

1.
 - 1 ref to operon;
 - 2 normally repressor substance bound to operator;
 - 3 prevents RNA polymerase binding (at promoter) / prevents transcription;
 - 4 lactose binds to repressor;
 - 5 changes shape of protein molecule;
 - 6 unable to bind (to operator);
 - 7 RNA polymerase binds (at promoter) / transcription occurs / genes switched on;
 - 8 AVP; e.g. production of lactose permease / production of beta-galactosidase;

max 5

[5]

2. a change in the genetic material;
unpredictable / AW;
extra detail; e.g. addition / substitution / deletion / frame shift / small part of chromosome / may code for different protein / may code for no protein

[2]

3. *1 mark max for general effect of mutations:*
mutation may give different, amino acid / primary structure;
A ref stop codon
some mutations alter, molecular shape / tertiary structure / binding;
max 3 for explaining data in Table:
so unable to, accept / transport, HCO_3^- ;
unable to bind ATP;
so increase in acidity / decrease in pH;
effect on mucus;
effect on enzyme(s) / ref pH optimum of enzyme(s);
poor digestion of, protein / lipid / starch;
AVP; e.g. some mutations, give some transport / have less effect.
> 33% (of norm) allows normal digestive function / < 6%
[A very low] does not.

max 3

[3]

4. *allow max 5 for following:*
transcription;
DNA unzips / H bonds break;
exposing required, gene / sequence of bases;
RNA nucleotides align with DNA;
U with A, A with T, C with G, **and** G with C;
RNA polymerase;
mRNA formed (using DNA strand as template);
leaves nucleus through pore;

allow max 5 for following:

translation;

mRNA attaches to ribosome;

tRNA brings amino acid (to, ribosome / mRNA);

each tRNA attached to specific amino acid;

tRNA binds to mRNA using complementary, base triplet / anticodon;

peptide bond formed between amino acids;

DNA / mRNA, (nucleotide / base) sequence determines sequence of amino acids;

AVP; e.g. 2, base triplets / codons, in ribosome

AVP; e.g. ref. to : start / stop, codons

polysomes

large and small subunit in ribosome

Mg²⁺

[10]

5. 1 mark per correct row

*Look for both ticks and crosses.**If a table consists of ticks ONLY or crosses ONLY, then assume that the blank spaces are the other symbol.**If a table consists of ticks, crosses and blanks then the blanks represent no attempt at the answer.*

Nucleotides line up along an exposed DNA strand.	✓	✓;
The whole of the double helix 'unzips'.	✓	✗;
Uracil pairs with adenine.	✗	✓;
A tRNA triplet pairs with an exposed codon.	✗	✗;
Both DNA polynucleotide chains act as templates.	✓	✓;
Adjacent nucleotides bond, forming a sugar-phosphate backbone.	✓	✓;
The original DNA molecule is unchanged after the process.	✗	✓;
Adenine pairs with thymine.	✓	✓;

[8]

6. (a) (i) U A C C G G A U U C A C;;

*1 error = 1, 2 errors = 0**allow 1 mark for giving T throughout instead of U**(i.e. T A C C G G A T T C A C = 1 mark)*

2

(ii) transcription / transcribed; **R** transcriptase

1

- (b) (i) **J** anticodon; **R** anticodons
K transfer RNA / tRNA;
L ribosome / rRNA;
M codon; **R** codons 4

- (ii) **1** DNA triplet / codon / **M** / mRNA triplet, codes for specific amino acid;
2 order of, triplets / bases, determines the order of amino acids;
3 tRNA / **K**, has, corresponding / complementary, triplet / anticodon;
4 (tRNA / **K**) attached to specific amino acid;
5 activation of amino acid;
6 2 (tRNA) binding sites on the ribosome;
7 codon and anticodon bind; **A** match
8 A to U and C to G;
9 adjacent amino acids join;
10 peptide bond; 4 max

- (c) **1** attaches to ribosome;
2 removes, base / portion, of ribosome;
A stops ribosome assembling / changes shape of ribosome
3 prevents ribosome, attaching to / reading, mRNA;
4 prevents codons being exposed;
5 prevents, tRNA / anticodon, attaching to, mRNA / codon;
6 prevents / inhibits enzyme responsible for, formation of peptide linkages;
7 AVP; e.g. further detail of any of the above points 2 max

[13]

7. (a) (i) mRNA leaves nucleus; *ora*
mRNA, translated / used to make, protein;
DNA, transcribed / used to make, mRNA;
mRNA short-term / DNA (long-term) store; 2 max
- (ii) siRNA smaller / fewer nucleotides / only matches part of gene; *ora*
siRNA double-stranded; *ora* 2

