AQA A-LEVEL · 7402

BIOLOGY



MARK SCHEME

3.4.1 DNA, GENES AND CHROMOSOMES

SCORE	PERCENTAGE
/236	%

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Q1.

(a) **Comparisons**

1. Nucleotide structure is identical;

   Accept labelled diagram or description of nucleotide as phosphate, deoxyribose and base

2. Nucleotides joined by phosphodiester bond;

OR

Deoxyribose joined to phosphate (in sugar, phosphate backbone);

3. DNA in mitochondria / chloroplasts same / similar (structure) to DNA in prokaryotes;

   Accept shorter than nuclear DNA/is circular not linear/is not associated with protein/histones unlike nuclear DNA;

Contrasts

4. Eukaryotic DNA is longer;

5. Eukaryotic DNA contain introns, prokaryotic DNA does not;

6. Eukaryotic DNA is linear, prokaryotic DNA is circular;

7. Eukaryotic DNA is associated with / bound to protein / histones, prokaryotic DNA is not;

5 max

(b) 1. Mutations change base / nucleotide (sequence);

   Reject if mutation in amino acid

2. (Causing) change in amino acid sequence;

3. Mutations build up over time;

4. More mutations / more differences (in amino acid / base / nucleotide sequence / primary structure) between distantly related species;

OR

Few(er) mutations / differences (in amino acid / base / nucleotide sequence / primary structure) in closely related species;

5. Distantly related species have earlier common ancestor;

OR

Closely related species have recent common ancestor;

Accept "order" for "sequence"

If neither MP4 or MP5 accept for 1 mark, idea of more mutations /differences as evidence of earlier common

ancestor OR converse

5

[10]

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.

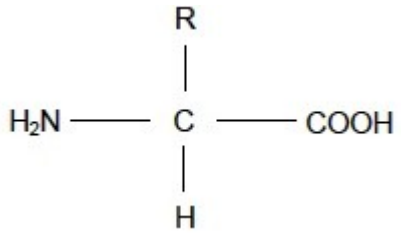
Ignore descriptions of eukaryotic DNA alone.

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 <u>active site</u>
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. **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]

Q5.

(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]

Q6.

(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]

Q7.

(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]

Q8.

(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]

Q9.

(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]

Q10.

(a) Locus;

Accept: loci

1

(b) Differences in DNA / differences in base sequence of DNA;

Accept: number of different alleles / size/variation in gene

pool

Reject: genes

1

(c) 1. Jack Russell (genetic) diversity is (significantly) greatest;

2. Bull terrier (genetic) diversity is (significantly) smallest / is most inbred;

3. Miniature terrier and Airedale terriers are similar;

1-3: do not credit just a list of values

4. Standard deviations do not overlap / do overlap with correct ref to significance;

Reference to significance must be relevant to examples given

Max 3

(d) 1. (Bull terrier) breeding has included a genetic bottleneck/ small population/more inbreeding/ greater selection (pressure);

Accept: founder effect

2. Reduced number of different alleles/size of gene pool;

Reject: decrease in number of genes

Ignore ref to mutations

OR

3. Miniature (terrier) breeding has included more outbreeding/less selection (pressure);

4. Increased number of different alleles/larger gene pool/more variety of alleles;

Reject if genes used instead of alleles

Reject: lower frequency of alleles

Ignore ref to mutations

2

[7]

Q11.

(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 triplets 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]

Q12.

(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]

Q13.

(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]

Q14.

(a) (i) 4;

1

(ii) 1. Change in amino acid / (sequence of) amino acids / primary structure;
1. Reject = different amino acids are 'formed'

2. Change in hydrogen / ionic / disulphide bonds alters tertiary structure / active site (of enzyme);
2. Alters 3D structure on its own is not enough for this marking point.

