AQA A-LEVEL · 7402

# BIOLOGY



## MARK SCHEME

### 3.4.2 DNA AND PROTEIN SYNTHESIS

| SCORE | PERCENTAGE |
| --- | --- |
| /445 | % |

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## Q1.

(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 longer 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]**

## Q2.

(a) 1. The (individual) chromosomes are visible because they have condensed;

*Both parts of each answer are required – evidence and explanation.*

*For 'they' accept 'chromosomes/chromatin/DNA'*

*Accept 'tightly coiled' or 'short and thick' for condensed but do not accept 'contracted'.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

2. (Each) chromosome is made up of two chromatids because DNA has replicated;

*Both parts of each answer are required – evidence and explanation.*

*Accept 'sister chromatids' for 'two chromatids'.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

3. The chromosomes are not arranged in homologous pairs, which they would be if it was meiosis;

*Both parts of each answer are required – evidence and explanation.*

*Accept not meiosis because bivalents/chiasmata/crossing over not seen.*

*Ignore references to nucleus/nucleolus/nuclear membrane.*

**2 max**

(b) Automarked q – ✔ prophase

**1**

(c) 1. Water moves into the cells/cytoplasm by osmosis;

*Reject water moving into chromosomes/nucleus.*

2. Cell/cytoplasm gets bigger;

*Accept idea of cell/cytoplasm has greater volume/swells/expands.*

*Ignore references to pressure changes, turgidity and chromosomes being more dilute.*

*Ignore references to changing water/fluid contents of the cell.*

*Allow ECF for 'nucleus expands' but not for 'chromosomes expand'.*

**2**

(d) Differences in base sequences

**OR**

Differences in histones/interaction with histones

**OR**

Differences in condensation/(super)coiling;

*Answer must be in context of differences in arrangement of chromosomes not just related to the properties of the stain.*

*Accept spec section 8 ideas e.g. different methylation/acetylation*

*Accept different genes*

*Reject different alleles*

**1**

(e) (Two chromosomes that) carry the same genes;

*Reject 'same alleles'*

*Accept 'same loci' (plural) or 'genes for the same characteristics'*

**1**

(f) (Prokaryotic DNA) is

1. Circular (as opposed to linear);

2. Not associated with proteins/histones ;

3. Only one molecule/piece of DNA
**OR**
present as plasmids;

*Max 1 if prokaryotic DNA only found as plasmids OR if prokaryotic DNA is single stranded.*

*Ignore references to nucleus, exons, introns or length of DNA. Do not credit converse statements.*

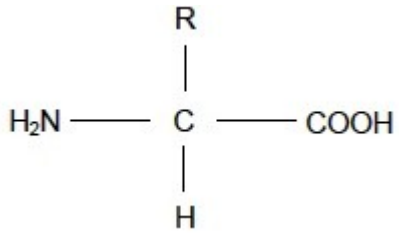
*Ignore descriptions of eukaryotic DNA alone.*

**2 max**

**[9]**

## Q3.

(a)




*Accept other correct representations.*

**1**

(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**

(d) ✔CAA → CGA

**1**

(e) 1. (Both) negatively charged to positively charged change in amino acid;

2. Change at amino acid 300 does not change the shape of the active site
**OR**
Change at amino acid 300 does not change the tertiary structure OR Change at amino acid 300 results in a similar tertiary structure;

*Reference to 'shape' of active site only needed once.*

3. Amino acid 279 may have been involved in a (ionic, disulfide or hydrogen) bond **and** so the shape of the active site changes
**OR**
Amino acid 279 may have been involved in a (ionic, disulfide or hydrogen) bond **and** so the tertiary structure changed;
**OR**
Amino acid 279 may be in the active site **and** be required for binding the substrate;

*Reference to 'shape' of active site only needed once.*

*Both parts are required for each mark option.*

*For 'a bond' reject peptide bond.*

**3**

**[8]**

## Q4.

(a) 1. (µg because) very little ammonia (in soil);

2. (µg because) avoids use of (lots of) decimal places (in their results) / avoids the use of powers of 10 / avoids the use of standard form;

*Accept makes numbers more manageable*

*Accept makes easier to plot graph*

3. ($g^{-1}$) to allow comparisons (between samples);

**2 max**

(b) Answer between 4.5 and 4.6 µg $g^{-1}$ $day^{-1}$;;

Award 1 mark for correct number but wrong / no units

*Ignore plus or minus signs*

*Accept 'per gram' **AND / OR** 'per day'*

**2**

(c) 1. pH 4.3 / B has fastest rate of breakdown (of ammonia);

2. A + B / mixture at pH 6.9 slowest / slower (than A or B);

*Not just ref. to A and then B on their own*

3. Suggests (community / bacteria at) pH 4.3 / B doesn't work (well) at pH 6.9 / pH of mixture;

*Accept converse that only (community / bacteria at) pH 6.9 / A is working in the mixture*

**3**

(d) (Species **S** because) no mark

1. Species **S** change of 990,000 (per gram of soil);

*Award MP1 and 2 OR MP3 and 4*

*Accept standard forms $9.9 \times 10^5$ and $9.9 \times 10^3$ for either*

*Accept for 1 mark for 100 times greater in correct context with no other calculations shown*

2. Species **T** change of 9,900 (per gram of soil);

*Accept standard forms $9.9 \times 10^5$ and $9.9 \times 10^3$ for either*

**OR**

(Species **T** because) no mark

3. Species **S** has 99% change;

4. Species **T** has 9900% change;

**2**

(e) 1. They didn't count bacteria / cells / population(s);

*Ignore ref. to other factors / other named factors affecting growth*

2. Copies / number of mRNA related to amount of enzyme / amoA produced / translated;

3. Don't know how much mRNA / amoA produced by each cell;

*Accept some bacteria produce more mRNA / amoA than others*

4. Don't know if amoA (mRNA / enzyme) is linked to cell division / growth (of population);

*Amount of amoA does not show cell division / growth*

*Reject references to mitosis / meiosis*

**4**

(f) 1. Suitable method;
eg in boiling water / steam / autoclave / wash in disinfectant / wash in alcohol

*Ignore heat unqualified*

*Ignore flaming of bottle*

*Accept radiation*

2. (Reason) to remove / kill other bacteria / organisms that might break down ammonia;

*Ignore ref to removing bacteria that 'affect the result'*

*Accept other bacteria producing amoA*

*Accept other bacteria compete with / kill bacteria that produce amoA*

*Ignore contamination unqualified*

**2**

**[15]**

## Q5.

(a) 1. Low starch, fewer copies;

2. Ranges overlap almost completely;
**OR**
Ranges overlap from 2 − 13 copies;
3. (surprisingly) very few / 2 or 3% have only 2 copies / are diploid;
4. the mode / highest percentage for low starch is 4 copies and for high starch is 6;
5. the range / spread is greater with high starch;

*4. "most people" is not equivalent to mode*

**3 max**

(b) 1. More mRNA / more transcription;
2. More translation / enzyme;
3. So reaction faster;

*The idea of "more" must be stated at least once.*

*2. Accept 'amylase' for enzyme*

*3. "More starch digested" is insufficient*

**3**

(c) 1. Mutation(s) produce extra copies of (*AMY1*) gene;
2. Those with more copies / this adaptation/mutation reproduce / survive better on high starch diet;
2. And pass on multiple copies / this adaptation/mutation (to offspring);

*Ignore ref. to single allele/gene*

**3**

**[9]**

## Q6.

(a) 1. Water lost from leaf because of transpiration / evaporation of water (molecules) / diffusion from mesophyll / leaf cells;
**OR**
Transpiration / evaporation / diffusion of water (molecules) through stomata / from leaves;
2. Lowers water potential of mesophyll / leaf cells;
3. Water pulled up xylem (creating tension);
4. Water molecules cohere / 'stick' together by hydrogen bonds;
5. (forming continuous) water column;
6. Adhesion of water (molecules) to walls of xylem;

*2. Accept Ψ or WP*

**5 max**

(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) nucleotides 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]**

## Q7.

(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]**

## Q8.

(a) 1. Degenerate: more than one (base) triplet for each amino acid;

2. Non-overlapping: each base is part of only one triplet.

*Accept codon (as would be applicable to mRNA code)*

**2**

(b) A = adenine

C = cytosine

G = guanine

U = uracil

*All four correct = 2*
*One error = 1*
*Two or more errors = 0*

**2 max**

(c) <u>AGT</u>;

**1**

**[5]**

## Q9.

(a) 1. DNA of eukaryotic cell has non-coding regions / introns within gene

*Allow converse: (But) a prokaryotic cell does not have non-coding regions / introns in DNA;*

**OR**

pre-mRNA contains non-coding regions / introns;

2. (After transcription / during modification) these regions are removed from (pre-)mRNA;

*Ignore references to 'cells need / bacteria do not need'*

**2**

(b) 1. mRNA longer

**OR**

Has more nucleotides than tRNA;

2. mRNA is a straight molecule but tRNA is a folded molecule / clover-leaf shaped molecule;

3. mRNA contains no paired bases / hydrogen bonds but tRNA has some paired bases / hydrogen bonds.

**2 max**

**[4]**

## Q10.

(a) 2 to 11;

**1**

(b) ± 2.0;

Data show great variation (around mean)
**OR**
4.4 ± 2 × SD includes most of the values measured.

**2**

(c) 1. Shows a positive correlation;

2. Their probability of getting this correlation by chance is less than 0.0001;

*Allow less than 0.01%*

3. Correlation is highly significant.

*Reject 'results' are significant / not due to chance*

**3**

(d) 1. Little digestion of starch by salivary amylase
**OR**
starch in mouth for a short period
**OR**
salivary amylase inactivated by stomach acid;

2. Amylase also secreted by pancreas;

3. So (most) starch digestion occurs in small intestine.

3

**[9]**

## Q11.

(a) 1. Hydrogen bonds between the base pairs holds two strands together

2. Many hydrogen bonds provides strength

*Reject strong hydrogen bonds*

2

(b) (Because) ribosomes assemble polypeptides using mRNA code
**OR**
DNA has two strands each with a different (complementary) base sequence;

1

(c) Codon;

1

(d) 1. (Because) some amino acids have more than one codon / mRNA code;

2. Correct example from table.

2

(e) 1. Stop translation;

2. Result in detachment of polypeptide chain from ribosome.

2

(f)

| | | |
|---|---|---|
| CAC | ATG | ACC |
| Val | Tyr | Trp |

*Mark each row*

2

**[10]**

## Q12.

(a) (Molecule contains) more than one polypeptide (chain).

*Accept: has four polypeptides*

1

(b) $\frac{\text{oxygenated haemoglobin}}{\text{maximum saturation}} \times 100$

1

(c) 1. At low partial pressure of oxygen, little increase in saturation as oxygen increases;

2. (then) rapid rise as it gets easier for oxygen to bind.

*Accept use of appropriate numbers from graph*

2

(d) Ensures rapid / more intake of oxygen in lungs / release of oxygen in tissues.

**1**

(e) Volume of blood leaving heart = (0.6 × 0.6) $dm^3$ $minute^{-1}$ = 3.6 $dm^3$ $minute^{-1}$

Mass of haemoglobin in this volume of blood = (3.6 × 150) g = 540g

Volume of oxygen at 100% saturation of this haemoglobin = (540 × 1.35) = 729 $cm^3$

The graph shows 60% of this volume of oxygen has been released to the tissues, so final answer is (729 × 0.6) = 437.4 $cm^3$ $minute^{-1}$

**3**

**[8]**

## Q13.

(a) Translation.

**1**

(b) Transfer RNA / tRNA.

**1**

(c) TAC;

UAC.

**2**

(d) Have different R group.

*Accept in diagram*

**1**

(e) 1. Substitution would result in CCA / CCC / CCU;
2. (All) code for same amino acid / proline;
3. Deletion would cause frame shift / change in all following codons / change next codon from UAC to ACC.

**3**

**[8]**

## Q14.

(a) 1. Helicase;
2. Breaks hydrogen bonds;
3. Only one DNA strand acts as template;
4. RNA nucleotides attracted to exposed bases;
5. (Attraction) according to base pairing rule;
6. RNA polymerase joins (RNA) nucleotides together;
7. Pre-mRNA spliced to remove introns.

