthesis phase	takes place throughout interphase
10	important in, cell division / mitosis / meiosis	for, polypeptide / protein, synthesis

[max 3]

(b) change / alteration / AW, in sequence / order / arrangement, of, bases /nucleotides (of DNA / gene) ; change to give a new allele ;

one additional detail ;
(may result in) altered, changed / non-functioning / no, polypeptide / protein
ref. to changed genetic code / different codons
different sequence of amino acids / different primary structure
named type of mutation
example e.g. HbS [max 2]

Q13.

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2 **(a)** **(i)** cells have machinery for protein synthesis / AW ;
A plant / animal, cells have RER
(assumption that) cells will continue to produce protein at high rate ;
large number of / many / AW, ribosomes ;
available supply of / AW, amino acids ;
ref. to presence of tRNA molecules ;
ATP available ;
ref. to easier to harvest high levels of protein ; [max 2]

(ii) *idea that* any added mRNA, has easier access to / can reach, ribosomes / RER ;
so that the cell's own, DNA / mRNA can be accessed / AW ;
easier to, harvest / extract, protein products ; [max 1]

(iii) only the desired protein is produced / AW ; ora
unwanted protein does not have to be separated from desired protein ;
idea that inefficient process if translation machinery used to produce other proteins ;
cell's proteins may, inhibit / affect / hinder / AW, process ; [max 1]

(iv) ref. to ribosome function not altered ;
R ref. to prokaryotic and eukaryotic ribosomes being the same
mechanism of translation / described, is the same in all cells ;
e.g. tRNA can respond to introduced mRNA
all types of cells use mRNA for protein synthesis ;
mRNA only has one role ;
genetic code / codons, are the same in all cells ;
A genetic code is universal
mRNA, contains only exons / introns removed, so translation can occur ; [max 2]

(b) different, structure / rRNA, (of ribosomes) ;
(ribosomes), larger / 80S, in eukaryotes *or* smaller / 70S in prokaryotes ;
(some) attached to / AW, (eternal surface of) RER in eukaryotes ; ora
A only found in cytoplasm in prokaryotes [max 2]

(c) other organelles / components, damaged *or* whole cell all organelles intact ;
some, ribosomes / RER, lost / damaged ;
idea that cell-free system is disorganised ; ora
fewer amino acids available ; ora
no / reduced, respiration ; AW
other, components / AW, required are, lost / at lower levels ;
organelles / components, not replaced ; ora
ref. to difficulty in creating identical conditions to cell environment ;
may be able to use cells that can replicate (hence continuous production) ;
AVP ; [max 1]

[Total: 9]

Q14.

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(c) (i) **mRNA** CGU ; UGC / UGU ; GAA

DNA GCA ACG / ACA CTT ; [3]

(ii) many / several / more than one, triplet for each amino acid ; **A** codon
an e.g. from Table 3.1 ;
degenerate code / description e.g. 64 possible triplets for 20 amino acids ; **A** codons
AVP ; e.g. may be an intron in this region, different nucleotides at the beginning (signal sequence) [2 max]

Q15.

(c) (i) AUG ; [1]

(ii)
1 secondary structure / α-helix / β-(pleated) sheet ;
2 tertiary structure / description / folding / complex 3D shape ;
3 formation of named bond(s) ; **R** if peptide bond in list
4 quaternary structure / description (e.g. assembly of polypeptides) ;
5 glycosylation / formation of glycoproteins / addition of carbohydrate(s) *or* sugar(s) ; **R** hydrocarbon chain
6 addition of, non-protein portion(s) / prosthetic group(s) / named example ; **A** haem / iron / Fe / copper / Cu / magnesium / Mg / AW
7 removal of some amino acids ; **R** one amino acid
8 polypeptide(s) cut into two or more pieces ;
9 AVP ; e.g. ref. to exposure to water molecules and folding **R** ref. to amino acids coded for by stop codons [max 2]

Q16.

