1. (a) Gene is a (length) of DNA;
Gene is a sequence of bases/chain of nucleotides;
Triplet (base) code/read in three's;
On sense/coding strand;
Triplet coding for amino acid;
Degenerate code; non-overlapping; start/stop code;
Sequence of triplets/bases code for protein; max 4

(b) Restriction enzymes;
Cut DNA; at specific base sequences;
Same (restriction) enzyme also cuts DNA; into which gene is inserted/plasmid/virus/Agrobacterium;
(DNA) ligase;
Joins two pieces of DNA together/forms recombinant DNA;
Vector needed to insert DNA into host/plasmid enters host/second organism;
Correct ref. to sticky ends; Reverse transcriptase; mRNA → DNA; max 6

(c) Unwinding/unzipping of DNA;
involving breaking of hydrogen bonds;
Assembly of mRNA nucleotides;
Complementary base pairing/example;
Role of polymerase enzymes;
mRNA enters ribosomes;
Specific tRNA molecule associated with specific amino acid;
Codon - anticodon relationship;
Formation of peptide bonds;
Specific role of ATP/energy; Reference to gene switched on; max 7

Quality of language

Aspect of work

Grammar, punctuation and spelling of an acceptable standard	1
Material presented in an appropriate scientific style with due regard to correct use of technical terms	1
Argument clearly and logically presented	1

[20]

2. (a) (i) Alike

both have phosphate/phosphoric acid/PO_4;
bases/named bases/accept letters;
nucleotides;
pentose sugar;

Different

DNA deoxyribose;
DNA thymine;
DNA double stranded;
DNA larger/longer;
DNA one form RNA 3 types; max. 5

(ii) Alike

H bonds break/DNA unwinds/DNA unzips;
between (complementary) bases;
complementary nucleotides/bases added/DNA acts as template;
same, correctly named, enzymes e.g. polymerase;

Different

uracil/thymine used;
all copied or only section copied respectively;
one strand used transcription, two in replication;
DNA/mRNA produced;
enzymes that are different, correctly named; max. 6

(b) Only some genes transcribed;
only one strand transcribed;
different protein/enzyme required by different cells;
intron ref/some DNA does not code/non sense codes/junk DNA;
stutter sequences/repeat DNA; max.2

[13]

3. (a)

DNA has thymine/T	**AND**	RNA has uracil / U;
DNA has deoxyribose	**AND**	RNA has ribose;
DNA is double-stranded	**AND**	RNA is single-stranded;
DNA larger	**AND**	RNA smaller; max. 3

(b) (i) Arg –Pro –Ala – Gly; 1

(ii) **T C T G G C C G A C C T;** 1

(iii) Mutation still codes for Ala / same amino acid; 1

[6]

4. (a) (i) P = Adenine
Q = Guanine
R = Thymine
S = Cytosine; 2

All four correct = 2 marks
Two or three correct = 1 mark

(ii) Complementary base pairing / purines = pyrimidines / A = T and C = G; 1

(ii) Not all DNA is coding / non-coding DNA / introns / start codes / stop codes; 1

(b) 608; 1

(c) Template for new sense strand (during DNA replication); 1
OR
Provides DNA molecule with stability (via base pairing hydrogen bonding);

[6]

5. (a) (i) Nucleus; **I** nucleolus 1

(ii) Translation **I** protein synthesis 1

(b) (i) mRNA and tRNA; 1

(ii) (each type) carries <u>specific</u> amino-acid / has an anti-codon;
3 bases on tRNA bind to 3 bases on mRNA / codon and anticodon interaction;
tRNA attaches to ribosomes / holds amino acid in place; max 2

(c) 94 **OR** 282 ÷ 3 ; **A** 92 or 93 if correct reference to stop / start codons. 1

[6]

6. (a) (i) Does not code for protein / amino acid / polypeptide / regulates gene expression / unknown function; **I** "junk" or introns reference 1

(ii) Breaks <u>hydrogen</u> bonds; 1

(b) $\mathbf{T} = \mathbf{N} \times 2^{\mathbf{C}}$; **A** $T = N.2^{C}$ **A** correct derivative of this 1

(c)

✓	✓	X
✓	✓	✓
X	X	X

Mark horizontally 3

[6]