- (b) (complementary) base-pairing;
hydrogen bonding;
between purines and pyrimidines;
A with U; **R** A with T
C with G;
ref to 2 or 3 bonds (correct context); 3 max [7]
8. (i) (*CCR5 / macrophages*)
(siRNAs continue to work) in long-lived cells;
only one treatment needed for macrophages / *CCR5*;
(siRNAs diluted) as lymphocytes divide; *ora*
repeat treatments needed for, lymphocytes / *CD4*; 2
- (ii) (*CCR5*)
because no essential function in body / absence not a problem; 1 [3]
9. (a) (i) steep increase, for the first 1 - 2 hours / till 2.2 - 3.8 (a.u) ; **A** linear,
steady became constant at, 3 hours / 4.3 (a.u) ;
if no figs in description, e.g. 'rose then constant' award 1 mark max 2
- (ii) (increased as) enzyme working / rate of reaction high / reaction
proceeding ;
(increased as) substrate converted into, drug / product ;
(levelled off / became constant, after the) enzyme, became inactive /
was denatured;
(levelled off / became constant) because product inhibits, reaction /
enzyme ;
R references to enzyme or substrate being used up **R** T °C limiting 2
- (b) pH ;
degree of mixing ;
enzyme concentration ;
AVP ; e.g. ref to concentration of inhibitors 1 max

- (c) *max of 2 marks for predicting or explaining*
- P1** concentration of drug higher / AW ;
P2 rate of reaction slower / AW ;
P3 may not level off (in time scale shown on graph) ;
P4 time taken to reach the maximum yield (approximately) doubles ; (c.f. 15 °C)
- E1** not denatured ;
E2 adapted to 5 °C / optimum / body / usual, temperature ;
E3 ref to Q_{10} of about 2 ;
E4 ref to lower kinetic energy / AW ;
E5 ref to E-S, collisions / complexes ;
- AVP ; e.g. ref to active site 3 max
- (d) (i) (shaded amino acids) form the active site ;
 substrate may not attach to the active site ;
 enzyme-substrate complex may not be formed / AW ; 1 max
- (ii) 44 and 66 not part of active site ;
 hold, active site / 3° structure / 3D structure, in shape ; **A** stop denaturing
 hydrogen bonds weak ;
 easily broken by, vibration / heat ; **A** pH
 disulphide bridge strong ;
 not broken by heat ; 2 max
- (e) nucleotide / base/ DNA, sequence codes for, protein / amino acid, sequence ;
 changes DNA ; **A** change triplet
 makes different mRNA ; **A** change codon
 transcription ;
 different tRNAs line up ; **A** change anticodon
 translation ;
 different (amino acid sequence in), enzyme / protein / polypeptide ; 2 max
- 10.** (a) estimate of role of genotype in phenotypic variation / AW ;
 heritability = V_G / V_P ;
 when heritability high much of variation is, genetic / not environmental
 / ora ;
 high heritability will result in successful selective breeding / ora ; 2 max

[13]

- (b) single / major / Mendelian, gene ;
 large effect ;
 little environmental effect ;
 dominant allele T expressed in homo- and heterozygote ;
 not polygenic ;
 not additive ;
 discontinuous variation / not continuous variation ;
 qualitative / not quantitative ; 2 max
- (c) (i) triplet of bases that does not code for an amino acid ;
 ATT / ATC / ACT ;
 code to mark end of gene ;
 code to stop transcription / ref to disengagement RNA polymerase ; 2 max
- (ii) transcription halted early / AW ;
 protein will, be smaller / have fewer amino acids ;
 tertiary structure / 3D shape different ;
 binding / affinity, different ;
 protein inactive ; 3 max
 ref to *lac* operon ;
- (iii) ref to, promoter / operator / 'on' switch ;
 allele T is regulator ;
 (protein) binds to DNA ;
 (protein) binds to repressor and prevents it binding to DNA ;
 allows RNA polymerase to bind ;
 AVP ; e.g. enzyme affecting transcription 2 max
- (d) (i) tt + T / AW, increases number of tillers per plant ;
 and number of branches per tiller ;
 ref to comparative figures ; 2 max
- (ii) inserted into genome randomly / cannot choose where it is inserted ;
 may be within a frequently expressed gene ;
 may be after an 'on' switch ;
 lacks normal controls ;
 AVP ; e.g. no other alleles affecting it
 different promoter 2 max

11. plant signal used by earworms ;
J switches on gene coding for **E** ;
 can then break down insecticide ;
 effect on transcription ; (× 5.5)
 reduces mortality ;
 even in absence of insecticide ;
 in absence of **J**, mortality, high / c. 87% ;
 ref to comparative figures ;
 e.g. 87 to 48% / almost halved, in presence of insecticide
 16 to 7% / more than halved, in absence of insecticide
 slight expression of **E** in absence of **J** caused by insecticide ;

4 max

[4]

12. (a) *plasmid DNA* *protein*
- | | |
|--|--|
| nucleotides / sugar + phosphate + base ; | amino acids ; |
| 4 different subunits ; | 20 different subunits ; |
| phosphodiester bonds ; A phosphoester | peptide bonds / polypeptide ; |
| contains P ; | contains S / disulphide bonds ; |
| double-stranded / double helix ; | may have 4° structure ; |
| circular ; | ref to, 2° / 3°, structure / AW ; |
| AVP ; e.g. role of H bonds | 3 max |