**6 max**

(b) 1. Polymer of amino acids;
2. Joined by peptide bonds;
3. Formed by condensation;
4. Primary structure is order of amino acids;
5. Secondary structure is folding of polypeptide chain due to hydrogen bonding;

*Accept alpha helix / pleated sheet*

6. Tertiary structure is 3-D folding due to hydrogen bonding and ionic / disulfide bonds;

7. Quaternary structure is two or more polypeptide chains.

**5 max**

(c) 1. Hydrolysis of peptide bonds;
2. Endopeptidases break polypeptides into smaller peptide chains;
3. Exopeptidases remove terminal amino acids;
4. Dipeptidases hydrolyse / break down dipeptides into amino acids.

**4**

**[15]**

## Q15.

(a) 1. Reduction in ATP production by aerobic respiration;
2. Less force generated because fewer actin and myosin interactions in muscle;
3. Fatigue caused by lactate from anaerobic respiration.

**3**

(b) Couple **A**,
1. Mutation in mitochondrial DNA / DNA of mitochondrion affected;
2. All children got affected mitochondria from mother;
3. (Probably mutation) during formation of mother's ovary / eggs;

Couple **B**,
4. Mutation in nuclear gene / DNA in nucleus affected;
5. Parents heterozygous;
6. Expect 1 in 4 homozygous affected.

**4 max**

(c) 1. Change to tRNA leads to wrong amino acid being incorporated into protein;
2. Tertiary structure (of protein) changed;

3. Protein required for oxidative phosphorylation / the Krebs cycle, so less / no ATP made.

**3**

(d) 1. Mitochondria / aerobic respiration not producing much / any ATP;
2. (With MD) increased use of ATP supplied by increase in anaerobic respiration;
3. More lactate produced and leaves muscle by (facilitated) diffusion.

**3**

(e) 1. Enough DNA using PCR;
2. Compare DNA sequence with 'normal' DNA.

**2**

**[15]**

## Q16.

(a)

| **Feature** | **Bacterium** | **Human immunodeficiency virus (HIV) particle** |
|---|---|---|
| RNA | ✔ | ✔ |
| Cell wall | ✔ | |
| Enzyme molecules | ✔ | ✔ |

| | | |
|---|---|---|
| Capsid | | ✔ |

*1 mark for each correct vertical column*

**2**

(b) 1. (Complementary) nucleotides/bases pair
**OR**
A to T **and** C to G;

*Ignore '(DNA polymerase) forms base pairs/nucleotide pairs'*

2. DNA polymerase;
3. Nucleotides join together (to form new strand)/phosphodiester bonds form;

*Ignore '(DNA polymerase) forms base pairs/nucleotide pairs'*

*If clearly writing rote answer about DNA replication **2 max***
*e.g. helicase or separating strands*

**3**

(c) 1. DNA double stranded/double helix **and** mRNA single-stranded;

*Contrast requires both parts of the statement*

2. DNA (very) long **and** RNA short;

*Accept 'RNA short**er**' or 'DNA bigg**er**/long**er**'*

3. Thymine/T in DNA **and** uracil/U in RNA;
4. Deoxyribose in DNA **and** ribose in RNA;

***R** Deoxyribonucleic/ ribonucleic acid*

***Ignore** ref. to histones*

***Ignore** ref. to helix and straight chain alone*

5. DNA has base pairing **and** mRNA doesn't/ DNA has hydrogen bonding and mRNA doesn't;
6. DNA has introns/non-coding sequences **and** mRNA doesn't;

***Ignore** ref to splicing*

**3 max**

**[8]**

## Q17.

(a) Quaternary (structure);

*Accept phonetic spelling eg quarternary/quarternery /4°*

*Award no mark for quaternary as part of a list*

**1**

(b) 423;

**1**

(c) 1. Oxyhaemoglobin formed/ haemoglobin is loaded/ uptakes/associates/binds with oxygen in area of higher $ppO_2$ / in gas exchange surface/lungs/gills;

*Reference to "react with" = max 1*

*Accept: reversible interaction with oxygen*

*Ignore: haemoglobin is carried / contained in red blood cells*

2. (oxygen) unloaded/dissociates from/released (in area of lower $ppO_2$ / in capillaries/to cells/tissues);

**2**

(d) (i) 56(%);

*Accept responses in the range 54-58(%)*

**1**

(ii) 1. (Anaemia curve shifted to right) haemoglobin has lower affinity for oxygen / binds less tightly;

*Assume reference is to haemoglobin of anaemia unless stated*

2. releases more oxygen / oxygen is released quicker / oxygen dissociates/ unloads more readily to muscles/tissues/cells;
3. (For) respiration;

*Accept: even with a lower haemoglobin concentration / meet demand for ATP/energy;*

**3**

**[8]**

## Q18.

(a) 1. (Reaction with ATP) breaks/allows binding of myosin to actin/ actinomyosin bridge;

2. Provides energy to move myosin head;

*1. Credit 'breaks' or 'allows' binding to actin (because cyclical)*

*2. Allow in context of 'power stroke' or 're-cocking' (because cyclical)*

*2. Ignore contraction on its own*

**2**

(b) (i) Any value between 68.5 and 69.49 (%);;

If get difference of 0.9 but calculation of percentage incorrect, then award 1 mark;

**2**

(ii) (Mutant mice)

1. Unable to make phosphocreatine/ less phosphate available to make/recycle ATP;
2. So less energy/so less ATP available for contraction/fast muscle fibres;

*1 and 2. Reject production/creation of energy once*

*2. Accept less energy for grip*

*2. Accept no energy/no ATP for contraction/fast muscle fibres*

**2**

(c) 1. (Heterozygous) have one dominant/normal allele (for creatine production);

2. (This) leads to production of enough/normal amount of creatine;

*1. Accept has one allele/one copy of the gene for/that is making creatine*

**2**

**[8]**

## Q19.

(a) (i) 1. (Tumour suppressor) gene inactivated / not able to control / slow down cell division;

*Ignore: references to growth*

2. Rate of cell division too fast / out of control.

*1 and 2 Accept: mitosis*

*1 and 2 Reject: meiosis*

**2**

(ii) 1. (Genetic) code degenerate;

*Accept: codon for triplet*

*Accept description of degenerate code, e.g. another triplet codes for the same amino acid*

2. Mutation in intron.

*Accept: mutation in non-coding DNA*

**1 max**

(b) 1. Antibody has specific tertiary structure / binding site / variable region;

*Do not accept explanations involving undefined antigen*

2. Complementary (shape / fit) to receptor protein / GF / binds to receptor protein / to GF;

*Ignore: same shape as receptor protein / GF*

3. Prevents GF binding (to receptor).

**3**

**[6]**

## Q20.

(a) 1. Sugar-phosphate (backbone) / double stranded / helix **so** provides strength / stability / protects bases / protects hydrogen bonds;

*Must be a direct link / obvious to get the mark*

*Neutral: reference to histones*

2. Long / large molecule **so** can store lots of information;

3. Helix / coiled **so** compact;

*Accept: can store in a small amount of space for 'compact'*

4. Base sequence allows information to be stored / base sequence codes for amino acids / protein;

*Accept: base sequence allows transcription*

5. Double stranded **so** replication can occur semi-conservatively / strands can act as templates / complementary base pairing / A-T and G-C so accurate replication / identical copies can be made;

6. (Weak) hydrogen bonds **for** replication / unzipping / strand separation / many hydrogen bonds **so** stable / strong;

*Accept: 'H-bonds' for 'hydrogen bonds'*

**6**

(b) 1. (Mutation) in **E** produces highest risk / 1.78;

2. (Mutation) in **D** produces next highest risk / 1.45;

3. (Mutation) in **C** produces least risk / 1.30;

*Must be stated directly and not implied*

***E*** > ***D*** > ***C*** = *3 marks*

*Accept: values of 0.78, 0.45 and 0.30 for MP1, MP2 and MP3 respectively*

*If no mark is awarded, a principle mark can be given for the idea that all mutant alleles increase the risk*

**3**

(c) **180**;

**1**

(d) **(Similarities):**

1. Same / similar pattern / both decrease, stay the same then increase;

2. Number of cells stays the same for same length of time;

   *Ignore: wrong days stated*

**(Differences):**

(Per unit volume of blood)

3. Greater / faster decrease in number of healthy cells / more healthy cells killed / healthy cells killed faster;

   *Accept: converse for cancer cells*

   *Accept: greater <u>percentage</u> decrease in number of cancer cells / greater <u>proportion</u> of cancer cells killed*

4. Greater / faster increase in number of healthy cells / more healthy cells replaced / divide / healthy cells replaced / divide faster;

   *Accept: converse for cancer cells*

   *For **differences**, statements made must be comparative*

**3 max**

(e) 1. More / too many healthy cells killed;

2. (So) will take time to replace / increase in number;

   *Neutral: will take time to 'repair'*

3. Person may die / have side effects;

**2 max**

**[15]**

## Q21.

(a) (i) (In all organisms / DNA,) the same triplet codes for the same amino acid;

*Accept codon / same three bases / nucleotides*

*Accept plurals if both triplets and amino acids*

*Reject triplet<u>s</u> code for an amino acid*

*Reject reference to producing amino acid*

**1**

(ii) 64;

**1**

(b) Splicing;

*Ignore deletion references*

*Accept RNA splicing*

**1**

(c) (i) 1. (Mutation) changes triplets / codons after that point / causes frame shift;

*Accept changes splicing site*

*Ignore changes in sequence of nucleotides / bases*

2. Changes amino acid sequence (after this) / codes for different amino acids (after this);

*Accept changes primary structure*

*Reject changes amino acid formed / one amino acid changed*

3. Affects hydrogen / ionic / sulfur bond (not peptide bond);

4. Changes tertiary structure of protein (so non-functional);

*Neutral 3-D structure*

**3 max**

(ii) 1. Intron non-coding (DNA) / only exons coding;

*Context is the **intron***

*Do not mix and match from alternatives*

*Neutral references to introns removed during splicing*

*1.and 2. Ignore ref. to code degenerate and get same / different amino acid in sequence*

2. (So) not translated / no change in mRNA produced / no effect (on protein) / no effect on amino acid sequence;

*Accept does not code for amino acids*

***OR***

3. Prevents / changes splicing;

4. (So) faulty mRNA formed;

*Accept exons not joined together / introns not removed*

5. Get different amino acid sequence;

**2 max**

**[8]**

## Q22.

(a) 1. (Protein / molecule) that moves from cytoplasm to DNA;

*Accept 'it' as TF.*

*Accept moves into nucleus*

2. (TF) binds to specific gene / genes / to specific part of / site on DNA / binds to promoter / RNA polymerase;

*Accept regulator / enhancer region*

3. Leads to / blocks (pre)mRNA production / allows / blocks binding of RNA polymerase (to DNA) / allows RNA polymerase to work;

*Ignore translation unless context wrong*

*Max 1 if refer to oestrogen as a transcription factor*

**2 max**

(b) 1. (Binding to CREB) prevents transcription / mRNA formation;

*Accept that lack of protein leaves NAD reduced*

2. (Binding of huntingtin) prevents production / translation of protein (that removes electrons / protons from NAD);

3. Fewer electrons to electron transport chain / electron transport chain slows / stops / stops / slower oxidative phosphorylation;

4. Fewer protons for proton gradient;

5. Not enough ATP produced / energy supplied to keep cells alive / anaerobic respiration not enough to keep cell alive;

*Accept neurones require ATP for active transport of ions*

*Ignore references to resting potential*

**3 max**

(c) 1. Mitochondrion has two membranes / inner and outer membranes;

*Accept cristae for inner membrane*

2. For each (different) membrane a (different) carrier required;

*Ignore reference to channel proteins*

**2**

**[7]**

## Q23.

(a) 250 000;

**1**

(b) (i) Loss of 3 bases / triplet = 2 marks;;

*'Stop codon / code formed' = 1 mark max unless related to the last amino acid*

Loss of base(s) = 1 mark;

*eg triplet for last amino acid is changed to a stop codon / code = 2 marks*

*3 bases / triplet forms an intron = 2 marks*

*Accept: descriptions for 'intron' eg non-coding DNA*

*'Loss of codon' = 2 marks*

**2**

(ii) 1. Change in tertiary structure / active site;

*Neutral: change in 3D shape / structure*

2. (So) faulty / non-functional protein / enzyme;

*Accept: reference to examples of loss of function eg fewer E-S complexes formed*

**2**

[5]

## Q24.

(a) One / an amino acid (can be) coded for by more than one triplet;

*Accept codon for triplet*

*Accept description of triplet − <u>three</u> bases / nucleotides*

1

(b) 1. Triplet / three bases on mRNA;

