# Mark schemes

(a) (i) Does not code for amino acid/tRNA/rRNA;

1

\_ \_ \_ \_ ,

Accept 'does not code for production of protein/polypeptide' Reject 'that produces/makes amino acid'

- Deletion mutation; Accept 'deletion' Ignore references to splicing
- (b) (The) polymerase chain reaction; Accept PCR

1

1

1

- (c) 1. Probes are single stranded / have a specific base sequence;
  - 2. Complementary base sequence on (specific) spacer

## OR

(ii)

- 3. Complementary/specific to (particular) spacer;
- 4. (In white squares probe) binds (to single-stranded spacer) and glows/produces light/fluoresce;
  - 2. Need idea of complementary to spacer
  - 3. Accept converse for dark squares

3

- (d) 1. To see if strain is resistant to any antibiotics;
  - 2. So can prescribe effective/right antibiotic;

## OR

- 3. To see whether (any) vaccine works against this strain/ seewhich vaccine to use/ to produce specific vaccine;
- 4. (So) can vaccinate potential contacts/to stop spread;

## OR

- 5. Can test other people to see if they have the same strain/ totrace where people caught TB;
- 6. Allowing control of spread of disease/vaccinate/treat contacts (of people with same strain) before they get TB;

Do not allow mix and match of points from different alternative pairs

2 max

(a) 1. Cut (DNA) at same (base) sequence / (recognition) sequence;

Accept: cut DNA at same place

- (So) get (fragments with gene) R / required gene.
   Accept: 'allele' for 'gene' / same gene
- (b) 1. Each has / they have a specific base sequence;
  2. That is complementary (to allele r or R). Accept description of 'complementary'

2

2

 (c) 1. Fragments L from parent rr, because all longer fragments / 195 base pair fragments;

> Ignore: references to fragments that move further / less, <u>require</u> identification of longer / shorter or 195 / 135 Accept: (homozygous) recessive

2. Fragments N from parent RR, because all shorter fragments / 135 base pairfragments;

1 and 2 Accept: A3 for 195 and A4 for 135

- 2. Accept: (homozygous) dominant
- 3. (M from) offspring heterozygous / Rr / have both 195 and 135 base pairfragments.
   Accept: have both bands / strips Reject: primer longer / shorter

3

2

2

- (d) 1. (Cells in mitosis) chromosomes visible;
  2. (So) can see which chromosome DNA probe attached to.
- (e) (i) 1. For comparison with resistant flies / other (two) experiments / groups;
   Ignore: compare results / data / no other factors
  - To see death rate (in non-resistant) / to see effect of insecticide in non-resistant / normal flies. Accept: 'pesticide' as 'insecticide' Accept to see that insecticide worked / to see effect of enzyme
  - (ii) (PM must be involved because)
    - 1. Few resistant flies die (without inhibitor);
    - 2. More inhibited flies die than resistant flies;
    - 3. (PM) inhibited flies die faster (than resistant flies);
    - (Other factors must be involved because)
    - 4. Some resistant flies die;
    - 5. But (with inhibitor) still have greater resistance / die slower thannon-resistant flies.

2

[15] (a) Reverse transcriptase;

3			1										
	(b)	1. Probe (base sequence) complementary (to DNA of allele A / where A is (and) binds by forming base pairs / hydrogen bonds; <i>Accept gene A</i>											
		<ol> <li>So (only) this DNA labelled / has green dye / gives out (green) light;</li> <li>Accept glows for green light</li> </ol>											
	(c)	(i) 1. More probe binding / more cDNA / mRNA / more allele / gene A meansmore light;											
			2. DNA (with <b>A</b> ) doubles each (PCR) cycle;										
			<ol> <li>So light (approximately) doubles / curve steepens more and more (eachcycle) / curve goes up exponentially / increases even faster;</li> <li>3</li> </ol>										
		(ii)	( <b>G</b> because)										
			<ol> <li>(Heterozygous) only has half the amount of probe for A attaching / only half the amount of DNA / allele A (to bind to); Accept only one A to bind to</li> </ol>										
			<ol> <li>(So,) only produced (about) half the light / glow / intensity (of H) (per cycle of PCR);</li> <li>If reference to 'half' for point 1, allow 'less light' in 2.</li> </ol>										
4			[8] (a) (i) 1. Negative correl	ation;									
			Accept: description for 'negative correlation' Neutral: 'correlation' Reject: positive correlation										
			2. Wide range;										
			3. Overlap;										
			<ul> <li>4. (Graph suggests that) other factors may be involved (in age of onset);</li> <li>2 / 3 Accept the use of figures from the graph</li> <li>2 / 3 Can refer to age of onset or number of CAG repeats</li> <li>Ignore references to methodology</li> <li>3 max</li> </ul>										

