Mark schemes

**Q1.**

(a)  1.    Hydrogen (bonds);

2.    Phosphodiester (bonds);
*Accept ester/covalent bond*

**2**

(b)  Correct answer for 2 marks = 1489/1489.2;;

Incorrect answer but for 1 mark accept:

876

**OR**

1861 - 1862

**2**

(c)  1.    tRNA is 'clover leaf shape', mRNA is linear;
*Must be a comparison*
*Reject tRNA is double stranded*
*Accept tRNA is folded for tRNA is 'clover leaf shaped'*

2.    tRNA has hydrogen bonds, mRNA does not;

3.    tRNA has an amino acid binding site, mRNA does not;
*Accept 'CCA end' for amino acid binding site*

4.    tRNA has anticodon, mRNA has codon;

**2**

(d)  1.    mRNA fewer nucleotides

**OR**

Pre-mRNA more nucleotides

**OR**

mRNA has no introns/has (only) exons

**OR**

Pre-mRNA has (exons and) introns;
*Accept mRNA is shorter OR pre-mRNA is longer*

2.    (Because of) splicing;

**2**

**[8]**

**Q2.**

(a)  1.  tRNA brings specific amino acid (to ribosome);

2.  Anticodon (on tRNA) binds to codon (on mRNA);

3.  Amino acids join by condensation reaction (using ATP)

   **OR**

   Amino acids join to form a peptide bond (using ATP);

**3**

**Q3.**

(a)  1.  (Free RNA) nucleotides form complementary base pairs;
          *Accept A-U, G-C **OR** combination of those pairs*

2.  Phosphodiester bonds form;
          *Accept linkages for 'bonds'*

3.  By (action of) RNA polymerase;

**3**

(c)  Serine Alanine Glycine Proline;
          *Must be in this order Accept Ser Ala Gly Pro / S A
          G P*

**1**

**Q4.**

(a)  1.  Hydrogen bonds (between DNA bases) break;
          *Ignore DNA helicase.*
          *Reject hydrolysing hydrogen bonds.*

2.  (Only) one DNA strand acts as a template;

3.  (Free) RNA nucleotides align by complementary base pairing;
          *For 'align by complementary base pairing', accept
          'align to complementary bases' or 'align by base
          pairing'.*

4.  (In RNA) Uracil base pairs with adenine (on DNA)

   OR

   (In RNA) Uracil is used in place of thymine;
          *Do not credit use of letters alone for bases.*

5.  RNA polymerase joins (adjacent RNA) nucleotides;
          *Reject suggestions that RNA polymerase forms
          hydrogen bonds or joins complementary bases.*

6.  (By) phosphodiester bonds (between adjacent nucleotides);

7.    Pre-mRNA is spliced (to form mRNA)

OR

Introns are removed (to form mRNA);

**5 max**

(b)    1.    (mRNA attaches) to ribosomes

OR

(mRNA attaches) to rough endoplasmic reticulum;

2.    (tRNA) anticodons (bind to) complementary (mRNA) codons;

3.    tRNA brings a specific amino acid;

4.    Amino acids join by peptide bonds;

5.    (Amino acids join together) with the use of ATP;

6.    tRNA released (after amino acid joined to polypeptide);

7.    The ribosome moves along the mRNA to form the polypeptide;

**6 max**

## Q5.

(a)    (The proteome is the full) range of / number of different proteins that a cell is able to produce (at a given time);

**OR**

(The proteome is the full) range of / number of different proteins the genome / DNA is able to code for;
   *Do not accept number of proteins unqualified*

**1**

(b)    1.    mRNA does not have hydrogen bonds / base pairing, tRNA does;
**OR**
mRNA is linear / straight chain, tRNA is cloverleaf;

2.    mRNA does not have an amino acid binding site, tRNA does;
   *Accept mRNA cannot carry an amino acid, tRNA
   can*

3.    mRNA has more nucleotides;
   *Accept mRNA is long<u>er</u> or converse*

4.    (Different) mRNAs have different lengths, all tRNAs are similar / same length;

5.    mRNA has codons, tRNA has an anticodon;
   *Statements must be comparative*

**2 max**

(c)  1.    mRNA associates with a ribosome / ribosome attaches to mRNA;
           *Idea of association is required*

     2.    Ribosome moves to / finds the start codon / AUG;

     3.    tRNA brings / carries (appropriate / specific) amino acid;
           *Must be explicitly stated and not inferred.*

     4.    Anticodon (on tRNA complementary) to codon (on mRNA);

     5.    Ribosome moves along to next codon;
           **OR**
           Ribosome 'fits' around two codons / can fit two tRNAs;
           *Must be explicitly stated and not inferred.*

     6.    (Process repeated and) amino acids join by peptide bonds /
           condensation reaction (to form polypeptide);
           **OR**
           (Process repeated and) amino acids joined using (energy from) ATP
           (to form polypeptide);

                                                                      **5**

                                                                          **[8]**


## Q6.

(b)  1.    More than one codon codes for a single amino acid;
           *Accept 'triplet' or 'sequence of 3 bases/nucleotides'*
           *for 'codon'.*
           *Reject 'production/produces' for 'codes for'.*
           *Do not infer mp1 from mp2.*

     2.    Suitable example selected from Table 1;

                                                                      **2**

(c)  1395;

           *Accept 1398 and 1401 (for those that include start*
           *and/or stop codons)*
           *Allow 2796 or 2802 or 2790*
           *Ignore 'bases/base pairs/bp/bps' written after the*
           *numerical answer.*

                                                                      **1**


## Q7.

(b)  1.    The DNA strands separate by breaking the H bonds;
           **OR**
           H bonds broken between (complementary) (DNA) bases;
     2.    (Only) one of the strands/template strand is used (to make
           mRNA/is transcribed);
     3.    (Complementary) base pairing so A → U, T → A, C → G, G
           → C;

4.    (RNA) <u>nucleotides</u> joined by RNA polymerase;
5.    pre-mRNA formed;
6.    Splicing / introns removed to form mRNA;

       *1.    Ignore 'hydrolysis' of bonds*

       *1.    Accept DNA "unzips" by breaking the H bonds*

       *6.    Accept 'non-coding' sections for introns*

       **5 max**

       **[10]**

## Q8.

(a)    1.    **One of** RNA / ribonucleic acid(s) / nucleotide(s)/nucleic acid(s) /
rRNA / ribosomal RNA / ribosomal ribonucleic acid
**and**
**one of** protein(s) / polypeptide(s) / amino acid(s) / peptide(s) /
ribosomal protein;

       *Reject DNA, deoxyribonucleic acid, tRNA, transfer
RNA, transfer ribonucleic acid, mRNA, messenger
RNA, messenger ribonucleic acid.*

       *Ignore enzyme(s), base(s).*

       **1**

(b)    1.    mRNA binds to ribosome;
2.    Idea of <u>two</u> codons / binding sites;
3.    (Allows) tRNA with <u>anticodons</u> to bind / associate;
4.    (Catalyses) formation of <u>peptide</u> bond between **amino acids**
(held by tRNA molecules);
5.    Moves along (mRNA to the next codon) / translocation
described;

       *Assume 'it' refers to ribosome.*

       **3 max**

(c)    TGCGTAATA;
Any errors = 0 marks

       **1**

(d)    1.    Introns (in pre-mRNA);
2.    Removal of sections of (pre-mRNA) / splicing;

       *Introns removed' scores 2 marks.*

       *Reference to 'introns present in mRNA' disqualifies
mp1 but allow ECF for mp2.*

       *Accept for 1 mark mRNA contains <u>only</u> exons.*

       **2**

       **[7]**