*1. Accept nucleotide for base*

*1. Accept DNA for mRNA*

*1. Ignore references to RNA unqualified*

2. That code for an amino acid;

*2. Accept code for stop / start*

2

(c) (i) To join <u>nucleotides</u> together to form mRNA / premRNA / RNA;

*Reject forming base pairs*

*Accept checking and correcting mismatched base pairs*

1

(ii) Reverse transcriptase;

*If they give two enzymes, no mark*

1

(d) GGATCC same as CCTAGG in opposite direction;

*Accept reads same both ways / same forward and back*

*Neutral bases are the opposite of each other / reference to base pairs*

1

[6]

## Q25.

(a) (i) Repeating units / nucleotides / monomer / molecules;

*Allow more than one, but reject two*

1

(ii) 1. C = hydrogen bonds;

2. D = <u>deoxy</u>ribose;

*Ignore sugar*

3. E = phosphate;

*Ignore phosphorus, Ignore molecule*

3

(iii)

| Name of base | Percentage |
|---|---|
| Thymine | 34 |

| | |
|---|---|
| Cytosine / Guanine | 16 |
| Adenine | 34 |
| Cytosine / Guanine | 16 |

*Spelling must be correct to gain MP1*
*First mark = names correct*
*Second mark = % correct, with adenine as 34%*

**2**

(b) (i) 153;

**1**

(ii) Some regions of the gene are non-coding / introns / start / stop code / triplet / there are two DNA strands;

*Allow addition mutation*
*Ignore unqualified reference to mutation*
*Accept reference to introns and exons if given together*
*Ignore 'junk' DNA / multiple repeats*

**1**

**[8]**

## Q26.

(a) (i) UGC;

**1**

(ii) TGCTAC;

**1**

(b) (DNA) contains introns / non-coding bases / mRNA only contains exons / coding bases;

*Assume that 'it' refers to DNA*
*Neutral: DNA contains introns and exons*
*Neutral: 'splicing'*
*Neutral: pre-mRNA contains introns*
*Ignore refs. to start and stop codons*

**1**

(c) Different primary structure / amino acid sequence / amino acid coded for;

*Reject: different amino acids produced / formed*
*Neutral: refs. to bonds*

**1**

(d) 1. Acetylcholine not broken down / stays bound to receptor;

2. $Na^+$ ions (continue to) enter / (continued) depolarisation / $Na^+$ channels (kept) open / action potentials / impulses fired (continuously);

3. (Intercostal) muscles stay contracted / cannot relax;

*'Muscles contract' is not enough*
*Accept: diaphragm stays contracted / cannot relax*

**3**

**[7]**

## Q27.

(a) (i) 9;

*Accept: nine*

**1**

(ii) Introns / non-coding DNA / junk DNA;

Start / stop code / triplet;

*Neutral: Repeats.*

*Accept: 'Introns and exons present'.*

*Reject: 'Due to exons'.*

**1 max**

(b) Change in amino acid / s / primary structure;

Change in hydrogen / ionic / disulfide bonds;

Alters tertiary structure;

*Reject: 'Different amino acid is formed' – negates first marking point.*

*Neutral: Reference to active site.*

**3**

(c) Number of bases

| | Number of bases | | | |
|---|---|---|---|---|
| | C | G | A | T |
| Strand A | 26 | **19** | **20** | **9** |
| Strand B | 19 | **26** | 9 | **20** |

Second column correct;

Columns three and four correct;

**2**

**[7]**

## Q28.

(a) (i) Phosphate and ribose;

*Accept in either order. Both correct for one mark.*

*For phosphate accept $PO_4$ / Pi / Ⓟ but not P.*

*Do not accept phosphorus.*

*Ignore references to pentose / sugar.*

**1**

(ii) TAGGCA;

1

(b) (i) Does not contain hydrogen bonds / base pairs / contains codons / does not contain anticodon / straight / not folded / no amino acid binding site / longer;

*Assume that "it" refers to mRNA.*

*Do not accept double stranded.*

1

(ii) (pre-mRNA) contains introns / mRNA contains only exons;

*Assume that "it" refers to pre-mRNA.*

*Accept non-coding as equivalent to intron.*

1

(c) (i)

| Part of chromosome | U |
|---|---|
| Middle | 18 |
| End | 21 |

*One mark for both figures correct*

1

(ii) 1. Have different (base) sequences / combinations of (bases);

2. (Pre-mRNA) transcribed from different DNA / codes for different proteins;

2

**[7]**

## Q29.

(a) 1. Hydrolysis breaks proteins / hydrolyses proteins / produces amino acids (from proteins);

2. Protein synthesis involves condensation;

2

(b) Amino acids (from calliphorin) can be joined in different sequences / rearranged;

1

(c) 1. Fall, rise and fall;

2. Rise after 40 and fall after 80;

*Ignore concentration values.*

2

(d) (i) Fall / increase then fall;

Lysosomes associated with tissue breakdown;

2

(ii) 1. Tissues / cells are being broken down;

2. RNA is digested / hydrolysed / broken down;

3. By enzymes from lysosomes;

4. New proteins not made / no new RNA made;

**2 max**

(e) 1. (RNA) associated with making protein;

2. New / adult tissues are forming;

**2**

(f) 1. In the first 6 days no / little oxygen supplied / with breakdown of tracheae, no / little oxygen supplied;

2. (Without tracheae) respire anaerobically;

3. Anaerobic respiration involves reactions catalysed by enzyme **B** / conversion of pyruvate to lactate / involves lactate production;

4. Enzyme **A** / Krebs cycle is part of aerobic respiration;

*Or, with emphasis on aerobic respiration:*

*1. Tracheae supply oxygen / after 6 days oxygen supplied;*

*2. (With tracheae) tissues can respire aerobically.*

**4**

**[15]**

## Q30.

(a) Banding pattern changes as cheetah gets older / difficult to judge as tail is short / fluffy;

**1**

(b) (i) Mean not (always) a whole number;
Standard deviation not (always) zero;

**2**

(ii) Movement of tail / angle of sight / confused it with another band / subjective estimation;

*Accept reference to **Figure 1***

*E.g. Bands 2 and 3 have same thickness but look different*

**1**

(c) Band width not the same on both sides of tail;

**1**

(d) Offspring of the same family will be more similar genetically;
As have same mother (and father) / parent;
Expect to see more differences in randomly chosen cheetahs;

**3**

**[8]**

## Q31.

(a) Introns;

**1**

(b) Ile Gly Val Ser;

**1**

(c) (i) Has no effect / same amino acid (sequence) / same primary structure;

***Q*** *Reject same amino acid formed or produced.*

1

Glycine named as same amino acid;

1

*It still codes for glycine = two marks.*

(ii) Leu replaces Val / change in amino acid (sequence) / primary structure;

Change in hydrogen / ionic bonds which alters tertiary structure / active site;

***Q*** *Different amino acid formed or produced negates first marking point.*

Substrate cannot bind / no longer complementary / no enzyme-substrate complexes form;

*Active site changed must be clear for third marking point but does not need reference to shape.*

3

(d) (i) Interphase / S / synthesis (phase);

1

(ii) DNA / gene replication / synthesis occurs / longest stage;

*Allow 'genetic information' = DNA.*

*Allow 'copied' or 'formed' = replication / synthesis*

1

**[9]**

## Q32.

(a)

| | | |
|---|---|---|
| DNA | ✓ | 2 |
| mRNA | ✗ | 1 |
| tRNA | ✓ | 1 |

*One mark for each correct column*
*Regard blank as incorrect in the context of this question*
*Accept numbers written out: two, one, one*

2

(b) (i) Marking principles
1 mark for complete piece transcribed;

*Correct answer*
*UGU CAU GAA UGC UAG*

1 mark for complementary bases from sequence transcribed;

*but allow 1 mark for complementary bases from section transcribed, providing all four bases are involved*

2

(ii) Marking principle

1 mark for bases corresponding to exons taken from (b)(i)

*Correct answer*
*UGU UGC UAG*
*If sequence is incorrect in (b)(i), award mark if section is from exons. Ignore gaps.*

**1**

**[5]**

## Q33.

(a) RNA polymerase;

*DNA polymerase is incorrect*
*Ignore references to RNA dependent or DNA dependent*
*Allow phonetic spelling*

**1**

(b) (i) (Receptor / transcription factor) binds to promoter which stimulates RNA polymerase / enzyme X;

Transcribes gene / increase transcription;

**2**

(ii) Other cells do not have the / oestrogen / ERα receptors;

*But do not accept receptors in general.*

**1**

(c) Similar shape to oestrogen;

Binds receptor / prevents oestrogen binding;

Receptor not activated / will not attach to promoter / no transcription;

*Accept alternative*
*Complementary to oestrogen;*
*Binds to oestrogen;*
*Will not fit receptor;*

**2 max**

**[6]**

## Q34.

(a) Will replace themselves / keep dividing / replicate;

Undifferentiated / can differentiate / develop into other cells / totipotent / multipotent / pluripotent;

*Accept tissues*

**2**

(b) Reverse transcriptase;

*Allow phonetic spelling*

**1**

(c) (i) Alters base / nucleotide sequence / causes frame shift;

Different sequence of amino acids in polypeptide / protein / primary structure alters the tertiary structure;

*Accept any reference, such as adding bases, to changing*

*the base sequence of the gene. Reject deletion / substitution.*
*Idea of sequence essential so not makes different amino acids.*
*Accept answers involving stop / start codons and effect on protein.*

**2**

(ii) Affects tumour suppressor gene;

Inactivates (tumour suppressor) gene;

Rate of cell division increased / tumour cells continue to divide;
*Ignore answers relating to oncogenes. May gain third point.*

**2 max**

(d) Yes
SCID patients unlikely to survive / quality of life poor unless treated;
Cancer that develops is treatable / only affects 25% / five children;

No
Risk of developing cancer is high / 25%;
Cancer may recur / may not be treated successfully in future / only short time scale so more may develop cancer;
*No mark for yes or no. Marks are for supporting argument based on biological reasoning.*
*Accept any points*

**2 max**

**[9]**

## Q35.

(a) (i) Deoxyribose;
*pentose / 5C sugar = neutral*

**1**

(ii) Phosphate / Phosphoric acid;
*phosphorus / P = neutral*

**1**

(b) Hydrogen (bonds);

**1**

(c) 381 / 384 / 387;

**1**

(d) (Gln) Met Met Arg Arg Arg Asn;

**1**

(e) Change in (sequence of) amino acids / primary structure;

Change in hydrogen / ionic / disulfide bonds leads to change in tertiary structure / active site (of enzyme);

Substrate cannot bind / no enzyme-substrate complexes form;
***Q** Reject = different amino acids are formed*

**3**

**[8]**

## Q36.

(a) Phosphate;

Deoxyribose;

***Q*** *Candidates must specify deoxyribose. This term is a specification requirement.*
*Ignore anything that is not incorrect.*

**2**

(b) 4;

**1**

(c) (i) 14;

**1**

(ii) 36;

*If (c)(i) incorrect accept [50 – (c)(i)]*

**1**

(d) Different genes;

Different (DNA) base sequences;

**2**

**[7]**

## Q37.

(a) GCAAUG; ;

*Allow one mark if T instead of U, i.e. GCAATG*

**2**

(b) (i) DNA is edited / introns present in DNA;

*Allow reference to 'junk' or non-coding DNA*

**1**

(ii) 220; allow 218 or 219-allow 2
Three bases / nucleotides code for one amino acid;
Correct explanation for 218 or 219;

**2**

(c) mRNA has no base-pairing, tRNA has base-pairing / mRNA linear, tRNA cloverleaf shape; mRNA has no binding site for amino acids, tRNA has; mRNA different for each gene / many kinds, only few / 20 / 64 kinds of tRNA; accept mRNA longer / larger / more nucleotides than tRNA

**max 2**

**[7]**

## Q38.

(a) (i) ACG;

**1**

(ii) serine;

**1**

(b) idea that DNA contains introns / mRNA is only exons / mRNA is "edited';
*(allow junk / non-sense DNA)*

**1**

(c) binds to / blocks codon / triplet on mRNA so anticodon / tRNA will not fit in / base-pair;
amino acids not delivered / joined;

*Accept translation will not occur for 1 mark*

**2**

**[5]**

## Q39.

(a) antibiotic has diffused / spread / moved into agar;
killed / inhibited bacteria;

**2**

(b) largest clear area / inhibition zone / killed the most bacteria;