3. Substrate not complementary / cannot bind (to enzyme / active site) / no enzyme- substrate complexes form;

3

(b) 1. Lack of skin pigment / pale / light skin / albino;

2. Lack of coordination / muscles action affected;

2 max

(c) Founder effect / colonies split off / migration / interbreeding;

Allow description of interbreeding e.g. reproduction between individuals from different populations

1

[7]

Q15.

(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]

Q16.

(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]

Q17.

(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]

Q18.

(a) More that one polypeptide / chain;

Ignore references to haem / other groups

1

(b) (i) 141;

1

(ii) 1. Stop / start sequences;

2. Non coding DNA (in the gene) / introns / multiple repeats / junk DNA;

Do not credit "some bases repeated"

3 Two chains / a non-coding strand / complementary base pairs;

4. Addition of base by mutation;

2 max

(c) Different primary structure / amino acids / different number of polypeptide chains;

Question is about haemoglobin so do not credit differences in DNA

1

(d) 1. Low partial pressure of oxygen in lungs;

2. (Llama) haemoglobin able to load more oxygen / (llama) haemoglobin saturated (at low / particular partial pressure of oxygen);

3. Higher affinity for oxygen;

The terms used in the graph (or near approximations) should be used in this answer.

Ignore references to unloading

The answer must relate to llamas

3

[8]

Q19.

(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]

Q20.

(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]

Q21.

(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]

Q22.

(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]

Q23.

(a) a length of DNA;
that codes for a single protein / polypeptide;

2

(b) by heating;
to break the H-bonds (between complementary bases);

2

(c) (i) to allow the DNA polymerase to attach / start addition of nucleotides / mark start and end of sequence to be copied / prevents strands re-joining;

1

(ii) because the sequences at the ends of the target sequence are different / one is at the beginning and one at the end;

1

(d) 8;

accept 7

1

[7]

Q24.

(a) (i) actin (*Accept* tropomyosin);

1

(ii) myosin head;

1

(b) (i) Ca^{2+} binds to [part of] the actin / troponin;
this causes tropomyosin to be displaced;
uncovers [myosin] binding sites [on actin] / allows actin to bind;

max 2

(ii) myosin heads bind to actin / cross bridge formation / actomyosin formed;
myosin heads / crossbridges swivel / ratchet mechanism;
causing actin to slide relative to myosin;
energy provided by hydrolysis of ATP;

max 3

(c) (i) (number lightly stained fibres / total number of fibres) × 100;
(actual numbers are 10 / 18 × 100)

1

(ii) sample not representative / large enough / individual muscle fibres different sizes / contain different number of myofibrils;

1

(d) all some stain = 1
fast dark and slow lighter = 2

2

(e) change in base sequence in DNA / addition / deletion / substitution of a base in DNA of the gene which codes for myosin;
change in amino acid sequence / primary structure;
causes a different tertiary structure;
which alters the binding properties of myosin;

4

[15]

Q25.

(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]

Q26.

(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]

Q27.

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]

Q28.

(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]

Q29.

(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]

Q1.

In question (a), it was clear that some students had been taught how to respond to the command ‘compare and contrast’. They produced well-organised answers, although these largely concentrated on the differences between the two types of DNA and seldom referred to similarities. Students who wrote lists about each type of DNA and did not make clear comparisons and contrasts, did not gain marks. A significant number of students compared prokaryotic cells with eukaryotic cells (such as “DNA floats in the cytoplasm, but in eukaryotes it is contained in a nucleus”) or they compared DNA with RNA. Misconceptions were common; for example, “prokaryotic DNA is single stranded”, “it contains uracil”, “it is not replicated semi-conservatively”, “it contains ribose”, “viruses are prokaryotes”, “DNA is an alpha helix”, “all prokaryotes have plasmids”. Very few students (0.3%) achieved five marks and not many (1.9%) got four marks. Many answers showed little evidence of knowledge beyond GCSE level; for example, “DNA consists of four named bases”, “DNA is made of a sugar, a phosphate and four bases”. Knowledge about nucleotides was given in very few answers. The low quality of answers (the mean mark on this question was only 0.79 out of 5), along with evidence of frequent misconceptions, gave examiners a sense that section 3.4.1 of the specification about DNA structure is not well understood.