7. (a) (i) (Some) amino acids have more than one coding triplet / eq. ; 1

(ii) Two marks for two of:

DNA	RNA
double (helix)	single strand
larger	smaller
contains T (not U)	contains U (not T)
sugar is deoxyribose	sugar is ribose
A = T, C = G	variable amounts
transcription	translation

I (treat as neutral) references to base pairing. max 2

(b) (i) (Incorporated) in(to) cell membrane;
Viscous mucus formed; 2

(ii) **X**-transcription; 1

[6]

8. (a) (i) Region of non-coding DNA / degenerate DNA; 1

(ii) A-T / C-G 1

(b) (i) Cut vector / plasmid DNA with restriction enzymes / endonucleases;
Use (DNA) ligase;
To join sticky ends / description; 2 max

(ii) (Plasmid) DNA **base sequence** / gene (function) altered /
different proteins made; 1

(c) (i) Arrow pointing downwards
AND
lightest molecules move the furthest / fastest / ora; 1

(ii) 5; 1

(iii) Probe binds to **complementary** base sequence in gene;
Position determined by radioactivity / fluorescence; 2

(d) DNA unzips / unwinds / splits / separates / hydrogen bonds break;
To allow assembly of mRNA;
Using RNA nucleotides;
Via RNA polymerase;
Complementary sequence / eq;
mRNA joins to ribosome (*accept travels to ribosome*);
tRNA carries a specific amino acid;
Codon-anticodon relationship / explained;
Peptide bonds form between adjacent amino acids; 6 max

[15]

9. (a) (Yes)
The bands in the baby that don't come from the mother are
shared with the footballer; 1

(b) Cuts the DNA at the same base sequence / specific points;
Allow 'cuts at same minisatellite'
Gives repeats of the same piece of DNA; 1

(c) DNA is not visible on the gel / radioactivity can be (easily) detected;
Shows up on photographic film / autoradiography; 2

(d) Idea of pairing animals with dissimilar fingerprints; 1

[5]

10. (a) Carrier of foreign DNA / gene; 1

(b) (i) *Pst* I; 1

(ii) (Loss of) marker gene;
Genetic code / base sequence / DNA altered;
(So) gene no longer functional; 2 max

(iii) Separate DNA strands to expose sense strand / probe only a single strand;
Probe contains a complementary base sequence to gene;
Attaches to complementary sequence if gene present;
Presence / location indicated by radioactivity / fluorescence; 3 max

(c) So cells cannot conjugate / link;
To stop transfer of DNA;
To reduce risk of other organisms in environment getting altered genes; 2 max

[9]

11. (a) (i) tRNA / transfer-RNA; *[not 'transport-RNA']* 1

(ii) UAG; 1

(b) Different tRNA/X for each amino acid / TRNA joins to one type of amino acid;
mRNA determines which tRNA/X binds (to ribosome) / reference to codon-anticodon pairing/<u>complementary</u> base pairing;
Sequence of bases (in MRNA) determines sequence of amino acids / sequence of codons/triplets determines sequence of amino acids; 3

[5]

12. (a) DNA has deoxyribose, RNA has ribose;
DNA has thymine, RNA has uracil;
DNA double-stranded, RNA single-stranded; 3

(b) Attachment of amino acid; 1

(ii) Allows binding/ joining/ attaching to mRNA;
Codon/ complementary base sequence; 2

(c) (i) Each base is part of only one codon / TRNA 'reads' three bases, then the next three; 1

(ii) Some amino acids are coded for by more than one codon/ base sequence; 1

[8]

13. (a) (i) Translation; 1

(ii) Amino acid; 1

(b) CAT (1 mark)
CAU (2 marks) 2

(c) (i) Bind to CCC/codon;
Hydrogen bond/complementary base-pairing;

(ii) Joins to amino acid/molecule P/peptide/polypeptide;
By peptide bond/condensation; max 3

[7]

14. (a) (i) C → B → E → F → A → D 2

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

(iii) nucleus; 1

(iii) A, D, F; *(ignore E if evident)* 1

(b) (i) Isoleucine; 1

(ii) TGG; 1

[6]

15. (a) Protein made of (chain of) amino acids;
Each amino acid has its own base code/code;
Triplet codes; max 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]

16. General Principles for marking the Essay:

Four skill areas will be marked: scientific content, breadth of knowledge, relevance and quality of language. The following descriptors will form a basis for marking.