**1**

(c) disrupts cell wall / prevents cell wall synthesis;
stops DNA replication;

**2**

**[5]**

## Q40.

(a) Protein made of (chain of) amino acids;
Each amino acid has its own base / triplet code;

**2**

(b) UCA = 2 marks
TCA – 1 mark;

**2**

(c) CCG;
GGG GGG;

**2**

(d) (i) Changes base sequence;
Of later triplets / amino acid codes;

**2**

(ii) S-phase / interphase;

**1**

(e) 1. mRNA leaves (nucleus) through nuclear pore;
2. To ribosome;
3. tRNA molecules bring amino acids (to ribosome);
4. Specific tRNA molecule for specific amino acid;
5. Anticodon of tRNA corresponds / complementary to codon on mRNA;
6. Peptide bonds form between amino acids;
7. tRNA detaches and collects another amino acid;
8. Ribosome moves along mRNA;

**max 6**

**[15]**

## Q41.

(a) (i) C → B → E → F → A → D

*Mark links: 5 correct = 2, 4 correct = 1, <4 correct = 0*

**2**

(iii) nucleus;

**1**

(iii) A, D, F; *(ignore E if evident)*

**1**

(b) (i) Isoleucine;

**1**

(ii) TGG;

**1**

**[6]**

## Q42.

(a) (i) join / attach nucleotides, to form a strand / along backbone / phosphodiester bonds;

*(reject reference to H bonds, complementary base pairing)*

**1**

(ii) ribosome / RER;

**1**

(b) (i) CGTTACCAA;

**1**

(ii) CGU UAC CAA;

**1**

(c) substitution;

**1**

(d) (i) alanine;

**1**

(ii) (mutation 1)
no change(to sequence of amino acids);
codon for alanine / degenerate codon / same amino acid coded for;

**2**

(mutation 2)
(change in sequence) valine replaced by alanine / codon for alanine;
folding / shape / tertiary structure / position of bonds may change;

*(reject peptide bonds)*

**2**

**[10]**

## Q43.

(a) side effects / allergic reactions / low toxicity to cells;
interaction with other drugs / effective in conditions of use / reasonably stable;
should only act on the problem bacteria / narrow spectrum;
how much resistance the bacteria have built up;

**2 max**

(b) (i) tetracycline
prevents tRNA binding to ribosomes / amino acid / mRNA;

**1**

amino acids not available / brought / picked up;

**1**

chloramphenicol
prevents amino acids being joined / prevents primary structure forming;

**1**

no enzymes / no structural proteins formed;

*(accept cell wall formation if qualified) (prevents protein synthesis gains one mark in either section, once only)*

**1**

(ii) only prevents tRNA binding to 70S / prokaryotic / bacterial ribosomes / human ribosomes are different sizes / shapes / structure;

**1**

**[7]**

## Q44.

(a) AGC; TTC;

**2**

(b) anticodon complementary to codon / reads message on mRNA;
specific amino acid;
carried / transferred (to ribosome);
correct sequence of amino acids along polypeptide;

**3 max**

(c)

| | | | | | | |
|---|---|---|---|---|---|---|
| (Met) | Phe | Gln | Gln | Lys | Gln | Phe |

**2**

*(three / four / five correct 1 mark; six correct 2 marks)*

**[7]**

## Q45.

(a) high energy radiation / ionising particles;
named particles / α, β, γ;
colchicine;
x rays / cosmic rays;
uv (light);
carcinogen / named carcinogen;
mustard gas / phenols / tar (qualified);

**1 max**

(b) (i) removal of one or more bases / nucleotide;
frameshift / (from point of mutation) base sequence change;

**2**

(ii) sequence of bases in mRNA would change;
(sequence of) amino acids different / different primary structure;

(active site / enzyme 1) changed tertiary shape / changed active sites;
white pigment does not bind;
lilac pigment not produced / white pigment remains unchanged / enzyme 1 does not function;

**4 max**

(iii) blue and lilac; white;

| *colour of petal* |
|---|
| *(white)* |
| blue |
| lilac; |
| white; |

**2**

**[9]**

## Q46.

(a) chloroplast, so cell photosynthesises and moves to optimum / best light intensity for photosynthesis;
avoids damage due to bright light;

**2**

(b) (i) 2700

**1**

(ii) $\frac{242 \times 7500 \times 900}{60}$ = 27 225 000 / 27 × $10^6$ = *2 marks*

*(allow 1 mark for principle:* $\frac{amino\ acids \times proteins}{time}$ *)*

**2**

(c) (i) rate slightly slower / not affected in first 20 / 30 minutes / lower peak than control;
then decreases / much lower (than control);
*(allow 1 mark for increase in first 20 / 30 minutes, then decreased, if not compared with control / normal)*
*(disqualify flagellum grows longer)*

**2**

(ii) 1. actinomycin has no effect (on growth of flagella);
even though mRNA production / transcription prevented;
*(accept references to 'expt 1')*
2. (re)growth little affected by puromycin at first;
protein synthesis inhibited, so likely to be using proteins present;

**4**

**[11]**

## Q47.

(a) 387;

**1**

(b) (i) CCAG;

**1**

(ii) 5;

**1**

(c) high energy radiation / X rays / ultraviolet light / gamma rays;
high energy particles / alpha particles / beta particles;
named chemical mutagens e.g. benzene / caffeine / pesticide / mustard gas / tobacco tar / free radicals;
*(two named examples of any of the above = 2 marks)*
length of time of exposure (to a mutagen);
dosage (of mutagen);

**2 max**

(d) (i) UAC UUA UGG;

**1**

(ii) addition and deletion (of bases / nucleotides);
thymine added;
adenine deleted;
*(addition of thymine and deletion of adenine = 3 marks)*
*(allow addition of adenine (RNA) and deletion of uracil (RNA) = 2 marks)*

**3**

**[9]**

## Q48.

(a) (i) number of bases = 4440

*allow 4446 if they refer to start / stop*

each amino acid coded for by triplet / three bases
(so three times more bases than amino acids);

**2**

(ii) deletion;
(deletion) of three bases;
because substitution / addition would change amino acid(s);

**2 max**

(b) codon on mRNA;
specific / complementary base pairing with;
anti-codon on tRNA;
specific tRNA for each amino acid;
protein formed by condensation reactions /
peptide bonds formed;

**4 max**

**[8]**

## Q49.

(a) memory B / T cells do not recognise (new antigens);
antibodies previously produced are not effective

as shape not complementary to new antigen;

**2**

(b) (i) antigen in membrane presented to lymphocytes / produce cytokinins;

**1**

(ii) mitochondria provide (more) ATP / energy;
(more) RER / ribosomes synthesise proteins;
(more) Golgi body secretes / modifies or packages proteins / produces glycoproteins;
(B lymphocytes) produces antibodies;

**4**

**[7]**

## Q50.

change in base / nucleotide (in DNA);
change in base sequence of mRNA / change in codons / idea of frameshift following deletion or addition / incorrect tRNA / anticodon;
incorrect amino acids / different primary structure / fomation of new stop codon;
different tertiary structure / different 3D structure / different polypeptide / shortened polypeptide;
different shape of active site / no active site present;

**[5]**

## Q51.

(a) mutation changes the amino acid sequence / primary structure of Factor VIII protein;
changes the tertiary structure / 3D shape;

**2**

(b) (mutant) Factor VIII protein is non-functional / does not work with Factor IX;
so no conversion of Factor X to active form and pathway blocked;

**2**

(c) boy's blood contains (active) Factor VIII;
Factor VIII haemophiliac's blood contains (active) Factor IX;
the mixture has both Factors and so the pathway can complete / blood clots;

**2 max**

**[6]**

## Q52.

(i) mRNA attaches to ribosome;
codon on mRNA;
binds to an anti-codon on tRNA;
each tRNA brings a specific amino acid;
sequence of codons / bases on mRNA determines order of amino acids;
formation of peptide bonds / amino acids joined by condensation reactions;

**4 max**

(iii) inserted gene / mRNA complementary to normal gene / mRNA;
binds to it to prevent protein synthesis / form double strand / prevents mRNA binding to ribosomes;

will not stop all translation, some mRNA reaches ribosomes /
because not all mRNA is bound by inserted gene mRNA;

**2 max**

**[6]**

## Q53.

(a) (Gene 1) allele A makes enzyme converting J to K / colourless to red;
Allele a produces no / non-functional enzyme;
(Gene 2) allele B makes enzyme converting K to L / red to purple;
Allele b produces no / non-functional enzyme;
("Recessive alleles produce no / non-functional enzyme" = 2)
White flowers result from genotype aa;
... regardless if B or b / even if aaB_ ;
Colourless (substance) / J produces white;
Red flowers when A_ bb / enzyme 1 only;
Purple flowers when A_ B_ / enzymes 1 and 2;

**6 max**

(b) (i) (1) (red parent) AAbb;

(2) (white parent) aaBB;

**2**

(ii) $F_1$ are AaBb;
$F_2$ ratio of 9 : 3 : 4;
Purple : red : white;
Suitable working shown;

**4**

(c) (i) aabb, aaBb, and aaBB; (allow aabb & aaB_)

**1**

(ii) (Crush each type of white petal to make an extract, and) add some of the (red) pigment / K, to petal OR incubate with K;
(extract becoming) purple is identified as aaBB OR that staying red, after K is added, is aabb;

**2**

**[15]**

## Q1.

Only 17.9% of students scored the mark on (a). Although this term is clearly defined in the first sentence of section 3.4.2 of the specification, few students seem to have learnt it. Wrong answers were often pure guesses, such as ‘where proteins are stored’ or ‘where tRNA is made’. 13% of students did not even attempt the question.

(b) was generally well answered; those who failed to score two, once again, did not state a clear difference, e.g. that “tRNA is clover leaf, but mRNA is linear”. There were also students who thought tRNA was a double-stranded molecule.

(c) tested recall, with a specific instruction not to include descriptions of transcription and splicing in answers. Many did include this, or *only* discussed this. Only 8.4% of students scored all five marks. Many described mRNA leaving the *cell* to associate with a ribosome, and there were many who also stated that RNA polymerase joins amino acids or forms peptide bonds. Start codon and first codon were ‘synonyms’ for many students. Overall this question discriminated well.

## Q2.

This question was loosely based on the skills students would have developed when completing required practical activity 2 – “Preparation of stained squashes of cells from plant root tips; set-up and use of an optical microscope to identify the stages of mitosis in these stained squashes and calculation of a mitotic index”. Students should have observed cells undergoing mitosis surrounded by many cells that were not and, therefore, should have considered why they looked different.

Many incomplete answers were seen to question (a). Students were required to give evidence **and** to explain that piece of evidence, but often only gave half the story. Some students used **Figure 2** rather than **Figure 1** and some tried to explain which stage of mitosis was shown, rather than simply that it was happening. Confusion was demonstrated here and in question (e) between a homologous pair of chromosomes and a pair of chromatids in a single chromosome. Worryingly, 62% of students failed to score on this opening question; only 5.8% gained both marks.

In part (b), 69.3% of students correctly identified that these cells were in prophase.VWithin required practical activity 2, students needed to spread the cells out to gain a clear view; question (c) was based on a similar principle, but using a different method. It required standard knowledge of osmosis, but the novel context threw many students. The majority could state that the water would move into the cells by osmosis, but then often referenced increased pressure, rather than the idea of the volume of the cells increasing. Some complex, incorrect answers were seen in which students attempted to describe changes in polar interactions between the chromosomes and water, and how these would change.

Question (d) tested Assessment Objective 2 (application of knowledge) and there were several parts of the specification from which students could select material to support their answer. 42.2% did this successfully; those who did not often did not describe sufficiently how a feature would be different along the length of the chromosome to result in the striped appearance. For example, mentioning “histones” or “bases” alone was not creditworthy.

In question (e), only 36.9% of students could define the term ‘homologous chromosome’. It is likely that more students could have written about independent segregation or crossing over of homologous chromosomes, but this question revealed that they did not

fully understand this biological term. Many students only referred to the origin of the chromosomes as paternal and maternal.VFor question 01.6, most students (83.2%) scored at least one mark, but there were many good answers limited to one out of two by demonstration of fundamental misunderstanding. The most common of these was that only eukaryotic DNA is a double helix and that prokaryotic DNA is single-stranded.

## Q3.

64.5% of students could answer question (a), a test of recall from section 3.1.4.1 of the specification.