In (b), it was evident that students had difficulty with this topic and many answers (56.4%) gained no credit. Some students were diverted because the question referred to haemoglobin, and went into long detail on levels of protein structure and physiological adaptations to different oxygen environments; for example, mammals at different altitudes. Those who discussed evolutionary relationships often gave vague answers that referred to sharing a common ancestor or being related, rather than use ideas like more differences would indicate a more distant relationship and an earlier common ancestor. Very few students considered what caused the differences in the primary structure of haemoglobin, consequently little mention was made of mutation, which is the process underpinning species change in evolution. Few considered why these differences accumulated over time. Many answers achieved two marks, and rarely more than three marks. The mean mark on this question was only 0.46 out of 5.

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.

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.

Q10.

(a) Over three quarters of students correctly identified 'locus' as the position of a gene on a chromosome with 'allele' and 'exon' given frequently as incorrect answers.

(b) Most students correctly defined the term 'genetic diversity', usually by referring to the number of different alleles. 'Genes' was used instead of 'alleles' by more than a few and some tried to hedge their bets by quoting 'genes/alleles'. Imprecise expressions like 'the range of alleles', 'variation of alleles' or 'number of alleles' were not credited, but often seen.

(c) This question tested students' ability to select and translate appropriate information from tabulated form and it differentiated well. Most achieved two marks and many got all three. Concise reference was often made to 'overlapping standard deviations showing no significant difference between mean values' and demonstrated that there is sound awareness of this principle. Nevertheless, some misread the table and quoted Airedale as being the most diverse and others failed to make a comparison, but relied simply upon using a list of numbers. Occasionally, students failed to identify the breed of dog in the comparison they made, leaving the onus on the examiner to decipher what they really meant. Some commented correctly on 'low values of standard deviations showing that there was high reliability', but this did not answer the question. Misconceptions, such as 'high diversity shows more genes are involved' and 'overlapping standard deviations show breeds are closely related' were not uncommon.

(d) This question proved beyond most students because they did not link the data to human involvement in the selective breeding of domesticated animals. Many thought incorrectly that frequent mutations caused the changes in genetic diversity, and many thought speciation had occurred which involved isolating mechanisms such as island populations or river barriers. Some put the changes down to environmental causes. Reproducing Miniature terriers with other breeds was often correctly given to indicate that they were more outbred, and 'selection of specific traits in Bull terriers' was accepted at the lowest level for inbreeding. References to a gene pool or to changes in the number of different alleles were rare. Some students referred to the terriers as different species, but then bred them and their offspring successfully, which suggested there is a misconception with the concept of species.

Q11.

(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.

Q12.

(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.

Q13.

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.

Q14.

(a) (i) Over 90% of students correctly determined that base sequence could code for a maximum number of four amino acids.

(ii) The vast majority of students gained at least one mark, often by mentioning a change in the sequence in amino acids. However, a significant number of students incorrectly referred to 'different amino acids being formed'. Most students gained a second mark for explaining that the active site/ tertiary structure would be altered. Over 50% of students gained maximum marks either by linking this to enzyme-substrate complexes not being formed or to changes in hydrogen bonds.

(b) Most students had little difficulty in using the information to give two symptoms of phenylketonuria and gained both marks.

(c) The majority of students obtained this mark, often by referring to migration or by describing interbreeding. However, over a third of students failed to gain credit and often accounted for the spread of phenylketonuria by horizontal or vertical gene transfer.

Q15.

(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.

Q16.

(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.

Q17.

(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.

Q18.

(a) Although there were various interpretations of the diagram, most candidates correctly indicated the presence of more than one polypeptide chain.