Scientific Content (maximum 16 marks)

Category	Mark	Descriptor
	16	
Good	14	Most of the material of a high standard reflecting a comprehensive understanding of the principles involved and a knowledge of factual detail fully in keeping with a programme of A-level study. Some material, however, may be a little superficial. Material is accurate and free from fundamental errors but there may be minor errors which detract from the overall accuracy.
	12	
	10	
Average	8	A significant amount of the content is of an appropriate depth, reflecting the depth of treatment expected from a programme of A-level study. Generally accurate with few, if any fundamental errors. Shows a sound understanding of most of the principles involved.
	6	
	4	
Poor	2	Material presented is largely superficial and fails to reflect the depth of treatment expected from a programme of A-level study. If greater depth of knowledge is demonstrated, then there are many fundamental errors.
	0	

Breadth of Knowledge (maximum 3 marks)

Mark	Descriptor
3	A balanced account making reference to most if not all areas that might realistically be covered on an A-level course of study.
2	A number of aspects covered but a lack of balance. Some topics essential to an understanding at this level not covered.
1	Unbalanced account with all or almost all material based on a single aspect
0	Material entirely irrelevant.

Relevance (maximum 3 marks)

Mark	Descriptor
3	All material presented is clearly relevant to the title. Allowance should be made for judicious use of introductory material
2	Material generally selected in support of title but some of the main content of the essay is of only marginal relevance.
1	Some attempt made to relate material to the title but considerable amounts largely irrelevant.
0	Material entirely irrelevant or too limited in quantity to judge.

Quality of language (maximum 3 marks)

Mark	Descriptor
3	Material is logically presented in clear, scientific English. Technical terminology has been used effectively and accurately throughout.
2	Account is logical and generally presented in clear, scientific English. Technical terminology has been used effectively and is usually accurate.
1	The essay is generally poorly constructed and often fails to use an appropriate scientific style and terminology to express ideas.
0	Material entirely irrelevant or too limited in quantity to judge.

[25]

Additional notes

Care must be taken in using these notes. It is important to appreciate that the only criteria to be used in awarding marks to a particular essay are those corresponding to the appropriate descriptors. Candidates may gain credit for any information providing that it is biologically accurate, relevant and of a depth in keeping with an A-level course of study. Material used in the essay does not have to be taken from the specification, although it is likely that it will.

These notes must therefore be seen merely as guidelines providing an indication of areas of the specification from which suitable factual material might be drawn.

In determining the mark awarded for breadth, content should ideally be drawn from each of the areas specified if maximum credit is to be awarded. Where the content is drawn from two areas, two marks should be awarded and where it is taken only from a single area, one mark should be awarded. However, this should only serve as a guide. This list is not exhaustive and examiners should be prepared to offer credit for the incorporation of relevant material from other areas of study.

17. (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) translation cannot occur; binds to/blocks codon/ triplet on mRNA; anticodon/tRNA will not fit in/base-pair; amino acids not delivered/ joined; 2 max

[5]

18. General principles for marking the Essay:

Four skill areas will be marked: scientific content, breadth of knowledge, relevance and quality of language. The following descriptors will form a basis for marking.

Scientific content (maximum 16 marks)

Category	Mark	Descriptor
	16	
Good	14	Most of the material of a high standard reflecting a comprehensive understanding of the principles involved and a knowledge of factual detail fully in keeping with a programme of A-level study. Some material, however, may be a little superficial. Material is accurate and free from fundamental errors but there may be minor errors which detract from the overall accuracy.
	12	
	10	
Average	8	A significant amount of the content is of an appropriate depth, reflecting the depth of treatment expected from a programme of A-level study. Generally accurate with few, if any fundamental errors. Shows a sound understanding of most of the principles involved.
	6	
	4	
Poor	2	Material presented is largely superficial and fails to reflect the depth of treatment expected from a programme of A-level study. If greater depth of knowledge is demonstrated, then there are many fundamental errors.
	0	

Breadth of Knowledge (maximum 3 marks)

Mark	Descriptor
3	A balanced account making reference to most if not all areas that might realistically be covered on an A-level course of study.
2	A number of aspects covered but a lack of balance. Some topics essential to an understanding at this level not covered.
1	Unbalanced account with all or almost all material based on a single aspect
0	Material entirely irrelevant.