For question (b), 67.5% of students achieved both marks. Those who could not define 'degenerate' in the context of the genetic code often failed to gain credit through not using appropriate terminology, for example referring to 'bases' rather than 'base triplets/codons' or stating that base triplets 'produce' amino acids rather than 'code for' amino acids.

Question (c) was an interesting question as it could be interpreted as a straightforward 465 amino acids multiplied by three to give the 1395 bases of the gene. Students could also add three or six bases to this, for a start and/or stop codon. Some students appreciated that a gene would be made up of double-stranded DNA so would comprise double this number of bases – this was also awarded credit. 67% of students could complete this calculation.

Question (d) showed that multiple-choice questions are not always simplistic or based on recall. This question required students to interpret **Table 1**, convert the mRNA codon to a DNA base triplet, and also notice in the question that this was a single base substitution. Only 9.6% successfully achieved all of this. The majority of students ticked box 2 that did show a Val to Ala change, but with a mutation in the mRNA (not DNA) and of 2 bases.

The answers to question (e) revealed much misunderstanding of the principles of the link between DNA, polypeptides and proteins, as many students discussed the changes in amino acid in terms of silent mutations or frameshift mutations. The instruction to use all the information required the students to look back at **Table 1** and use the key showing the properties of the R group of the amino acid. Very few students could apply this information and link the reduction in rate of reaction with the R group of amino acid 279 changing from being negatively-charged to being positively-charged. Imprecise biological language was also often seen, for example omitting to reference the 'shape' of the active site and discussing the 3-D structure of the protein rather than its tertiary structure. Just over half of the students (54.2%) managed to score at least one mark here; only 3.2% gained maximum credit.

## Q4.

On reflection, in question (a), it would have been better not to try and 'help' students by splitting the answer space into μg and $g^{-1}$ and just let them answer as they saw fit. In any event, the question discriminated well. Some 22% obtained both marks, 44% one mark and 31% failed to score. All three marking points appeared with roughly equal frequency. Quite a few students seemed to miss the point entirely, writing about μg being used because ammonia is a small molecule.

Question (b) proved much more difficult than expected. Many students appeared to have difficulty extracting data from the graph, often apparently mis-reading the scale. 20% of students obtained both marks. Another 13% obtained one mark because they calculated the correct number but made a mistake with the units. The commonest error was to use a solidus to represent 'per'; so, /day instead of $day^{-1}$. For many years, AQA has followed the convention of using a solidus to separate units from the name of whatever is being presented. In this case, that would mean, "Difference in rate / μg $g^{-1}$ $day^{-1}$". The question

did discriminate reasonably well.

Question (c) proved too challenging for most students. They were asked to identify evidence that supported the idea of different communities of bacteria in soils A and B. This would suggest that the bacteria (bacterial populations) in each soil would be those adapted to a certain soil pH. Many misinterpreted the graph at the start and thought that ammonia was being made; thus thinking A+B gave the fastest rate. Others focused almost entirely on how much ammonia was left at the end of 20 days and/or described the lines on the graph. Some 29% did note that the mixture of A and B had the slowest rate of breakdown of ammonia and obtained one mark. Another 15% obtained a further mark by deducing that it must be bacteria from soil B that weren't working well at pH 6.9; or that only bacteria from soil A were working. Only 3% obtained all three marks by linking their deductions to bacteria from soil B having the fastest rate of ammonia breakdown in their own soil condition (pH 4.3).

Question (d) discriminated quite well and showed which students were able to use data presented in logarithmic form. The examiners allowed calculations of changes in numbers of copies of mRNA, or calculation of percentage changes. 42% of students obtained both marks. Some 7% of students obtained one mark for calculating one correct change. Some who failed to score used the 'power' numbers as simple numbers; so, for species S they said the fall was 2 and it was the same for species T. One mark was awarded if they gave an answer of 100 times with no further explanation.

Question (e) was the worst answered on the paper and 11% did not attempt it. This might indicate that more guidance should have been included in the stem of the question, or it should have been worth only three marks. All four marking points were seen but students often focused on one or two at great length. Since the command word was 'explain', there were only four marking points, for four marks. Few students noted that the population growth could not be determined using the method outlined because at no point were the bacteria counted. The method simply gives an indication of the amount of amoA enzyme produced. About 28% obtained one mark, usually for noting that the number of mRNA molecules produced might well vary from cell to cell. Some 8% obtained two marks, often for the previous point and suggesting that it is not known if there is a link between expression of *amoA* and population/cell growth/division.

Question (f) tested knowledge of aseptic technique and its use in the context used in the question. The examiners expected students to suggest methods for sterilising whole bottles before use. Many students wrote about flaming the necks of the bottles, ignoring the inside (and outside). Others made vague references to 'heating the bottles', with no detail about how or to what sort of temperature. The mark scheme gave acceptable examples such as autoclaving, using boiling water and washing in alcohol. 36% of students obtained one mark, usually for suggesting a suitable method for sterilisation. The explanations of the reason for sterilising were usually very weak and did not link directly to this investigation. So, most explanations were restricted to statements about getting rid of contaminants or bacteria. The examiners were looking for ideas relating to the removal of bacteria that might compete with or kill the bacteria being studied, or removal of other bacteria that might produce amoA. Only 4% of students made these sorts of statements.

## Q5.

Students clearly have difficulty in describing data with almost a quarter gaining no marks at all for question (a), and many of these confusing data for low-starch and high-starch diets. However, most could state that a low-starch diet was linked to fewer copies of the gene and many correctly identified the modal values. There were few references to the overlapping ranges and the higher range in populations with a high-starch diet. Students would benefit from learning to use terms such as mode and range in their answers to similar questions.

In answers to question (b), students seemed less confident in their knowledge of protein synthesis than in their knowledge of enzyme action. Consequently, very few students could explain that, with more copies of the gene, there would be more transcription or more mRNA formed. However, most realised that there would be more enzyme present and then went on to explain the advantage in terms of faster starch digestion.

Often students failed to use the information given to them in question (c) and wrote generic answers about natural selection which failed to gain any marks. Examiners were looking to award marks for points made in the context of multiple copies of the *AMY1* gene. Those students who did this often gave excellent answers referring to mutation resulting in extra copies; they then went on to explain that this mutation resulted in a higher chance of survival and reproduction in populations with a high-starch diet, with the beneficial mutation being passed on to their offspring.

## Q6.

There was a wide range in the quality of the responses to question (a), with 16% gaining 4 or 5 marks and approximately the same percentage gaining zero marks. Many students did not seem to understand what is meant by the cohesion-tension hypothesis and complicated their answer with unnecessary and lengthy accounts of the movement of water across a root, root pressure and even translocation. Those who understood the scope of the question were frequently able to access the mark scheme, with most writing about hydrogen bonding between water molecules resulting in cohesion and water being pulled up the xylem as a continuous column. Many wrote about transpiration from the leaves though few explained how this would result in a lower water potential in the leaf cells. Only a small number of students referred to adhesion of water molecules to the walls of the xylem vessels.

Question (b) discriminated well, with approximately 20% of students gaining 4 or 5 marks and 28% gaining no marks (although quite a few of these may well have been as a result of students running out of time). Some excellent answers were seen in which students wrote logically and clearly using accurate scientific terminology, though even these students rarely gave the full information for complementary base pairing. A high percentage of students gained the 2 marks available for describing how the pre-mRNA formed is cut and spliced to form mature mRNA. The role of RNA polymerase was often incorrectly stated and students frequently stated that plant DNA does not contain introns.

## Q7.

It was hoped that this would provide a reasonably straightforward start to the paper, assessing AO1 on topics 3.1.5.1 and 3.4.2.

(a) Only 22% of students could correctly name the types of molecule that make up a ribosome.

(b) This question was answered much more successfully than (a), with 48% of students gaining all three marks.

(c) This question proved to be very accessible, with 96.3% of students gaining the mark.

(d) Although 83% of students scored 2 marks for this question, there were some incorrect answers, e.g., indicating that the introns removed from the pre-mRNA were made of DNA.

## Q16.

The factual recall question, (a), proved far more challenging than intended. Only 5% of students obtained both marks and 54% failed to score. There was no particular pattern to the wrong answers.

Question (b) discriminated very well, with 15% obtaining three marks and 21% scoring zero. There were good, concise answers that scored three marks for including complementary base pairing and the role of DNA polymerase in joining nucleotides together to form the new DNA strand; often in two or three lines.

Many students failed to read the question carefully and did not answer the question as set. They wrote at length about DNA replication, starting with DNA helicase. These answers were awarded a maximum of two marks, because the question specifically asked how the complementary strand of HIV DNA is made. Many students appeared to believe that DNA actively pulls free nucleotides into place and makes them base pair; some even wrote about condensation reactions. There were students who confused transcription with replication and gave accounts of mRNA production.

Some students appeared to focus on 'HIV' and 'replication' and gave an extended account of how HIV infects cells, uses reverse transcriptase to make DNA, incorporates its DNA into host DNA, takes over the cell, is replicated by the host cell, infects new cells and leads to AIDS. They often went onto an additional page, or wrote their answer under (c) on the next page, in breach of instructions given on the front of the exam paper. Many of these students may have found themselves short of time for later questions.

In (c), it was pleasing to find that many students did obey the command word to 'contrast' and gave full statements about the differences between DNA and RNA. Many students knew enough about the structures of DNA and mRNA to give correct contrasting features and 47% obtained all three marks.

## Q17.

(a) Most correctly identified 'quaternary' as the appropriate term to describe the protein's structure with 'tertiary' being a common misconception.

(b) The triplet nature of the DNA nucleotide code for amino acids is well understood. Very few failed to achieve the mark, although some students divided by three instead of multiplying by three.

(b) Detailed accounts of haemoglobin's allosteric properties, its structure, the Bohr shift or the number of oxygen molecules loaded per molecule were common, demonstrating where students had not read carefully enough the detail required in this question. Where students achieved only a single mark, they had usually not referred precisely to the location where haemoglobin associates with oxygen.

(d) (i) A vast majority of students successfully used the graph to find the correct difference in percentage saturation of haemoglobin with oxygen. A few failed to gain the mark despite having identified the correct values on the graph because they calculated a percentage change, rather than the difference.

(ii) This question discriminated well. Students who understand the transport of oxygen topic gave good responses that made clear a link to the context of anaemia with a sense that the shortage of haemoglobin molecules would, to some extent, be compensated for by the reduced oxygen affinity. Some did not make a direct reference to 'reduced affinity' although they demonstrated a good understanding of the principle. Occasionally students went off at a tangent by referring to the effects of altitude differences and some erroneously described the curve's shift to the right as representing an 'increase' in affinity.

## Q18.

(a) This question discriminated more than expected, with 34% obtaining two marks and 50% one mark. Most students wrote about ATP being used to make/break the binding with actin. A few failed to make any reference to actin and failed to score. Those who obtained the second mark went on to refer to ATP providing the energy to move the myosin head.

(b) (i) 63% of the students could calculate the correct percentage fall.

(ii) 63% of students obtained both marks and 30% obtained zero. Those who failed to score often wrote an account of what phosphocreatine is used for. 'These results' they were asked to explain included the mice being unable to produce creatine.

(c) 74% obtained one mark for the observation that the heterozygous mice have one dominant allele (of the gene for creatine production). Only 11% went on to say that this one allele allowed the mice to produce enough, or the normal amount of, creatine. Some said that the dominant allele masks the recessive allele, which is true but doesn't explain why the heterozygous mice can produce a similar force to normal mice.

## Q19.

(a) (i) The examiners wanted a statement that a mutation could make the gene inactive and that this would lead to uncontrolled, or very rapid, cell division. About half of students obtained both marks. Some students did not mention cell division but just stated that a tumour would grow; apparently taking 'growth' to mean cell division. The examiners did not accept these terms as equivalent. Some students got into long explanations of how a mutation could lead to a faulty protein and eventually got the first mark point for an inactive gene. Some of these failed to score because they wrote about mutations leading to the production of faulty amino acids.

(ii) A large majority of students managed to convey the idea of the genetic code being degenerate.

(b) Very few students obtained all three marks in this part. This was because they didn't address the reference to 'this antibody' in the stem. The examiners were looking for an observation that 'this antibody' will have a specific tertiary structure, or binding site, or variable region. Some of those who did consider this aspect, failed to score because they referred to a specific 'active site'. Many students obtained two marks for suggesting that the antibody binds either to the receptor (protein), or growth factor, and this prevents growth factor binding to its receptor.

## Q20.

Parts (a), (b) and (d) proved to be good discriminators.

