

Q1.

Question	Expected Answers	Marks														
5 (a) (i)	U - phosphate / PO <sub>4</sub> ; R phosphoric acid / phosphorus / P W - deoxyribose; R pentose X - cytosine; R nitrogenous base / pyrimidine / C	3														
(ii)	Z - hydrogen; R H	1														
(b)	<p><i>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.</i></p> <table style="width: 100%; border: none;"> <tr> <td style="width: 50%; border: none;"><i>polypeptide</i></td> <td style="width: 50%; border: none;"><i>DNA</i></td> </tr> <tr> <td style="border: none;">amino acids</td> <td style="border: none;">nucleotides ;</td> </tr> <tr> <td style="border: none;">one / single strand / chain</td> <td style="border: none;">two / double strand / chains ;</td> </tr> <tr> <td style="border: none;">peptide bonds R between peptides / polypeptides</td> <td style="border: none;">phosphodiester ;</td> </tr> <tr> <td style="border: none;">20 monomers / sub units A &gt; 4 monomers / sub units</td> <td style="border: none;">only 4 monomers / sub units ; R 4 bases</td> </tr> <tr> <td style="border: none;">no phosphate / PO<sub>4</sub></td> <td style="border: none;">has phosphate / PO<sub>4</sub> ;</td> </tr> <tr> <td style="border: none;">2° / 3° structure</td> <td style="border: none;">double helix ;</td> </tr> </table>	<i>polypeptide</i>	<i>DNA</i>	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 <sub>4</sub>	has phosphate / PO <sub>4</sub> ;	2° / 3° structure	double helix ;	3 max
<i>polypeptide</i>	<i>DNA</i>															
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 <sub>4</sub>	has phosphate / PO <sub>4</sub> ;															
2° / 3° structure	double helix ;															

Q2.

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

- (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.**

- 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]

(b) answers must be in pairs

mRNA	DNA
ribose	deoxyribose ;
<i>differences between pentoses / sugar may be described in terms of OH on C2</i>	
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.

2 (a) one mark per complete correct row

DNA	RNA	
two, polynucleotides / chains / strands <b>A</b> double	single, polynucleotide / strand / chain	;
(double) helix	not a helix / straight chain ;	;
deoxyribose	ribose <i>differences between pentoses / sugar may be described in terms of OH on C<sub>2</sub></i>	;
<u>thymine</u> / no uracil	uracil / no <u>thymine</u>	;
hydrogen bonding (between all bases)	hydrogen bonds between some bases <b>A</b> 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.

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.

- 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<sup>-</sup>, from, carboxyl / -COOH / COO<sup>-</sup> (group) of one amino acid ;
- 3 H / H<sup>+</sup>, from, amine / NH<sub>2</sub> / NH<sub>3</sub><sup>+</sup> (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]

(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 requirements ;  
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<sub>2</sub> bond** [max 3]

Q12.

- 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*

	<i>DNA replication</i>	<i>DNA transcription</i>
1	DNA, formed / AW	mRNA / pre-mRNA (transcript) , (formed)
2	two (identical) DNA <u>molecules</u> formed	one mRNA <u>molecule</u> (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) <i>treat ref. to sense / antisense strands as neutral</i>
6	(involves / uses) DNA polymerase	RNA polymerase
7	(free) DNA nucleotides, required / used	RNA nucleotides
8	(process involves complementary) base pairing A–T <i>ignore C–G</i>	(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.

- 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, (external 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.

(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 /  $\alpha$ -helix /  $\beta$ -(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]

(d)

	<b>replication</b>	<b>transcription</b>
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]

- (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]

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.

- 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 6<sup>th</sup> triplet ;  
4 (so) mRNA has GUG as (6<sup>th</sup>) 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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