(b) six / first five and seventh, amino acids are the same ; ora amino acid at position 6 is different
both are 1. val-2.his-3.leu-4.thr-5.pro….7.glu ; *take from diagram*
variant 1 is, glutamic acid / glu (whereas), variant 2 is, valine / val ; [3]

Q17.

(c) condensation / polymerisation / esterification ; [1]

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(d)

	replication	*transcription*
1	DNA polymerase	RNA polymerase ;
2	(free activated) DNA nucleotides	RNA nucleotides ;
3	(complementary) base pairing A-T	base pairing A-U ;
4	both strands, involved / act as template / AW	one strand involved ;
5	all / AW, the DNA molecule, is copied / unzips / AW	part / gene(s), copied ;
6	(two) DNA molecules produced **A** DNA produced	messenger RNA / mRNA / pre-mRNA , produced ;
7	molecule(s) produced are double-stranded	single-stranded molecule produced ;
8	occurs, in late interphase / S-phase / prior to mitosis	occurs throughout interphase / AW ;
9	important in, mitosis / meiosis **A** cell / nuclear, division	important in, protein / polypeptide, synthesis ;
10	AVP ; e.g. Okazaki fragments / breaking and joining (of DNA) required	mRNA produced as continuous molecule

[max 4]

Q18.

5 (a) (i) box drawn round one phosphate, sugar and base ; [1]

(ii) label P to circle ; **A** phosphate / no label but clear a circle is intended [1]

(b) **1** DNA (double helix), unwinds / AW ; **A** uncoil
2 hydrogen bonds between (complementary) bases broken ;
ignore DNA unzips
3 complementary, base / nucleotide, pairing ; **A** A-T **and** C-G
4 phosphodiester bonds ;
5 both strands used as templates ; **A** both strands are copied
6 produces two identical DNA molecules ; **A** 'DNAs'
7 semi-conservative / each new DNA = one 'old' and one 'new' strand ;
8 ref to DNA polymerase ;
9 correct ref to other named enzyme ; e.g. helicase (unwinds), topoisomerase (cuts backbone), ligase (formation of phosphodiester bonds)
10 ref to Fig. 5.1 ; e.g. described dotted lines as H bonds that need to be broken
look for annotations on Fig. 5.1
11 AVP ; e.g. replication fork(s), replication bubble(s), antiparallel nature, Okazaki fragments, activated nucleotides (3 phosphate groups) [max 5]

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(c) **1** tRNA carries amino acid to ribosome ;
2 ref to specificity of amino acid carried ;
3 anti-codon on tRNA complementary to codon on mRNA ;
A example for complementary, e.g. AUG and UAC
4 ref to two sites / P(eptidyl) and A(mino-acyl) sites, of ribosome ;
5 peptide bond is formed between amino acids ; **R** 'polypeptide bond'
6 tRNA, can be re-used / collects another amino acid ; [max 3]

[Total: 10]

Q19.

5 **(a)** 1 complementary bases / base pairing, hold(s) strands together / AW;
2 (because of) many hydrogen bonds;
R if between adjacent nucleotides
if mp 1 and 2 not awarded
1/2 hydrogen bonds hold strands together;
3 sugar-phosphate backbone / AW, with covalent / phosphodiester, bonds;
4 double helix structure protects bases;
5 **AVP**; coiling protects from, chemical / enzyme, attack [max 2]

(b) 1 (information is) ref. (different) sequence / order of bases / nucleotides (in the polynucleotide strand);
A described in terms of sequence of bases
2 DNA / gene, contains / AW, information for the synthesis of a, polypeptide / protein / enzyme;
3 *idea that* (coded because) information becomes sequence of amino acids;
4 *idea that* information passed on (cell to cell / parent to offspring); [max 2]

(c) (late) interphase / S phase / synthesis phase; [1]