(a) It was disappointing that only just below 40% of students scored at least half marks. This was mainly due to simply describing the structure of DNA, without explaining how these features relate to its functions. Some students wrote about DNA structure and function in different paragraphs. This made it unclear which feature went with which function, as no direct links had been made. In contrast, there were some truly excellent responses, which had clearly been well planned before putting pen to paper. The most common mark points awarded were for the sugar-phosphate backbone providing strength or protecting bases, the helix allowing the molecule to be compact, weak hydrogen bonds allowing strand separation or replication and the

two strands acting as templates or allowing semi-conservative replication. Relatively few students linked complementary base pairing with accurate replication or the production of identical copies of DNA. Similarly, few students referred to DNA as a large molecule that can store lots of information, or the base sequence coding for amino acids. Weaker responses often mentioned this in the context of the genetic code being degenerate. Indeed, some students thought that the base sequence causes amino acids to be *produced*. The ability to convey that *many* hydrogen bonds provide stability was rarely seen. It was also unfortunate that a number of students wasted their time by writing about irrelevant topics such as the differences between prokaryotic and eukaryotic DNA and the role of histones. There were also some lengthy accounts of DNA replication, enzyme structure and the different levels of protein structure.

(b) Many students scored at least two marks for stating that a mutation in gene **E** produces the highest risk and a mutation in gene **C** produces the lowest risk. However, only the best responses also referred to gene **D**. Students who did not mention any of the genes usually picked up one mark for noting that all of the mutant alleles increase the risk of lung cancer. Surprisingly, some thought that a mutation in gene **D** produces the highest risk.

(c) Just fewer than 40% of students gave the correct answer of **180**.

(d) Two-thirds of students scored at least two marks. Many were able to identify the decrease, plateau and increase for healthy cells and cancer cells. However, relatively few made reference to the plateau occurring for the same length of time. Students who failed to gain a mark for a similarity usually ignored the plateau. Most students spotted that a greater number of healthy cells were killed or that they experienced a faster decrease in number. Similarly, it was impressive to see that some used data from the graph to calculate that a greater *proportion* of cancer cells were killed. Many students also noted the faster increase in the number of healthy cells.

(e) Half of students scored full marks. This was usually for mentioning that too many healthy cells would be killed, which could kill the patient or cause side effects. However, relatively few appreciated that it would take time to replace the healthy cells that had been killed.

## Q21.

(a) (i) This part asked students why the genetic code is described as universal. Universal in this context means found in all organisms. A large percentage of students wrote that it is universal because it is found everywhere. Only a quarter of students made correct references to the triplet code used in DNA. Some had the correct idea but wrote things such as, ‘The same triplet codes for all amino acids’ and failed to score.

(ii) 50% of students gave the correct answer.

(b) This part discriminated well, but with over 40% getting all three marks. Most stated or described the idea of a frame shift. However, some wrote that this changed the sequence of bases afterwards, rather than the sequence of codons. Another fairly common misconception was that mRNA leads to the synthesis, or formation, of amino acids.

(c) This part proved more challenging and only about a third obtained both marks. Most correct answers revolved around the idea of introns being non-coding and thus not affecting an amino acid sequence. Students who failed to score often ignored the

fact that the mutation was in an intron and wrote about possible effects of a substitution on amino acid sequences. In the figure, it clearly states that the intron is removed from pre-mRNA.

## Q22.

(a) In this part, many students expressed themselves unsatisfactorily and there were a number of misconceptions; almost half failed to score. Some simply said that a transcription factor affects transcription. Others attempted to use oestrogen as an example of a transcription factor, rather than a hormone that binds to a receptor to form a transcription factor. Yet others failed to state that a transcription factor binds to a *specific* site (or sites) on DNA (however expressed). Only about 20% of students obtained both marks.

(b) There were some very good, clear and concise answers to this part that obtained all three marks. All the points on the mark scheme were seen but perhaps the commonest observations were that binding of huntingtin to CREB stops production of the protein (that removes protons and electrons from reduced NAD). This stops / slows the electron transfer chain. This leads to not enough ATP being produced and the nerve cells die. A lot of students did not read the stem carefully and thought that CREB removes electrons and protons. Others made general references to respiration slowing but did not mention the electron transfer chain, or proton gradients, or ATP production.

(c) It was pleasing in this part to find many students connecting the requirement for two carriers for CREB to the two membranes of a mitochondrion; just over 50% obtained both marks. Some students had problems expressing themselves and others seemed genuinely confused about the membranes of the mitochondrion; for example, some wrote about a membrane round the cytoplasm and then the cristae.

## Q23.

(a) Nearly all students gave the correct answer of **250,000**.

(b) (i) One-third of students gained at least one mark. This question required students to apply the principle that three bases code for one amino acid to an unfamiliar context. However, other creditworthy approaches were used to explain why the faulty protein has one amino acid missing. This said, many students simply defined the term ‘mutation’ or repeated information given in the question stem. Consequently, there were many references to a *change* in the base sequence or amino acid sequence. Only the best responses mentioned a loss of bases. Students who took a different approach fell into one of two camps. Some suggested that a stop codon had formed for one mark. However, it was rare to see this related to the final amino acid of the protein. Similarly,others were clearly aware of introns but rarely mentioned that three bases may form an intron. Unfortunately, a minority of students provided a good response to (c) (ii) for this question part.

(ii) One-third of students gained full marks. Many were aware that the protein produced could be faulty or non-functional. However, the ability to explain this in terms of a change in tertiary structure or active site discriminated well. Unfortunately, some students went no further than to state that the protein would have a different primary structure. This was given in the question stem and therefore not credited.

## Q24.

This question was intended to provide an accessible start to the paper, since it was almost entirely factual recall. In the event, it proved challenging for many students.

(a) Just over forty percent failed to obtain the mark. Some students failed to make reference to triplets, or three bases and made statements along the lines of 'Many bases code for the same amino acid.' Others got the definition the wrong way round and said that one triplet codes for more than one amino acid. Quite a few got confused between the genetic code being degenerate and non-overlapping.

(b) About thirty percent obtained both marks. Some students again failed to refer to triplets, or three bases, and some failed to say that a codon is on mRNA (we accepted DNA).

(c) (i) This question demonstrated that the majority of students think that RNA polymerase causes base pairing, rather than joining together nucleotides that have already base paired.

(ii) About seventy-five percent of students correctly named the enzyme.

(d) A similar percentage obtained the mark for an explanation of what a palindromic recognition sequence is.

## Q25.

(a) (i) Students were aware that polymers were made of many monomers, but in many cases went on to include descriptions in their answers that implied they did not understand what the monomers in this case were. A number of answers suggested that each strand was a monomer or that the monomers were amino acids.

(ii) Most students knew the names of the parts of the diagram; the most common mistake was giving 'sugar' or 'ribose' instead of deoxyribose.

(iii) In order to gain both marks, students had to show that they knew the names of the bases. This proved very revealing in that almost all knew the initial letters of the four bases but only a minority could write down the names correctly. About half were able to complete the simple calculation to give the percentage of the other three bases.

(b) (i) Those who failed to gain credit often did so because they were, apparently, of the opinion that one base coded for three amino acids.

(ii) Introns, non-coding DNA, start and stop codes were all known to be non-coding DNA and, thus, adding to the length of the gene without contributing to the polypeptide. Some students also mentioned addition mutations or the fact that there are two strands. A minority of students incorrectly linked the degeneracy of the genetic code to the difference in number of bases.

## Q26.

(a) (i) Most students correctly gave the base sequence of the anticodon as **UGC**.

(ii) Almost all students correctly gave the base sequence of DNA as **TGCTAC**. However, a minority of weaker students failed to read the stem of the question carefully enough. They replaced the thymine bases in this sequence with uracil.

(b) Most students were aware that DNA contains introns or mRNA only contains exons. Weaker students were often let down by vague answers, such as 'mRNA contains exons' and 'mRNA is spliced'.

(c) It was widely appreciated that a change in the base sequence of mRNA could result in different amino acids being coded for or would produce a change in the primary structure of the toxin. A common response seen by a minority of weaker students was 'different amino acids are produced'. This was not credited.

(d) Most students gained at least one mark for stating that acetylcholine would not be broken down. However, the ability to tell the rest of the story correctly proved to be a good discriminator. Weaker students often thought that depolarisation would be prevented, resulting in the muscles not being able to contract. Some students attempted to explain this in terms of the inability to reabsorb acetylcholine into the presynaptic membrane. They thought that this would prevent any further release of acetylcholine. It was usually only better students who went on to describe the opening of sodium ion channels. Similarly, the importance of the 'continuous' aspect of muscle contraction was only appreciated by the best students.

## Q27.

(a) (i) Almost ninety percent of candidates were able to determine the maximum number of amino acids which could be coded for by the sequence of DNA bases provided.

(ii) There was almost an equal split here between candidates who correctly referred to introns or stop/start codons and those candidates who incorrectly provided an explanation in terms of the code being degenerate.

(b) This question proved to be a very effective discriminator. Most candidates gained at least one mark, often by mentioning a change in the sequence of amino acids. However, a significant number of candidates incorrectly referred to 'different amino acids being formed'. Many candidates gained a second mark for explaining that the tertiary structure would be altered. Better candidates gained maximum marks either by linking this to changes in hydrogen/ionic/disulfide bonds. Candidates were not penalised for references to 'active sites' even though the question did not indicate that the protein was an enzyme.

(c) Rather surprisingly, only half of the candidates gained marks on this question. Those that did gain credit usually obtained both marks by realising that it was important to match the number of complementary base sequences between strand A and strand B.

## Q28.

(a) Most candidates named the two substances required in answer to part (i) correctly, although there were responses such as sugar and pentose that lacked the necessary precision. Part (ii) was answered correctly by most candidates.

(b) In part (i), a few candidates attributed the properties of DNA in containing thymine being double stranded to one or other of the specified forms of RNA. Most, however, were able to explain that tRNA was folded and contained hydrogen bonds. Part (ii) was also answered well with only occasional confusion between exons and introns.

(c) Although part (i) was answered well, less able candidates experienced considerable difficulty with part (ii). There was much confusion between chromosomes and genes and there were frequent references to stop codons being found at only the end of

chromosomes. Equally worrying was the number who considered that as the base sequence on DNA was random, then the percentage of bases was also random.

## Q29.

This question was intended to be synoptic and as such required a basic understanding of principles established in other units. There were some outstanding answers but it was also disappointing to note that there were many candidates who clearly had little idea of the functions of cell organelles or of the role of ribosomes and RNA in protein synthesis.

(a) There were, perhaps inevitably, candidates who confused condensation and hydrolysis but most were able used the terms appropriately in the context of protein digestion and synthesis.

(b) Those who understood protein structure usually gained credit, but almost two-thirds of all candidates made no progress here. While the most frequent problems stemmed from confusing amino acids with bases, others appeared uncertain that proteins could be digested.

(c) Most, but by no means all, candidates identified the overall trend of decrease, increase, decrease but rather fewer supported this with data from the table relating to the age of the pupa. Where the age was quoted, it was not uncommon to see it given in days or years. A little common sense might have excluded the latter.

(d) Answers to part (i) might have been better had more candidates distinguished between the roles of lysosomes and ribosomes. There were many responses associating an increase in lysosomes with increased protein synthesis towards the end of the time spent as a pupa.

Others linked lysosomes with disease and answered in terms of increased exposure to bacterial infection. A major misconception in the answers to part (ii) was that protein synthesis would decrease RNA concentration as it was “used up” in the process.

(e) Although some of the candidates answering this part of the question were unable to identify the trend in the table, most recognised that tissue formation involved protein synthesis and hence the increase in RNA.

(f) This question discriminated very effectively over the range of available marks but, at all levels of ability, candidates appeared to find difficulty with spelling the words aerobic and anaerobic. Examiners try to avoid being unnecessarily pedantic over the spelling of technical terms but the onus is on candidates to make their intentions clear, particularly when the words concerned are closely similar. A considerable number of candidates failed to equate tracheae with insect gas exchange and wrote of breathing and the lungs.

## Q30.

(a) There was widespread recognition that tail band width would be likely to change with age.

(b) In part (a), many candidates lacked the mathematical understanding to appreciate that a mean which had a value with decimal places suggested that measurements of the same band must differ. Likewise, they did not appreciate that a standard deviation with a value other than zero indicated variation in the measurements of the same band. However in part (b), having read the description of the procedure, most recognised that viewing an animal's tail through binoculars from a moving vehicle

was likely to give rise to inconsistent data.