(b) In part (i), many candidates correctly identified the number of amino acids coded by this piece of DNA as 141. Incorrect responses were usually centred on multiplying the number of bases either by two or by three. In part (ii), the single mark that was most frequently awarded was for a reference to introns. Many candidates, however, interpreted the question as asking about the nature of the genetic code. There were many responses centred on there being "more than one code for an amino acid".

(c) Despite the mark allocation shown for this question, there were some very extensive answers involving the DNA base sequence and protein structure. Many of these accounts also reflected much confusion between the terms base and amino acid. There were occasional unfortunate references to the environment causing the difference in haemoglobin structure.

(d) Better candidates were able to identify the principle involved here and suggested an explanation based on the ability of haemoglobin to load more oxygen at lower partial

pressures. Where these candidates used the information from the graph and wrote of the partial pressure of oxygen and the percentage saturation of haemoglobin, they were usually able to gain full credit. There was, however, much imprecise wording and accounts were often marred by such phrases as there was “less air in mountains” and “the llama carries more oxygen”. Less able candidates frequently twist the wording of questions round. This question, for example, was occasionally answered as requiring an explanation of the adaptations of horses to living at low altitudes. Such an interpretation failed to gain credit.

Q19.

(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.

Q20.

(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.

Q21.

(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.

Q22.

(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.

Q23.

(a) Examiners were very disappointed to read so many incorrect definitions of a gene. The idea that a gene is a ‘strand of DNA’ seems a common misconception. Some indicated that a gene was the entire DNA or that it was part of a chromosome. Few referred to it coding for a polypeptide but instead gave a vague reference to ‘characteristics’ or used examples, e.g., eye colour. A significant number incorrectly believed that the gene was a protein.

(b) The concept of breaking bonds between the strands was well understood. However some failed to name the bonds correctly. Others incorrectly suggested that the bonds were broken by the action of enzymes (often restriction enzymes) rather than heat. Nevertheless, many candidates scored both marks here.

(c) A significant proportion of the candidates were unsure of the role of primers, and a larger number could not suggest why two different primers are required.

(d) Many candidates gave the correct answer of 8. Among the incorrect answers, the commonest were sixteen or six.

Q24.

(a) (i) and (ii) A majority of candidates were able to identify A as the myosin head, although rather fewer were able to name actin as the main protein in the thin filament.

(b) In general, the responses to this section of the question revealed a pleasing level of knowledge and understanding.

(i) Many candidates, including otherwise weaker candidates, were able to describe the role of calcium ions in binding to troponin and removing tropomyosin from the myosin binding sites on the actin molecule.

(ii) Again, a good number were able to describe the role of ATP and the two proteins in bringing about contraction of the myofibril.

(c) (i) Only better candidates realised that to calculate the percentage of fast fibres, the number of fast fibres (lightly stained fibres) must be divided by the *total* number of fibres and this figure then multiplied by one hundred. Many weaker candidates multiplied the ratio of the two fibres by one hundred.

(ii) Most candidates could explain that the figure obtained might not be typical as different regions of a muscle may have different proportions of the two fibres, or because the sample used is such a small one as to be not necessarily reliable.

(d) Only really able candidates realised that *all* the fibres would undergo glycolysis, whether respiring aerobically or anaerobically. However, those respiring anaerobically would undergo glycolysis only (and not any further stages of the aerobic pathway) and so produce the enzymes used in glycolysis in greater concentrations.

(e) Many candidates interpreted this question as another concerning natural selection, despite the clear instruction to explain how a new form of myosin could be *formed as a result of mutation*. Good candidates were able to explain how alterations to the base sequence of DNA could result in a different mRNA and, as a result, a different primary structure of the protein. They then went on to explain how this would result in different folding of the molecule, tertiary structure and properties as a result.

Q25.

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.

Q26.

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.

Q27.

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.

Q28.

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.

Q29.

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.