(d) 1 different sequence of bases / nucleotides;
2 (as a result of) mutation;
3 base substitution;
4 CTT replaced by CAT;
A GAA replaced by GUA (for mRNA codon)
5 glu(tamate) substituted by val(ine); [max 3]

(e) 1 increasing concentration of ara-ATP decreases enzyme activity;
can be comparison between 0 and 5 / 20 or between 5 and 20
A ref. to rate of DNA synthesis for enzyme activity
2 ara-ATP acting as an inhibitor;
3 substrate unable to bind with active site / fewer enzyme-substrate complexes (formed);
4 further detail;
for either competitive
e.g. competes with substrate for (binding to) the active site / similar, structure / shape, as substrate *or* complementary shape to active site
or non-competitive inhibition
e.g. binds to site other than active site / changes shape of active site [max 3]

[Total: 11]

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Q20.

5 (a) *all points except mp3 may be taken from a labelled/annotated diagram*

1 ref. to, attachment / AW, to mRNA ;
2 *idea of* two codon attachment, sites / space, for six bases *or* nucleotides ;
3 mRNA has code for sequence of amino acids (in a polypeptide) ;
4 (ribosome) provides sites for attachment of two tRNA (molecules) ;
A implied
5 each tRNA has a specific amino acid / AW ;
6 (mRNA) codon – anticodon (tRNA), binding ;
A description in terms of complementary base pairing
A 'matching'
7 formation of peptide bonds (catalysed by peptidyl transferase) ;
8 *idea of* ribosome moving along mRNA one codon at a time ; [max 4]

(b) (i) GGC ; [1]

(ii) CTA ; [1]

(c) 1 amino acid coded by codon 2 changed ;
2 *idea of* every subsequent codon changed ;
3 amino acids / protein sequence, up to and including codon 1 unaffected / AW
ora amino acid sequence from codon 2 onwards is changed ;
4 *idea of* premature chain termination (if stop codon further on) / AW ;
5 *idea of* change in, primary / secondary / tertiary, structure of protein ;
6 *idea of* protein non-functional ;
ignore 'affect / effect'
A in context of enzyme not functioning
R if this point is out of context
7 **AVP** ; e.g. frameshift (mutation) [max 3]

[Total: 9]

Q21.

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5 (a) (i) GTG ;

ACU ;

leu ; [3]

(ii) primary structure ; [1]

(b) 1 mutation ;
2 base substitution/T→ A in template strand of DNA/AW ;

transcription
3 DNA has CAC as 6th triplet ;
4 (so) mRNA has GUG as (6th) codon ;
allow one mark for altered mRNA codon *if no marks gained for mps 3 and 4*

translation
5 different tRNA involved/tRNA specific to val and not glu ;
6 anticodon on tRNA has CAC (with valine) ;
7 tRNA brings, incorrect amino acid/val, to ribosome ;
8 further detail ; e.g. incorrect amino acid incorporated into growing polypeptide chain [max 5]

[Total: 9]

Q22.

(b) UAC ; [1]

(c) mRNA, less stable / broken down sooner / used only for a short time / does not last long / is temporary / has short (half-) life ; **I** 'used up'
tRNA is re-used (for a longer time); no ora
unless correct ref. to mRNA 'shelf life' [max1]

(d) 1 translation (*in correct context*) / genetic code used to make a sequence of amino acids / AW ;
2 attach / assemble around / moves along / AW, mRNA ;
A ref. to bind mRNA / mRNA 'lies within' the ribosome
R mRNA enters ribosome
3 tRNA(s) carrying amino acid(s), bind to / AW, mRNA ;
A provides two sites for tRNAs carrying amino acids to bind to mRNA
4 binding / pairing / AW, between anticodon on tRNA to codon on mRNA ;
5 (catalyse) formation of peptide bond (to form polypeptide) ;
6 any further detail of translation ;
e.g. peptidyl transferase
ribosome moves along one codon at a time
start codon is AUG
stop codon *in context*
correct roles of P and A sites [max 3]

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