(c) Most candidates correctly used the data about the width of bands from the left and right sides of the tail as evidence that rings of equal width were not found.

(d) The most frequently awarded mark was for showing an understanding that unrelated animals would be expected to show more variation than animals from the same family. It was less usual to find a link to the idea that members of one family are genetically closely related, or a reference to the animals' parentage.

## Q31.

(a) Less than half the candidates correctly named introns as the non-coding sections of a gene.

(b) The vast majority of candidates correctly identified the amino acid sequence.

(c) (i) Most candidates obtained at least one mark for stating that the amino acid sequence would not change. However, less than half the candidates gained the second mark by explaining that the new base triplet would still code for glycine.

(ii) Most candidates gained at least one mark, often by mentioning a change in the sequence of amino acids. However, a significant number of candidates incorrectly referred to 'different amino acids being formed'. Many candidates gained a second mark for explaining that the active site/ tertiary structure would be altered. The best candidates gained maximum marks either by linking this to enzyme-substrate complexes not being formed or to changes in hydrogen or ionic bonds.

(d) (i) Almost two thirds of candidates correctly identified the part of the cell cycle as being interphase or the synthesis stage. Anaphase was a common incorrect response.

(ii) Most candidates obtained this mark, often by indicating that DNA replication occurs during interphase.

## Q32.

(a) This part of the question was often poorly answered. While errors in the first column were perhaps predictable, those not infrequently given in the second column suggested confusion between polynucleotide strands and bases or even chromosomes.

(b) This question was marked in such a way that a candidate who made a single error was still able to gain some credit. The answers to both parts were generally sound although there were occasional errors involving giving the base sequence on the complementary DNA strand, or resulting from uncertainty over splicing.

## Q33.

(a) The answers to this question and to Question 6 (b) suggested that many candidates were uncertain as to the roles of various enzymes used in gene technology.

(b) Although the majority of candidates clearly understood the basic idea of transcription, they tended to gain limited credit for part (i) of this question. This was largely because they failed to make effective use of the material with which they had

been provided. There were few references either to binding to the promoter or to stimulation of the enzyme. In part (ii), most candidates recognised the specificity of the receptors but were not always able to address the question of why oestrogen does not affect other cells. There was much discussion of oestrogen binding to receptors, but relatively little about receptors being confined to the cells of target organs.

(c) Most candidates recognised the molecular structures as being either complementary or similar and used this information to construct sensible suggestions about reduction in growth of breast tumours. The terminology used by many, however, suggested confusion with enzyme action.

## Q34.

(a) While most candidates recognised that stem cells are undifferentiated, many failed to point out that they were capable of replacing themselves. A reference to totipotency ensured this first mark, but a second could not be awarded for simply explaining what the term meant.

(b) The examiners were of the opinion that many candidates had encountered the word but had very little understanding of its meaning.

(c) In part (i), only the better candidates recognised and were able to describe the relationship between the altered sequence of nucleotide bases and the consequent change in the sequence of amino acids affecting the tertiary structure of the protein. There were many general answers that offered little more information than that the "gene was disrupted" or that a "different amino acid was made." Many candidates found part (ii) challenging and, although they were able to gain credit for a general statement relating to the uncontrolled division of cancer cells, they attributed this to insertion of the gene in the base sequence of either the tumour suppressor gene or into a proto-oncogene, thereby converting it into an oncogene.

(d) Many candidates had clearly given careful thought to their answers and made effective use of the data provided. They usually came to the conclusion that 25% was either an unacceptably high cancer risk or that 75% of children were unaffected by cancer. Many took the view that, as the cancer could be treated, whereas SCID was likely to prove fatal, this was an acceptable trial. Answers that adopted a more general approach, describing the trial as unethical, accusing the scientists concerned of "playing God" or commenting on children being unable to make informed judgement did not gain credit.

## Q35.

(a) (i) Most candidates correctly named part **R** as deoxyribose. Answers identifying part **R** as pentose or as a five carbon sugar were considered too imprecise due to the question clearly identifying the molecule as being DNA.

(ii) Most candidates correctly named part **Q** as a phosphate group or as phosphoric acid. Unfortunately, some candidates incorrectly named parts **R** and **Q** the wrong way round.

(b) Almost every candidate correctly stated 'hydrogen bonds'.

(c) Approximately fifty percent of candidates obtained this mark. Although there was a wide range of incorrect answers, the most common error was to divide, rather than multiply the number of amino acids by three.

(d) Over 90 % of candidates were able to correctly work out the sequence of amino acids.

(e) This question proved to be an effective discriminator. Most candidates gained at least one mark, often by mentioning a change in the sequence in amino acids. However, a significant number of candidates incorrectly referred to 'different amino acids being formed'. Many of these candidates gained a second mark for describing that the active site or tertiary structure would be altered. Better candidates gained maximum marks either by linking this to enzyme-substrate complexes not being formed or to changes in hydrogen/disulfide bonds.

## Q36.

(a) Most of the more able candidates recognised that the feature labelled **M** in the diagram represented the sugar-phosphate backbone of the molecule and identified phosphate and deoxyribose as the relevant components. Others enjoyed less success and offered such suggestions as base, nucleotide or, even, hydrogen bond.

(b) Although there were many candidates who identified the maximum number of amino acids coded by this piece of DNA as four, it was difficult to determine any pattern in the enormous range of incorrect responses. It was clear, however, that many candidates had little understanding of the concept of a triplet code.

(c) Part (c) (i) was answered correctly by most candidates, but a substantial number were unable to make use of their responses to determine the percentage of adenine bases in part (c) (ii). The incorrect answer 86% featured frequently.

(d) Better candidates were able to identify the principle involved here and suggest an explanation based on different base sequences coding for different proteins. This idea eluded many, however. Some clearly thought the question related to DNA hybridisation, while others attempted to derive answers from an uncertain understanding of ratios. A common problem arose from imprecise use of the term, genetic code. This should only be regarded as a base sequence coding for a specific amino acid. Answers that attempted to explain the observation described in the question in terms of changes in the genetic code of the bacteria were, therefore, clearly incorrect.

## Q37.

**Unit 2**

(a) Two marks were scored regularly. Confusion between T and A does exist in a significant number however, giving rise to the incorrect responses of GCAAUG and GCUUTG.

(b) In (i) the idea of editing of mRNA was well understood, although some did remove the exons and therefore retained the introns. Poor expression was in evidence here. A few thought that stop and start codons could account for the large difference in number of nucleotides. In (ii) some extremely good answers were seen. Once again many candidates failed to gain marks through poor quality of expression. Amino acids are not made from three bases and, unless qualified by referring to code, the mark was not allowed. Some believed there to be 290 amino acids, but for the correct reason. A significant number believed there to be two amino acids because they went back to the DNA sequence at the beginning of the question rather than the piece of mRNA 660 nucleotides long. This was, however, given credit.

(c) The examiners were very surprised to find this was badly answered, even by many

of the best candidates. Candidates do not appreciate the difference between structure and function. Equally they were unable to provide pairs of matching statements. Successful candidates discussed linear and clover-leafed structure or length of molecules. A major error in a significant number of responses was to imply that tRNA was only three nucleotides long. Amino acid binding sites were discussed in terms of carrying amino acids. It was obvious that many candidates mis-read the question and discussed differences between DNA and RNA, as they referred to the bases present in the molecules.

**Unit 3**

(a) This was a straightforward application question and most candidates gave the correct response.

(b) Part (i) was reasonably well answered. The most common incorrect response was to explain the difference in length in terms of the start/stop codons. Responses to part (ii) showed candidates often chose to refer to the original sequence for part (a) rather than the section in part (b) to which the question actually referred. The examiners credited a correct response regardless of which section of mRNA was being used.

(c) Only the most able candidates were able to give two structural differences. The vast majority of candidates gave a mixture of structural and functional differences.

## Q38.

(a) (i) Most correctly gave the coding sequence of ACG. The most common incorrect answer involved replacing A with T.

(ii) Most identified serine correctly.

(b) There was some good understanding of introns and many identified this correctly as the explanation for the different number of nucleotides. The main incorrect answer occurred when candidates concentrated solely on stop/start codons.

(c) This was poorly answered by many candidates. Most had some understanding of what was happening but only the better candidates could express this in enough detail to achieve full marks.

Weak candidates failed to use terms like codon, anticodon or translation, and often simply restated the question. Many referred to tetracycline carrying a stop codon.

## Q39.

(a) Almost all candidates scored one mark for the idea of bacteria being killed or inhibited but very few mentioned diffusion of the antibiotic. Candidates should note that two marks are rarely given for a single idea in a question of this type.

(b) Some candidates failed to gain marks by casual references to large or larger clear areas instead of saying this was the largest.

(c) Many candidates scored two marks but some, disregarding the question, wrote about protein synthesis or gave general statements about bactericidal or bacteriostatic compounds. Some were confused as to whether the cell wall or the cell membrane was disrupted.

## Q40.

**Unit 2**

(a) Much confusion was shown here between bases, amino acids, DNA and protein. Few were able to give a clear account and many discussed translation, mRNA and tRNA and stumbled on markworthy points almost incidentally.

(b) This usually scored two marks.

(c) Although many produced a correct 9-letter code, several gave CCC rather than CCG, and some listed every triplet mentioned in the question.

(d) This part of the question was not answered well. General accounts of mutation were often provided or changes other than addition of bases were given. Even those who were moving in the right direction failed to explain that the amino acid chain would only differ from this point onward. Many correctly identified the stage as interphase or the S phase but some offered translation or transcription.

(e) Examiners commented on the precise use of language here even in papers where it was lacking elsewhere. Many started with transcription but got into their stride and gained 6 marks easily. Not all mentioned nuclear pores or the tRNA collecting more of the same amino acid. Several made creditable attempts to say that the amino acid was specific to the anticodon. Problems arose in the location of peptide bonds which were thought to join codons to 'matching' anticodons and a few failed to mention amino acids at all.

**Unit 3**

In part (a), many candidates did not link the base code with different amino acids in the sequence. Weaker candidates were confused about DNA structure and referred to it containing amino acids. In (b), the correct base sequence was given by most candidates. In (c), many failed to give the correct answer, but produced a long list of triplet codes instead. In (d)(i), many did not link a change in the sequence of bases with a change in the amino acid sequence and, hence, a change in the protein. It was common to read that a change in base sequence gave a different protein without further detail. Most candidates gave the S-phase or interphase in (d)(ii) although some offered 'transcription' or 'replication'. Part (e) was surprisingly badly done by many candidates. Many started with transcription, but when they reached the required part of the story, described the process erroneously. Many did not refer to mRNA leaving the nucleus via nuclear pores, nor to the fact that tRNA brings *specific* amino acids. The complementary codon/anticodon binding was well described, but many candidates described anticodons attaching to amino acids. Many referred to polypeptide bonds instead of peptide bonds. Weaker candidates confused protein synthesis with DNA replication.

## Q41.

**BYA2**

Most candidates were able to give the correct sequence in (a) (i). In (a) (ii), almost everybody gave the correct answer of nucleus, though there were some references to cytoplasm. There were fewer correct answers to (a) (iii), however, as many candidates assumed that only one stage had to be chosen. Part (b) was well answered by most. A small number of candidates gave the complementary sequence for the tRNA anticodon, UAA, rather than the name of an amino acid in (b) (i). The commonest error in (b) (ii) was to include uracil in the base sequence.

**BYA3**

(a) The sequence of events was familiar to most. One mistake tended to lead to others, however. Nearly everyone was able to identify the nucleus. Some appeared to think only one letter was required in part (iii), but many successfully produced all three.

(b) This question was accessible to many although part (ii) offered more scope for errors and several did not work through all the steps needed.

## Q42.

Most candidates were able to apply their knowledge and gained credit but poor expression marred the answers of the weaker candidates.

(a) The role of RNA polymerase was not well known. There were very few answers worthy of credit. The majority of candidates described the role of RNA polymerase as catalysing complementary base pairing. Responses were often ambiguous and it was not clear if the enzyme was joining nucleotide to nucleotide along the backbone. In contrast, the vast majority could name the ribosome.

(b) The majority of candidates gained both marks.

(c) Well answered.

(d) Most candidates recognised the amino acid alanine. Very few candidates scored full marks in part (ii) and a substantial minority gained only one. The most common point to gain credit was reference to mutation 1 having no effect. Weaker candidates described the change in the DNA triplet as causing a different amino acid to be made as the result of mutation 2 and then failed to relate description of the change to the polypeptide in terms of shape or tertiary structure.