Relevance (maximum 3 marks)

Mark	Descriptor
3	All material presented is clearly relevant to the title. Allowance should be made for judicious use of introductory material
2	Material generally selected in support of title but some of the main content of the essay is of only marginal relevance.
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0	Material entirely irrelevant or too limited in quantity to judge.

Quality of language (maximum 3 marks)

Mark	Descriptor
3	Material is logically presented in clear, scientific English. Technical terminology has been used effectively and accurately throughout.
2	Account is logical and generally presented in clear, scientific English. Technical terminology has been used effectively and is usually accurate.
1	The essay is generally poorly constructed and often fails to use an appropriate scientific style and terminology to express ideas.
0	Material entirely irrelevant or too limited in quantity to judge.

[25]

Additional notes on marking

Care must be taken in using these notes. It is important to appreciate that the only criteria to be used in awarding marks to a particular essay are those corresponding to the appropriate descriptors. Candidates may gain credit for any information providing that it is biologically accurate, relevant and of a depth in keeping with an A-level course of study. Material used in the essay does not have to be taken from the specification, although it is likely that it will be. These notes must therefore be seen merely as guidelines providing an indication of areas of the specification from which suitable factual material might be drawn.

In determining the mark awarded for breadth, content should ideally be drawn from each of the areas specified if maximum credit is to be awarded. Where the content is drawn from two areas, two marks should be awarded and where it is taken only from a single area, one mark should be awarded. However, this should only serve as a guide. This list is not exhaustive and examiners should be prepared to offer credit for the incorporation of relevant material from other areas of study.

19. (a) GCAAUG; ; 2

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

(b) (i) DNA is edited/introns present in DNA; 1

Allow reference to 'junk' or non-coding DNA

(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]

20. (a) 1. Cut gene out of cell/make gene using mRNA/obtain gene with restriction enzymes;
2. Cut DNA using restriction enzyme/plasmid cut with restriction enzyme;
3. Correct reference to sticky ends;
4. Join DNA using ligase/insert gene into vector;
5. Plasmid/named vector transferred to cell;
6. Method of transfer e.g. heat shock;
7. Reference to marker gene;
8. Select bacteria containing new gene; max 6

(b) Cells can metastasise/break off;
Spread to other parts of the body;
Remaining cells continue to divide;
Forming a new tumour/secondary; max 2

(c) Antibodies specific;
Normal cells have different antigen/cancer cell has particular antigen;
Enzyme **only** present in cancer cells;
Drug **only** activated at/near cancer cells; max 3

(d) All cells contain DNA;
Would stop/inhibit DNA replication in normal cells;
Stops/inhibits cell division;
Named example on growth/repair e.g. no new blood cells made/no wound healing; 4

[15]

21. section of DNA unwinds / uncoils;
RNA nucleotides align;
complementary base pairing / example of pairing;
mRNA polymerase (joins nucleotides);
mRNA moves into cytoplasm / through nuclear pore / to ribosome;
tRNA carries specific amino acid;
mRNA read in codons / triplets;
anticodon of tRNA matches codon of mRNA;
ATP used in activation / joining amino acids;
amino acids join by peptide bonds;
tRNA used repeatedly;
sequence of bases / codons determines sequence of amino acids; max 8

[8]

22. (a) (i) ACG; 1

(ii) Serine; 1

(b) DNA contains introns / (pre) mRNA is edited; 1

(c) (Tetracycline) binds to/blocks mRNA triplet;
Anticodon/tRNA triplet cannot pair with mRNA triplet;
Amino acid not added to polypeptide chain;
Translation prevented; 2 max

[5]

23. (a) Strand of DNA;
Short strand / up to 20 bases long;
With base sequence that is complementary to part of target gene;
Radioactive labelling / fluorescent labelling; 3 max

(b) Identify carrier (of cancer gene);
Identify which (cancer) gene present;
Identify most effective treatment; 2 max

[5]