		(ii)	1.	Age of onset can be high / symptoms appear later in life; Accept: 'gene' for 'allele'	
			2.	(So) individuals have already had children / allele has been passed on;	
			OR		
			3.	Individuals have passed on the allele / already had children;	
			4.	Before symptoms occur; 2 n	nax
	(b)	(i)	1.	Person <b>K</b> ;	
			2.	(As has) high(est) band / band that travelled a short(est) distance / (er) so_has large(st) fragment / number of CAG repeats; <i>Must correctly link</i> distance moved and fragment size	2
		(;;;)	Dun	fragments of known longth / CAC repeats (at the same time):	
		(11)	Run	Accept: references to a DNA ladder / DNA markers	
				Do not accept DNA sequencing	
					1
		(iii)	Hom	ozygous / (CAG) fragments are the same length / size / mass;	
				Accept: small fragment has run off gel / travelled further	1
					-
	] (a)	1.	Car	riers are heterozygous / have one normal copy and one mutant copy of gene /	
5 ha	ave or	ne rec	essive	allele / don't have the condition;	
		2.	Both h carrie	nave DNA that binds (about) half / 50% amount of probe (that non- rdoes);	
		3.	Probe one co	binds to dominant / healthy allele so only one copy of exon in their DNA /have opy of gene without exon / base sequence for probe to bind to;	
				3. Accept normal and gene	
				3. Accept have <u>a</u> deletion mutation	3
	(b)	1. code	Intro e for a	ns not translated / not in mRNA / (exons) code for amino acids / introns donot mino acids;	
				1. Accept not expressed	
			1.	Accept polypeptide / protein for amino acids	
			2.	Mutations of these (exons) affect amino acid sequences (that produce) faultyprotein / change tertiary structure of protein;	
				2. Accept deletion leads to frameshift	
			2.	In this context, accept affects protein made	

[9

*3.* So important to know if parents' exons affected, rather than any other part of

DNA / introns;

Accept converse arguments involving - eg introns do not code for amino acids / proteins Reject references to making amino acids, once

- (c) 1. Restriction mapping / described;
  - 2. DNA / base sequencing (of fragments) / description / name of method;

[8] (a) 1. Closer the (amino acid) sequence the closer the relationship;

3

2

2

[4]

# 6

- (Protein structure) related to (DNA) base / triplet sequence;
   Amino acid sequence is related to (DNA) base / triplet sequence = two marks;
- (b) 1. Reference to base triplets / triplet code / more bases than amino acids / longer base sequence than amino acid sequence;

Different (base) triplets code for same amino acids = 2 marks; Degeneracy of triplet code = 2 marks

2. Introns / non-coding DNA / degeneracy of code / more than one code for each amino acid;

Ignore reference to codon.

## Essay Using DNA in science and technology

7
---

# **DNA and classification**

- 2.2 Structure of DNA
- 2.3 Differences in DNA lead to genetic diversity
- 2.9 Comparison of DNA base sequences

# Genetic engineering and making useful substances

2.5 Plasmids

5.8 The use of recombinant DNA to produce transformed organisms that benefit humans

# Other uses of DNA

2.5 Cell cycle and treatment of cancer

5.8	Gene	the	rapy;
-----	------	-----	-------

Medical diagnosis and the treatment of human disease;

The use of DNA probes to screen patients for clinically important genes.

To cut the DNA; (a) (i)

8			Reject breakdown, cutting out	
		(ii)	To separate the (pieces of) DNA;	1
	(b)	Con Labe	nplimentary base sequence / complementary DNA; binds to both (haplotypes); el would show up in both; Idea of complimentarity required	-
	(c)	(i)	Y chromosome inherited / comes from male parents / only found in males;	2
		(ii)	Mitochondria in egg / female gamete / no mitochondria come from sperm / malegamete;	1
	(d)	(i)	Allows comparison; Different (sized) areas covered;	2
		(ii)	Wolves do not eat all of prey animal / do not eat (large) bones / skin; Inedible parts make up different proportions / wolf eats different proportions;	2
	(e)	Lim Larg	ited by food / prey; as prey increases so do wolf numbers / positive correlation; e range so other factors involved;	2
9	(a)	Rest	triction (enzyme / endonuclease);	1
	(b)	Mov	e towards anode / move because charged;	

Different rates of movement related to charge / size;

(c) (i) Piece of DNA; 2

[12]