- (b) (i) stimulates, immune response / production of antibodies / T or B cells ; 1
- (ii) stimulate, cell-mediated immunity / T cells ;
 antigen, remains in body longer / continuously produced ;
 antigens in blood only stimulate, humoral immune system / B cells ;
 antigens (in blood) lost in urine / broken down in liver ;
 ref to MHC ; 1 max

- (c) (i) binds RNA polymerase ;
 allows, transcription / production of mRNA ;
 switches gene on / allows gene expression ; 2 max

- (ii) (protect against) more than one, strain / disease / pathogen / AW ;
 stronger immune response ;
 less likely mutant form will escape immune response / AW ;
 AVP ; cheaper / reduces number of vaccinations 2 max

- (iii) Golgi modifies protein / polypeptide / AW ;
 forms glycoproteins / add sugars *or* carbohydrate ;
 Golgi forms vesicles ;
 incorporated into cell membrane ; **R** exocytosis
 AVP ; 2 max

(d) *cells that take up DNA vaccine might*

- 1 function less well ;
- 2 be killed by immune system / trigger auto-immune response ;
- 3 have genes disrupted / mutation ;
- 4 new gene might be inherited / AW ;
- 5 plasmid could enter bacteria ;
- 6 superbug / create new disease / AW ;
- 7 effects unknown / new technology / no human trials ;
- 8 AVP ; ref ethics, ref irreversible

3 max

[14]

13. (a) (i) **AaBB** white;
aaBB black;
Aabb white;
aabb brown;

4

(ii) (dominant) epistasis;

1

- (iii) codes for inhibitor;
protein;
blocks transcription (of allele coding for pigment);
ref to, regulator / promoter;
blocks enzyme (producing pigment);
AVP; e.g. detail

max 3

(b) (i) $AaBb \times AaBb / AaBb \times Aabb$;

both must have A because they are white;

* both must, have a / not be homozygous AA, because some kittens coloured;

* both must have b to give brown kittens;

- '*must be heterozygous at both loci*' = 1 only

at least one / one or both, must have B to give black kittens;

credit ref to Punnett square showing genotypes;

credit ref to Punnett square showing phenotypes;

max 5

(ii) $AaBb \times AaBb$ 12 white : 3 black : 1 brown;;

$AaBb \times Aabb$ 6 white : 1 black : 1 brown;;

max 2

[15]

14. (i) RNA(i) combines with mRNA;
e.g. of base pairing (but not T) A-U / G-C;
stops translation;
ref to stops mRNA combining with ribosomes;
stops protein synthesis; max 3
- (ii) chemicals / enzymes in, mouth / toothpaste / bacteria;
denature / degrade, RNA;
RNA not normally taken up by bacterial cells;
short life of RNA;
RNA not replicated in bacteria when bacteria reproduce;
toothpaste in mouth only for short time;
AVP;
AVP; e.g. washed away by saliva max 2
- [5]
15. 1 ref to operon;
2 normally repressor substance bound to operator;
3 prevents RNA polymerase binding (at promoter) / prevents transcription;
4 lactose binds to repressor;
5 changes shape of protein molecule;
6 unable to bind (to operator);
7 RNA polymerase binds (at promoter) / transcription occurs
/ genes switched on;
8 production of lactose permease;
9 production of beta – galactosidase;
- [5]
16. 1 proteins needed for repair / AW;
2 more transcription of, DNA / genes;
3 more translation;
4 protein synthesis;
5 named protein; e.g. actin / myosin / troponin / tropomyosin
ignore all refs to muscle contraction
6 more aerobic respiration;
7 so more, energy released / ATP produced;
8 (energy required for) condensation / anabolic, reactions;
9 (energy required for) formation of peptide bonds;
10 (energy required for) formation of extra mRNA; max 5
- [5]

17. (a) provides sites for binding;
 ref to, spindle fibres / microtubules;
 ref to genes being spaced out along chromosome;
 places to break and rejoin (during meiotic division); **A** chiasmata formation
 'junk' implies no, function / purpose; *ora*
 function may not yet have been discovered;
 AVP; e.g. raw material for, evolution / natural selection,
 required for, cell division / mitosis / meiosis max 2

(b) straight line sloping up from left to right; (does not need to start at origin) 1

(c) ATP / NAD / NADP / RNA / phospholipid / GP / TP / RuBP / ADP /
 RUP / AMP / cAMP/ phosphocreatine / AVP; **R** DNA 1

[4]

18. DNA codes for, protein / polypeptide;
 transcription and translation (or described);
 enzyme is globular (protein);
 3 bases \equiv 1 amino acid;
 sequence of bases / triplets, determines, sequence of amino acids /
 primary structure;
 coiling / α helix / β -pleated sheet / particular secondary structure;
 determines projecting side groups;
 folding / bonding, for tertiary structure;
 3-D structure is tertiary structure;
 AVP; e.g. ref. active site related to shape
 2 or more genes produce quaternary structure 4 max

[4]