

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) | <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 border="0"> <tr> <td><i>polypeptide</i></td> <td><i>DNA</i></td> </tr> <tr> <td>amino acids</td> <td>nucleotides ;</td> </tr> <tr> <td>one / single strand / chain</td> <td>two / double strand / chains ;</td> </tr> <tr> <td>peptide bonds R between peptides / polypeptides</td> <td>phosphodiester ;</td> </tr> <tr> <td>20 monomers / sub units A > 4 monomers / sub units</td> <td>only 4 monomers / sub units ; R 4 bases</td> </tr> <tr> <td>no phosphate / PO₄</td> <td>has phosphate / PO₄ ;</td> </tr> <tr> <td>2^o / 3^o structure</td> <td>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 ₄ | has phosphate / PO ₄ ; | 2 ^o / 3 ^o 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 ₄ | has phosphate / PO ₄ ; | | | | | | | | | | | | | | | |
| 2 ^o / 3 ^o 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 A 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 C₂</i> ; |
| <u>thymine</u> / no uracil | uracil / no <u>thymine</u> ; |
| 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.

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⁻, from, carboxyl / -COOH / COO⁻ (group) of one amino acid ;
- 3 H / H⁺, from, amine / NH₂ / NH₃⁺ (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.

4 (a) J thymine ;
K guanine ;
L hydrogen bond ;
ignore H/H₂ 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 / 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]

(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]

- (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 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]