			Single stranded; Complementary to / binds to known base sequence / gene;	max 2	
		(ii)	DNA invisible on gel / membrane; Allows detection;	2	
			[7] (a) Mother and father both heterozygotes /	Tt / carri	ers;
10		Prob Prob	bability of thalassaemia 1/4 and female 1/2; bability of both 1/8;		
				3	
	(b)	(i)	Cut at same base sequence as same enzyme used; Fragments are same length / size / have same charge;	2	
		(ii)	Single base occurs many times; Sequence of 20 unlikely to occur elsewhere; Allow one mark for establishing the principle where neither marking point clearly made.		
			[7] (a) Endonuclease / restricti	2 on enzy	me;
11				1	
	(b)	DNA Each along	A made of base pairs; h base pair is same length / occupies same distance g backbone;	2	
	(c)	(i)	Second blank box from left labelled 6;	2	
		(ii)	Distance moved depends on length / number of base pairs / second longest fragment / second shortest distance identified;	1	
	(d)	5;		1	[0]
12	(a)	(i)	Different genes / characteristics / features;		[6]
			Reference to mutations; Or Base sequence determines protein; Different species have different protein sequences;	max 2	

		(ii)	Primer has different DNA sequence; DNA specific / complementary base-pairing;	2
		(iii)	Electrophoresis separates DNA; (So they can be) identified by position on gel; Smaller / shortest fragments travel furthest / quicker / or reverse argument;	3
	(b)	( <i>con</i> Each	<i>ventional</i> ) Many lengths / all DNA / ( <i>new</i> ) one length; n rung is DNA of one / specific length;	2
	(c)	1 He 2 Bre 3 Add 4 Add 5 Cod 6 (to 7 <u>DN</u> 8 Rol	eat DNA; eaks hydrogen bonds / separates strands; d primers; d nucleotides; ol; allow) binding of nucleotides / primers; <u>IA</u> polymerase; le of (DNA) polymerase;9 Repeat cycle many times;	
			[15] (a) 1 (DNA altered by	max 6
13		2 (m 3 of 4 of 5 ch 6 (tu 8 un 9 ma	nutation) changes base sequence; gene controlling cell growth / oncogene / that monitors cell division; tumour suppressor gene; ange protein structure / non-functional protein / protein not formed; mour suppressor genes) produce proteins that inhibit cell division;7 mitosis; controlled / rapid / abnormal (cell division); alignant tumour;	max 6
	(b)	canc	er cells die / break open;releasing DNA;	2
	(c)	norm sequ DNA	nal DNA and changed DNA have different iences; only binds to complementary sequence;	2
	(d)	fewe tumo locat	er abnormal / cancerous cells / smaller ours;less cell damage / less spread / fewer tions to treat;	2
	(e)	mRN struc / tum	IA base sequence has changed;gene / DNA cture is different / has mutated; cancer gene active nour suppressor gene inactive;	3

		DNA	from	two sp	ecies	/ 2 <u>typ</u>	<u>bes</u> of c	organisi	ms;							1	
	(ii)	carri	es ger	ne / DN	IA (into	o the o	other o	rganisr	n / gen	e carri	er);					1	
	(iii)	expo survi OR i marl e.g.	se cel ve; dentify ker pro radioa	ls to th / by ac bbe; de ctivity	ne fung Iding n escripti / fluore	gus;no narke ion of escen	n-resis r gene , positivo ce / coi	stant or / gene e result mplemo	nes die probe t entary	, resist / (quali <u>base</u> p	ified	ones ) ng;	3			2	
(b)	EITH OR 2 usi 3 cut 4 wit 5 ref 6 use 7 ret 8 use	HER ing DN t plasn h (san stick e (DN urn pla e of C	1 cu 2 us 1 use 2 an 1 ma IA pol nid op ne) re y ends A) liga asmid a <sup>2+</sup> / c	t desir ng res mRN d use r ke artii ymeras en; striction s / unpa se to ju to (bao alcium	ed ger trictior A from reverse ficial D se; n endo aired b oin / re cterial) salts /	ne (fro n endo n oat v e trans DNA w DNA w DNA w DNA w DNA w DNA w DNA w DNA w	m DNA onuclea which w scriptas ith corr ase / re attache tion; ; ric sho	A) of oa ase / re vill code se to fo rect sec estrictio ed; ck;	at plant strictio e for re orm des quence on enzy	; n enzy sistand sired D of bas yme; (if re 0] (a)	rme; ce; NA; ses; f. to pro	ʻinsu obe v	ulin' a will a	allow 5 ttach (	i max.) to mut	) max 6 tant al	lele);
	attac comj film / prese	ches to pleme / X-ray ent);	o <u>one</u> ntary / by a	DNA st base <u>p</u> autorac	trand; <u>airing;</u> diograp	as a r radio ohy (if	esult of activity mutan	f ⁄ detect t allele	ed on							4	
(b)	<u>for g</u> ene is only active in man obtain product / product produ offspring;						y cells in large	/ only a amou	affects nts / ge	milk / o ene pa	easy ssec	/ to d to				1	
	<u>agaii</u> explo shee	<u>nst</u> lor oitatio ep tiss	ig tern n e.g. ues / g	n effec use of genes;	ts not embry	knowr yos / e	n / qual effect of	lified re f inserte	ferenc ed gen	e to an e on o	nima ther	I					
												[6]	(a)	Corre	ect ans	1 swer:	1.25;