## Q43.

Many candidates gained at least five marks in this question with weaker candidates scoring at least three.

(a) Most candidates gained one mark. Cost was rarely mentioned. Answers were often vague and lacked precision.

(b) (i) Most identified protein synthesis. Candidates tended to just give the sequence of events rather than what would happen if they stopped. Weaker candidates just repeated the question. Some candidates were confused between transcription and translation and others wrote about DNA replication and mRNA production.

(ii) There were many good answers but some just said ‘different sizes’.

## Q44.

The majority of candidates gained the marks for application of knowledge. Straightforward recall proved difficult for some, through lack of adequate preparation for the examination.

(a) There was a very disappointing number of correct responses. The vast majority of candidates quoted ‘mRNA codons’ and gained no marks.

(b) Candidates who had not thoroughly learnt the factual material necessary to understand protein synthesis gave confused accounts and failed to gain any marks. Many candidates gained two marks but common omissions were failure to mention the specific nature of the amino acid carried and also failure to complete the story by reference to the correct sequence on the completed polypeptide.

(c) The vast majority of candidates gained both marks.

## Q45.

This question produced a very wide spread of marks. Candidates frequently failed to gain marks through their inability to select appropriate information to answer the specific question asked. This particularly applied to part (b) (ii). Again, inaccurate use of terminology compromised the marks gained by many candidates.

(a) The majority of candidates gained the mark, UV light being the most popular response. Vague reference to cigarettes or tar, without further qualification, did not gain credit.

(b) In part (i), most candidates recognised the loss of a base and the frame shift occurring in consequence and gained both marks. Weaker candidates confused the change in base sequence with amino acid sequence, seemingly unaware of the distinction between the two. Very few candidates scored full marks in part (ii) and a substantial minority gained only one. The most common point to gain credit was reference to the enzyme.s inability to function. Weaker candidates wrote in general terms about enzyme function and did not specifically refer to enzyme 1 in the question. Again, as in section (i), some candidates confused the structure of a gene with the structure of a protein and gained no marks. The change to the mRNA was rarely mentioned and descriptions of alteration to tertiary shape were too often vague and imprecise to gain credit. In part (iii), any candidates interchanged the lilac and blue colour when completing the table. Errors also included ‘no pigment’ and ‘albino’ for the unlabelled white petal.

## Q46.

(a) Although more demanding than the others, it was pleasing to find that many candidates performed well on this question, and that a considerable number gained at least 6 or 7 marks. In particular, an encouraging number managed to get to grips with part (c).

Surprisingly, this was rather poorly answered by many candidates. Often this was because they failed to use the diagram, and, for example, quite often the presence of the chloroplast was not related to photosynthesis. Very few suggested that the movements might position the cells in the optimum light intensity for photosynthesis. The commonest suggestion was that moving away from very bright light would avoid damage, more often to the eyespot than the chlorophyll. Some equated bright light with heat and suggested it would denature enzymes. Others were sidetracked into accounts of avoiding predators or referred to physiological processes that could not be seen in the diagram. Quite a few suggested that bright light was avoided so that the cells would not make too much starch or sugar and burst.

(b) (i) This proved more discriminating than expected, and only the better candidates simply multiplied the 900 amino acids by three.

(ii) There was a good proportion of correct answers, and many more made a sufficiently sensible attempt to gain a mark for the principle. Some gave a figure for two flagella, rather than for each flagellum, and others made errors with the number of zeros or the indices.

(c) (i) A good proportion of candidates gained both marks for this part, but quite a large number failed to compare the results for puromycin with those for the control. The latter group simply described the curve for puromycin. Some weaker candidates misinterpreted the graph and stated that the flagella stopped growing longer after 20 minutes.

(ii) This question was targeted at the more able candidates and the examiners were looking for a precise explanation of the evidence. It was, however, pleasing to note that large numbers of candidates were able to make the links between transcription and mRNA production and between translation and protein synthesis. Better candidates did point out that actinomycin D had no significant effect on regrowth of the flagella and that therefore the cells must be using existing mRNA. Fewer specified that the rate of regrowth declined after about 20 minutes in the presence of puromycin, so only some of the regrowth could be attributed to proteins already present in the cells.

## Q47.

Most candidates were able to score at last two marks on this question. However, very few candidates obtained maximum marks, usually because of their responses in part (d)(ii).

(a) The majority of candidates correctly gave 387 as the answer. However, a significant number of candidates divided the number of amino acids by three and gave an incorrect answer of 43.

(b) Part (i) caused few difficulties with the majority of candidates correctly giving CCAG as the complementary DNA sequence. A few candidates incorrectly gave CCTG. Part (ii) proved to be far more discriminating with many candidates giving seven as an answer rather than five, having failed to realise that two of the codons appeared twice.

(c) Most candidates were able to gain at least one mark by naming a specific mutagen. Unfortunately, a significant number of candidates were not specific enough, using vague references to ‘radiation’ and/or ‘chemicals’ which were not credited. Similarly, tobacco tar was credited but ‘smoking’ was not. Better candidates had no problem obtaining both marks by naming a chemical mutagen, e.g. benzene, and a named radiation source, e.g. ultraviolet rays. Answers referring to the length of time of exposure to a mutagen and to the dosage of mutagen were also credited.

(d) This proved to be the most difficult question on the paper. Most candidates incorrectly used a substitution mutation when determining the altered mRNA base sequence in part (i), rather than an addition and deletion. Consequently they had difficulty obtaining any marks for part (ii). Although approximately a third of candidates provided the correct mRNA base sequence in part (i), few of them gained more than a single mark in part (ii). A common error was to refer to amino acid mutations rather than to base mutations. Many candidates in part (ii) referred to RNA nucleotides rather than to DNA nucleotides, which restricted their maximum mark.

## Q48.

(a) (i) Most candidates calculated the number of bases correctly. Many obtained a

second mark for explaining that three bases on DNA (a triplet) code for each amino acid. A significant number did not get the second mark, because they stated or implied that bases are amino acids.

(ii) This proved very difficult for many candidates. Quite a large number obtained one mark for suggesting a deletion mutation but only the best candidates went on to suggest the deletion of a triplet of bases. Some candidates continued a misconception evident in (i) and stated that an amino acid was deleted. Credit was given to candidates who suggested another type of mutation affecting a terminal amino acid.

(b) There were many good answers to this question and many candidates obtained all four marks. Surprisingly few candidates made clear reference to complementary base-pairing between codon and anti-codon.

## Q49.

This question produced a wide range of marks and proved to be an effective discriminator.

(a) Answers to this question were rather disappointing, often lacking the precise details expected at Advanced level. Although some candidates referred to 'memory cells', many did not specify that these are T or B cells (lymphocytes). Better candidates did mention antibodies but they often failed to explain that antibodies previously produced were ineffective or that it takes time to produce new effective antibodies following infection by a new strain of the influenza virus.

(b) In part (c)(i), although many candidates appreciated that macrophages engulf pathogens, few candidates precisely described that the antigen is then displayed on the macrophage cell membrane. An alternative mark point credited was the role of macrophages in producing cytokinins which stimulate B lymphocytes. Part (c)(ii) was generally well answered with most candidates obtaining at least two marks. Many candidates explained that the mitochondria provide ATP and that the RER or ribosomes are involved in protein synthesis. Although some candidates then linked protein synthesis to antibody production, only the best candidates provided a correct function of the Golgi body in terms of packaging and/or secreting proteins or glycoproteins.

## Q50.

This question was often poorly answered with many candidates having insufficient synoptic knowledge to answer it. The most able candidates scored well, giving complete and accurate answers.

Although most candidates scored some marks, only a minority scored full marks by giving a full account explaining how a mutation would affect protein synthesis. There was a tendency for candidates to limit their account to the changes in amino acids and protein structure, making no reference to either mRNA or tRNA. Some candidates just gave an account of protein synthesis without any reference to the change that would occur. Many who did mention changes in the protein failed to describe the nature of the changes. There was considerable confusion between bases and amino acids in describing DNA and proteins. Many candidates also stated that amino acids are made in the process.

## Q51.

Quite a large number of candidates failed to perform well on this question because of poor use of language and terminology in parts (a) and (b).

(a) Most candidates obtained the mark for the idea that the mutation alters the amino acid sequence in Factor VIII protein. Good candidates then related this to a change in the tertiary structure (or three-dimensional shape) of the protein. Poorer candidates made vague references to changes in the protein, or it not being able to work.

(b) Most candidates scored one mark for the idea that the faulty Factor VIII leads to a failure of the activation of Factor X and blocking of the clotting pathway. Fewer candidates were able to give a reasonable description of Factor X not being activated, because non-functional Factor VIII cannot work with Factor IX. Weaker candidates misunderstood the diagram and thought that Factor IX and Factor VIII were used to make Factor X.

(c) Only the best candidates understood that the blood from each haemophiliac contained the functional factor that the other lacked. Some who understood this only gained one mark because they simply stated that the mixture contained both factors. The examiners wanted a clear statement for the second mark that blood from the boy with faulty Factor IX contained working Factor VIII and the blood from the haemophiliac with faulty Factor VIII contained working Factor IX. A common misconception was that the mutations to the genes for Factor VIII and Factor IX would produce proteins that were able to interact, because they were both the products of mutation.

## Q52.

Many candidates who had done very well throughout the paper displayed surprising gaps in factual knowledge in this question, or expressed themselves very poorly.

(i) This was well answered by the majority of candidates. Some failed to gain marks because they made reference to codons, anti-codons, messenger RNA and transfer RNA but made no attempt to say where the codons or anti-codons were found. A large number of candidates wrote about ‘amino acids’ being attached to tRNA rather than making the required point that each tRNA is specific to a certain amino acid. Weaker candidates were very confused in their terminology.

(iii) This question was only accessible to the best candidates. Weaker candidates tended to answer along the lines that the inserted gene produced an ‘anti-enzyme’ that worked in opposition to the normal enzyme. Quite a number of candidates did note that the softening gene and inserted gene mRNAs are complementary and gained one mark. Very few then linked this in some way to the idea that they might bind to each other and this would reduce synthesis of the softening enzyme. It might have helped some candidates if they had noted that this was part (ii) of a question which started in (i) with a request to describe translation, given that parts of questions are often linked to point candidates in the right direction.

## Q53.

This question involved epistasis and was based on the effect of two different enzymes in a biochemical pathway determining flower colour. Those candidates who were confident about genetics found little difficulty in gaining all 15 available marks in this question. In some cases, however, candidates answered in terms of monohybrid inheritance, even though two separate genes were clearly implicated. Some candidates gave answers in terms of multiple alleles, or even sex linkage, in which it appeared that they had confused the concepts of allele and gene.

In part (a), candidates could receive full credit by using a number of different approaches to explain how the two genes were involved in producing differently coloured flowers.

Some candidates concentrated purely on the alleles and their effect on the two enzymes and the pigments produced, whereas others tackled the question only in terms of the flower colour produced by different genotypes. To gain all six marks available it was necessary for candidates to explain aspects of both.

In part (b)(i), the parents were Aabb (red-flowered) and aaBB (white-flowered). Good answers to part (b)(ii) showed the purple-flowered offspring as AaBb, and proceeded to derive the offspring 2 ratio of 9:3:4, purple: red: white, showing appropriate working. Examiners were surprised and pleased to find that it was not impossible for candidates who had achieved no marks in (b)(i), having offered answers that were totally wrong, to recover and gain full credit in (b)(ii).

In part (c)(i), three different genotypes, aaBB, aaBb, and aabb, were required for the single mark. A proportion of candidates failed to score because they omitted one of these. In part (c)(ii), candidates gained credit by suggesting the addition of the red pigment, K, to extracts of each homozygous type of white petal, going on to achieve full marks for explaining that the extract of the aaBB petal would contain enzyme 2 and that this would catalyse the conversion of K to L, turning the extract purple. In contrast, the other white petal from the aabb flowers would remain red after K had been added. The most commonly encountered wrong approach was for the petals somehow to be ‘crossed’.

Genetics questions, as a rule at this level, tend to produce extremes of either very low or very high marks, depending on candidates’ understanding of the topic. This question, in requiring quite different skills in its three main parts, proved an exception to this, with many intermediate scores being achieved as well. Where candidates understood the concept of dihybrid inheritance and associated enzymes, answers were very good indeed and showed an improvement in the General standard seen at Advanced level in recent years.