14

15

Ignore working

**OR** (if wrong answer) measurement in µm measurement in mm 40000 40 = 1 mark125 but wrong order of magnitude = 1 mark C has myosin / thick (and actin / thin) filaments; 2 (ii) OR A has only actin / thin (/ no myosin / no thick) filaments; When contracted:

Thick & thin filaments/myosin & actin overlap more;

Interaction between myosin heads & actin / cross-links form;

Movement of myosin head;

Thin filaments / actin moved along thick filaments / myosin;

Movement of thin filaments / actin pulls Z-lines closer together;

Displacement of tropomyosin to allow interaction;

2+ Role of Ca;

Role of ATP;

Allow ref. to 'sliding filament mechanism' / described if no other marks awarded

4 max

1 max

(C) 8 has DMD but 3 and 4 do not / 12 has DMD but 6 and 7 (i) do not / neither parent has the condition but their child has;

Allow parents 3 and 4 give 8, parents 6 and 7 give 12

1

(ii) 4 **AND** 7;

> Parental genotypes:  $6 = \mathbf{X}^{D}\mathbf{Y}$  AND  $7 = \mathbf{X}^{D}\mathbf{X}^{d}$ 1 (iii)

AND

Gametes correct for candidate's P genotypes - e.g.

16

(b)

 $\mathbf{X}^{D}$  and  $\mathbf{Y} + \mathbf{X}^{D}$  and  $\mathbf{X}^{d}$ ;

Offspring genotypes correctly derived from gametes e.g.

$$\mathbf{X}^{\mathsf{D}}\mathbf{X}^{\mathsf{D}} + \mathbf{X}^{\mathsf{D}}\mathbf{X}^{\mathsf{d}} + \mathbf{X}^{\mathsf{D}}\mathbf{Y} + \mathbf{X}^{\mathsf{d}}\mathbf{Y};$$

Male offspring with MD correctly identified:  $X^{d}Y$ ;

Probability = 0.25 / correct for candidates offsprings genotypes; Accept <sup>1</sup>/<sub>4</sub> / 1 in 4 / 1:3 / 25% NOT '3:1' / '1:4'

4

1

2

3

1

1

(d) (i) No gene fragment G;

(ii) Only one copy of gene fragment **F**;

Male has only one X-chromosome / is XY (c.f. female has two / is XX);

#### (iii) 10 has only one copy of gene fragment G;

10 has only one normal X-chromosome / has one abnormal / d D d has only one normal allele / has one X / is X X / is heterozygous;

11 has two normal X-chromosomes / has 2 normal alleles / <sup>D D</sup>
<sup>d</sup>
is X X / has not got X / has 2 copies of (F and) G;

# (e) (i) To prevent rejection / prevent antibody production vs. injected cells / injected cells have (foreign) antigen (on surface);

- Shows effect of <u>cells</u> / not just effect of injection / not just effect of salt solution;
- (iii) Only one person tested so far need more to see if similar results /need more to see if reliable;

Need to assess if new (dystrophin positive) muscle fibres are functional / if muscle becomes functional;

Can't tell how widespread effect is in the muscle / sample taken near injection site;

Need to test for harmful side effects;

Need to test if successful for other mutations of dystrophin gene;

Need to assess permanence / longevity of result/insufficient time allowed in investigation;

(In this patient) only small response / %;

Further sensible suggestion;

4 max

[25] (a) Cocaine (binding) changes shape of transporter/prevents dopamine binding;

# 17

#### Reject references to active site

	Transporter cannot move (bound) dopamine (through membrane / protein / into cell);									
	Dopa	amine remains / builds up in synapses (leading to feelings of pleasure);	3							
(b)	(i)	Polymerase chain reaction / PCR;	1							
	(ii)	Single-stranded DNA;								
		Reject reference to a single strand of DNA								
		Bases / sequence complementary to DNA / gene to be identified;								
		(Radioactively / fluorescent) labelled so that it can be detected;	2 max							
(c)	Muta	ation changes base sequence of gene / DNA;								
		Accept references to active site								
	(Thus) changing amino acid sequence; Changes tertiary structure / shape of protein/transporter; Cocaine binding site changes/cocaine cannot bind; Dopamine can still bind (and be transported);									

3 max

[9]